

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 16:55:38 ; Search time 17269 Seconds
(without alignments)
11501.574 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaagaattgtgtg.....ttctcgagcagtgactgc 3106

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : GenBank:*

1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3106	100.0	3106	5	HUMKGFRA	M80634 Human kerat
2	3013.2	97.0	4574	2	CS115082	CS115082 Sequence
3	3013.2	97.0	4574	2	CS173036	CS173036 Sequence
4	3013.2	97.0	4574	2	DD187137	DD187137 Novel tar
5	2904.2	93.5	4587	2	CS115081	CS115081 Sequence
6	2904.2	93.5	4587	2	CS237527	CS237527 Sequence
7	2904.2	93.5	4587	2	DD187136	DD187136 Novel tar
8	2849.4	91.7	4575	2	CS031438	CS031438 Sequence
9	2849.4	91.7	4575	2	CS040390	CS040390 Sequence
10	2849.4	91.7	4575	2	CS115085	CS115085 Sequence
11	2806.2	90.3	3080	2	DD187140	DD187140 Novel tar
12	2806.2	90.3	3080	2	AR669941	AR669941 Sequence
13	2806.2	89.6	4268	5	HUMKGFRA	M97193 Homo sapien
14	2781.8	89.6	4268	2	AR669919	AR669919 Sequence
15	2781.8	89.6	4268	2	AX334811	AX334811 Sequence
16	2781.8	89.6	4268	2	AX334117	AX334117 Sequence
17	2781.8	89.6	4268	2	AX336422	AX336422 Sequence
18	2781.8	89.6	4268	5	HUMKSAWI	M87770 Human fibro

19	2747.4	88.5	4667	2	CS115090	CS115090 Sequence
20	2747.4	88.5	4667	2	DD187145	DD187145 Novel tar
21	2747.4	88.5	4667	2	AX587545	AX587545 Sequence
22	2728.6	87.8	2923	2	AR669936	AR669936 Sequence
23	2728.6	87.8	2923	2	AB030077	AB030077 Homo sapi
24	2723.4	87.7	2826	5	AR669937	AR669937 Sequence
25	2723.4	87.7	2826	5	AB030078	AB030078 Homo sapi
26	2723.4	87.7	3071	5	AB030075	AB030075 Homo sapi
27	2722	87.6	2868	5	AR669935	AR669935 Sequence
28	2722	87.6	2868	5	AB030076	AB030076 Homo sapi
29	2722	87.6	2876	5	AB030074	AB030074 Homo sapi
30	2722	87.6	2941	5	AR669934	AR669934 Sequence
31	2722	87.6	2941	5	AB030073	AB030073 Homo sapi
32	2714.2	87.4	3415	5	HSRGPFRB	X52832 Human bek m
33	2714.2	86.1	4142	2	CQ728285	CQ728285 Sequence
34	2674.4	85.0	3219	2	CS115087	CS115087 Sequence
35	2639.6	85.0	3219	2	CS115087	CS115087 Sequence
36	2639.6	85.0	3219	2	DD187142	DD187142 Novel tar
37	2556.8	82.3	3248	5	HSRGPFR2MR	Z71929 H.sapiens P
38	2556.8	82.3	3248	5	HSRGPFR2UA	Z69640 H.sapiens f
39	2556.8	82.3	3248	5	HSRGPFR2UB	Z69640 H.sapiens f
40	2506	80.7	3216	2	CS115086	CS115086 Sequence
41	2506	80.7	3216	2	DD187141	DD187141 Novel tar
42	2475	79.7	4310	2	CS115088	CS115088 Sequence
43	2475	79.7	4310	2	DD187143	DD187143 Novel tar
44	2404.4	77.4	4222	2	CS115092	CS115092 Sequence
45	2404.4	77.4	4222	2	DD187147	DD187147 Novel tar

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
HUMKGFRA	HUMKGFRA	Human keratinocyte growth factor receptor mRNA, complete cds.	M80634	M80634.1	GI:186740	keratinocyte growth factor receptor.	Homo sapiens (human)	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CS115090	CS115090	Sequence	CS115090	CS115090	CS115090	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
DD187145	DD187145	Novel tar	DD187145	DD187145	DD187145	Novel tar	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AX587545	AX587545	Sequence	AX587545	AX587545	AX587545	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AR669936	AR669936	Sequence	AR669936	AR669936	AR669936	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030077	AB030077	Homo sapi	AB030077	AB030077	AB030077	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AR669937	AR669937	Sequence	AR669937	AR669937	AR669937	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030078	AB030078	Homo sapi	AB030078	AB030078	AB030078	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030075	AB030075	Homo sapi	AB030075	AB030075	AB030075	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AR669935	AR669935	Sequence	AR669935	AR669935	AR669935	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030076	AB030076	Homo sapi	AB030076	AB030076	AB030076	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030074	AB030074	Homo sapi	AB030074	AB030074	AB030074	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AR669934	AR669934	Sequence	AR669934	AR669934	AR669934	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
AB030073	AB030073	Homo sapi	AB030073	AB030073	AB030073	Homo sapi	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
X52832	X52832	Human bek m	X52832	X52832	X52832	Human bek m	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CQ728285	CQ728285	Sequence	CQ728285	CQ728285	CQ728285	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CS115087	CS115087	Sequence	CS115087	CS115087	CS115087	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
DD187142	DD187142	Novel tar	DD187142	DD187142	DD187142	Novel tar	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
Z71929	Z71929	H.sapiens P	Z71929	Z71929	Z71929	H.sapiens P	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
Z69640	Z69640	H.sapiens f	Z69640	Z69640	Z69640	H.sapiens f	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CS115086	CS115086	Sequence	CS115086	CS115086	CS115086	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
DD187141	DD187141	Novel tar	DD187141	DD187141	DD187141	Novel tar	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CS115088	CS115088	Sequence	CS115088	CS115088	CS115088	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
DD187143	DD187143	Novel tar	DD187143	DD187143	DD187143	Novel tar	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
CS115092	CS115092	Sequence	CS115092	CS115092	CS115092	Sequence	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.
DD187147	DD187147	Novel tar	DD187147	DD187147	DD187147	Novel tar	Homo sapiens	1 (baaes 1 to 3106)	Miki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgees,W.H., Chan,A.M. and Aaronson,S.A.	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)	Gene	JOURNAL PUBLISHED	Original source text: Homo sapiens Mammary gland cDNA to mRNA.

AGEYI CKVSNYIGANOSAMLTVL PKQAPSEKEITIASPDYLIBAIIYCIYFIACM
VTYVILCKMKTNTKKPDESSOPAVHKLTIRIPLRQVTVSASSSSNNMNPVLRIT
RUSTADPEPLAGVSEYELPBDKPLTKPDLBEGFQGVVAEAGIDKDK
PEBAVTAIVKMLKDAATEKDLSDIVSEMMKMGIKHKT IMLCACTODGLYIV
VASKNTEVYIARRPGMEVSVDINRVEBQMTKFDVSCYOLABREYIASOKCI
HDLARBYLVTEBNVMKADPGLARDININDYKKTNGRLPYVMMAPEALFDVYT
HOSDWSFGLVMEI FTLAGSPYPGI PVBEFLKLBKGRMDKRPANCTHLYMRDRC
MHAIVSORPTFKQVLEDLRLITLTNBEYIDLSPLEQYSPSYEDTSSCSSGDSV
FSPDMPYRCPLOYPHINGSYKT"

ORIGIN

Query Match	100.0%;	Score 3106;	DB 5;	Length 3106;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3106;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCCGGAGCAAGTTGGTGGAGGCAACGCAAGCTGAGTCTTTCTTCTCTGTTCC	60	
Db	1	CCCGGAGCAAGTTGGTGGAGGCAACGCAAGCTGAGTCTTTCTTCTCTGTTCC	60	
QY	61	CAATCCGAGGAGCGCCGCGGCGTCATGCGCTCTCCGAGCCTGGGATAACGGTGA	120	
Db	61	CAATCCGAGGAGCGCCGCGGCGTCATGCGCTCTCCGAGCCTGGGATAACGGTGA	120	
QY	121	AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGCACTCTTCTGCGTTGSAAGTTGC	180	
Db	121	AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGCACTCTTCTGCGTTGSAAGTTGC	180	
QY	181	TCGCCGCAACCCCGGCGCTGCTGCTTCTCATCCGACCCAGCGCGGCGCGGAGCAAC	240	
Db	181	TCGCCGCAACCCCGGCGCTGCTGCTTCTCATCCGACCCAGCGCGGCGCGGAGCAAC	240	
QY	241	ACAGGTGCGGAGAGCGTTGCAATCAAGTGACTGCAAGAGCAGCGCAGCGCTGCGTT	300	
Db	241	ACAGGTGCGGAGAGCGTTGCAATCAAGTGACTGCAAGAGCAGCGCAGCGCTGCGTT	300	
QY	301	CCGAGACCCACCGCAGCTGAAGGCATTCGCGGTATGTCATCCCGTGAAGGAGTGTGA	360	
Db	301	CCGAGACCCACCGCAGCTGAAGGCATTCGCGGTATGTCATCCCGTGAAGGAGTGTGA	360	
QY	361	GATGGATTAACTGCAATGAGATATGGAAGAGCACGGGAGTTGTTACCGTAAACAT	420	
Db	361	GATGGATTAACTGCAATGAGATATGGAAGAGCACGGGAGTTGTTACCGTAAACAT	420	
QY	421	GGTCACTGGGGTCTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480	
Db	421	GGTCACTGGGGTCTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480	
QY	481	CCGCGCTCTCTTCAAGTTAGTGAATACCACTTAAGAGCCAGAGAGCCACCAACAA	540	
Db	481	CCGCGCTCTCTTCAAGTTAGTGAATACCACTTAAGAGCCAGAGAGCCACCAACAA	540	
QY	541	ATACCAAAATCTCAACCAAGATGTAAGTGTGCTGCGCAGGAGAGTCCGTAGAGGTGC	600	
Db	541	ATACCAAAATCTCAACCAAGATGTAAGTGTGCTGCGCAGGAGAGTCCGTAGAGGTGC	600	
QY	601	CTGCTGTTGAAAAGATGCGCGCGTATCACTTGAATGAAGATGGGGTGCACCTTGAGAG	660	
Db	601	CTGCTGTTGAAAAGATGCGCGCGTATCACTTGAATGAAGATGGGGTGCACCTTGAGAG	660	
QY	661	CAACAAATGAGCAGTGTCTTATTTGGGAGTACTTGCAATAAAGGCGCCACACTTAAGA	720	
Db	661	CAACAAATGAGCAGTGTCTTATTTGGGAGTACTTGCAATAAAGGCGCCACACTTAAGA	720	
QY	721	CTGCGGCTCTGATGCTGTACTGCAGTAGAAGTGTAGAGAGTGAACCTTGATCTTCAAT	780	
Db	721	CTGCGGCTCTGATGCTGTACTGCAGTAGAAGTGTAGAGAGTGAACCTTGATCTTCAAT	780	
QY	781	GATGAATGTCAAGATGCACTTCAATCCGAGATGATGAGAGTGAACCGATGGTGGGA	840	
Db	781	GATGAATGTCAAGATGCACTTCAATCCGAGATGATGAGAGTGAACCGATGGTGGGA	840	
QY	841	AGATTTTGTCACTGAGAACATTAACAAGAGGCACTATCTGAGCAACACAGAAA	900	

Db	841	AGATTTTGTCACTGAGAACATTAACAAGAGGCACTATCTGAGCAACACAGAAA	900	
QY	901	GATGAAAAAGGCTCCATGCTGTCCTGCGCCCAACCTGTCAAGTTTGGTGGCCAGC	960	
Db	901	GATGAAAAAGGCTCCATGCTGTCCTGCGCCCAACCTGTCAAGTTTGGTGGCCAGC	960	
QY	961	CGGGGGGAACCAAGCCAAACCATGCGGTGGCTGAAAAACGGGAAAGAGTTTAAAGAGA	1020	
Db	961	CGGGGGGAACCAAGCCAAACCATGCGGTGGCTGAAAAACGGGAAAGAGTTTAAAGAGA	1020	
QY	1021	GCATGCAATGAGGCTCAAGATGAGAAACAGCACTGAGACCTCATTAATGAAAAGTGT	1080	
Db	1021	GCATGCAATGAGGCTCAAGATGAGAAACAGCACTGAGACCTCATTAATGAAAAGTGT	1080	
QY	1081	GGTCCATCTGCAAGAGGAATTAATCTGTGTATGAGAGATGAATACGGGTCCATCAA	1140	
Db	1081	GGTCCATCTGCAAGAGGAATTAATCTGTGTATGAGAGATGAATACGGGTCCATCAA	1140	
QY	1141	TCACAGTACCACTGAGATGTTGAGAGGATGCGCTCACCGGCGCATCTTCAAGCCGG	1200	
Db	1141	TCACAGTACCACTGAGATGTTGAGAGGATGCGCTCACCGGCGCATCTTCAAGCCGG	1200	
QY	1201	ACTGCGGCAATGCTCCACAGTGTGAGAGAGCGTAAAGTTGTCTGCAAGGTTTA	1260	
Db	1201	ACTGCGGCAATGCTCCACAGTGTGAGAGAGCGTAAAGTTGTCTGCAAGGTTTA	1260	
QY	1261	CAGTATGCCAGCCCCACATCACTGATGATCAAGCACTGGAAGAAACGGAGTAAATA	1320	
Db	1261	CAGTATGCCAGCCCCACATCACTGATGATCAAGCACTGGAAGAAACGGAGTAAATA	1320	
QY	1321	CGGGCCGAGCGGGCTGCCCTTCAAGGTTCTCAAGCACTCGGGGATTAATAGTTCCAA	1380	
Db	1321	CGGGCCGAGCGGGCTGCCCTTCAAGGTTCTCAAGCACTCGGGGATTAATAGTTCCAA	1380	
QY	1381	TGCAGAGTCTGCTGCTTCAATGTGACCGAGGCGGATGCTGGGAAATATATATGTA	1440	
Db	1381	TGCAGAGTCTGCTGCTTCAATGTGACCGAGGCGGATGCTGGGAAATATATATGTA	1440	
QY	1441	GCTCTCAATTAATAGGCAAGCCCAACAGTCTGCTGCTCACTGCTGCTGCTGCTGCTGCT	1500	
Db	1441	GCTCTCAATTAATAGGCAAGCCCAACAGTCTGCTGCTCACTGCTGCTGCTGCTGCTGCT	1500	
QY	1501	GCAAGGCTGGAAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGATAGCCAT	1560	
Db	1501	GCAAGGCTGGAAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGATAGCCAT	1560	
QY	1561	TTACTGCATAGGGTCTTCTTAATGCTGTATGCTGTATGATCACTGCTGCTGCTGCTGCT	1620	
Db	1561	TTACTGCATAGGGTCTTCTTAATGCTGTATGCTGTATGATCACTGCTGCTGCTGCTGCT	1620	
QY	1621	GAAAGACAGACCAAGAACCCAGACTTCAAGCAAGCCGCGCTGTCACAAGCTGACAA	1680	
Db	1621	GAAAGACAGACCAAGAACCCAGACTTCAAGCAAGCCGCGCTGTCACAAGCTGACAA	1680	
QY	1681	AGTATCCCTGCGGAGCAGGTAACAGTTTCCGCTGAGTCAAGCTCTCATGATCACTC	1740	
Db	1681	AGTATCCCTGCGGAGCAGGTAACAGTTTCCGCTGAGTCAAGCTCTCATGATCACTC	1740	
QY	1741	CAACACCCGCTGTGAGATTAACAACGCTCTTCAACGCGACACCCCATGCT	1800	
Db	1741	CAACACCCGCTGTGAGATTAACAACGCTCTTCAACGCGACACCCCATGCT	1800	
QY	1801	GCGAGGGTCTCCGAGTATGAATCTTCAAGAGACCCAAATAGGAATTTTCAAGATTA	1860	
Db	1801	GCGAGGGTCTCCGAGTATGAATCTTCAAGAGACCCAAATAGGAATTTTCAAGATTA	1860	
QY	1861	GCTGACATGGGCAACCCCTGGGAGAGGTTGCTTGGCAAGTGTCAATGGCGGAAC	1920	
Db	1861	GCTGACATGGGCAACCCCTGGGAGAGGTTGCTTGGCAAGTGTCAATGGCGGAAC	1920	
QY	1921	AGTGGAAATTTGACAAAGCAAGCCCAAGAGGCGGTCACTGTCGCTGGAAGATGTTGA	1980	
Db	1921	AGTGGAAATTTGACAAAGCAAGCCCAAGAGGCGGTCACTGTCGCTGGAAGATGTTGA	1980	

QY	1981	AGATGATGCCACAGAGAAAGCCTTCTCGATCTGCGTGCAGAGATGAGATGAAGAT	2040
DB	1981	AGATGAATGCCACAGAGAAAGCCTTCTCGATCTGCGTGCAGAGATGAGATGAAGAT	2040
QY	2041	GATTGGGGAACACAGAAATATCATTAATCTTCTTGAGACCTGCACACAGATGGGCTCT	2100
DB	2041	GATTGGGGAACACAGAAATATCATTAATCTTCTTGAGACCTGCACACAGATGGGCTCT	2100
QY	2101	CTATGTCATATGTTGATGATATGCTCTTAAAGGCAACCTCCGAAATACCTCCGAGCCGAG	2160
DB	2101	CTATGTCATATGTTGATGATATGCTCTTAAAGGCAACCTCCGAAATACCTCCGAGCCGAG	2160
QY	2161	GCCACCCGGGATGAGATATCTCTTATGACATTAACCGTGTCTCTGAGAGCAGATGACCTT	2220
DB	2161	GCCACCCGGGATGAGATATCTCTTATGACATTAACCGTGTCTCTGAGAGCAGATGACCTT	2220
QY	2221	CAAGGACTTGGTGTCAATGACCTTACAGCTGGCCAGACGATGAGATATCTTGCTTCCCA	2280
DB	2221	CAAGGACTTGGTGTCAATGACCTTACAGCTGGCCAGACGATGAGATATCTTGCTTCCCA	2280
QY	2281	AAATATGATTCATGAGATTTTGAAGCCAGCAAAATGTTTTGTGTAAACAGAAAACAATGTGAT	2340
DB	2281	AAATATGATTCATGAGATTTTGAAGCCAGCAAAATGTTTTGTGTAAACAGAAAACAATGTGAT	2340
QY	2341	GAATAATGACAGACTTTGATCTGCGCAGAGATATCAACATATTAACATTAACAAAAAGAC	2400
DB	2341	GAATAATGACAGACTTTGATCTGCGCAGAGATATCAACATATTAACATTAACAAAAAGAC	2400
QY	2401	CACCAATGAGGAGCTTCCAGTCGAATGAGATGGCTCCAGAAACCGCTGTTGTATAGATATA	2460
DB	2401	CACCAATGAGGAGCTTCCAGTCGAATGAGATGGCTCCAGAAACCGCTGTTGTATAGATATA	2460
QY	2461	CACCTCATCAGAGTATGTCTGATCCTTGCGGGTGTATATGTGGAGATCTTCACTTTAGG	2520
DB	2461	CACCTCATCAGAGTATGTCTGATCCTTGCGGGTGTATATGTGGAGATCTTCACTTTAGG	2520
QY	2521	GGGCTCGCCCTACCCAGGAGATTCCTCGTGGAGAACTTTTAACTGCTGAAAGAAAGACA	2580
DB	2521	GGGCTCGCCCTACCCAGGAGATTCCTCGTGGAGAACTTTTAACTGCTGAAAGAAAGACA	2580
QY	2581	CAGAAATGATTAAGCAGGCAATCAGCAACAAAGAACTGTACATGATGATGAGGAGCTGTG	2640
DB	2581	CAGAAATGATTAAGCAGGCAATCAGCAACAAAGAACTGTACATGATGATGAGGAGCTGTG	2640
QY	2641	GCATGCAAGTGCCTCCCAAGAGACCAACGTTCAACAGAGTTGGTAAAGACTTGCATCGAAT	2700
DB	2641	GCATGCAAGTGCCTCCCAAGAGACCAACGTTCAACAGAGTTGGTAAAGACTTGCATCGAAT	2700
QY	2701	TCTCATCTCTCAACACCAATGAGAAATCTTGAACCTCAGCCAACTCTCGAACAGTATTC	2760
DB	2701	TCTCATCTCTCAACACCAATGAGAAATCTTGAACCTCAGCCAACTCTCGAACAGTATTC	2760
QY	2761	ACCTAATGTTACCTTGCACACAGAAAGTTCTTGTCTTCAAGAGATGATTTCTGTTTCTCC	2820
DB	2761	ACCTAATGTTACCTTGCACACAGAAAGTTCTTGTCTTCAAGAGATGATTTCTGTTTCTCC	2820
QY	2821	AGACCCCATGCTTACAGAACCATGCTCTCCAGATATCAACATTAACGSCAGGTAA	2880
DB	2821	AGACCCCATGCTTACAGAACCATGCTCTCCAGATATCAACATTAACGSCAGGTAA	2880
QY	2881	AACATGATATGACTGTGTCTGCTGTGCCCAACAGGACCTGAGAACTTACCTTAC	2940
DB	2881	AACATGATATGACTGTGTCTGCTGTGCCCAACAGGACCTGAGAACTTACCTTAC	2940
QY	2941	TGAGCAGGGAACCATATGCTCTCCAGAGCTTGTGTCTCAGCTGTATATATGATATCAGAG	3000
DB	2941	TGAGCAGGGAACCATATGCTCTCCAGAGCTTGTGTCTCAGCTGTATATATGATATCAGAG	3000
QY	3001	GAGTAAATATATGAAATAGTATGCAATATGTGTAAAGATTTATACGTTGAATACTTG	3060
DB	3001	GAGTAAATATATGAAATAGTATGCAATATGTGTAAAGATTTATACGTTGAATACTTG	3060

[illegible]

593 GAGTGCCTGCTGCTGTTGAAGAATGCCGCGTGATCATGTTGAAGTATGAGTGCAC 652
767 GAGGTGCGGTGCTGTGTTGAAGAATGCCGCGTGATCATGTTGAAGTATGAGTGCAC 826
653 TTGGGGCCCAACATATGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCGCA 712
827 TTGGGGCCCAACATATGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCGCA 886
713 CTTAGAGATCTCCGGGCTTATGCTTGTATCTGACAGTATGAGTATGAGTATGAGTATG 772
887 CTTAGAGATCTCCGGGCTTATGCTTGTATCTGACAGTATGAGTATGAGTATGAGTATG 946
773 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
947 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
833 GGTGCGGAAGATTTTGTCACTGAGAACATGTTACAAACAGAGACATCTTGGACCAAC 892
1007 GGTGCGGAAGATTTTGTCACTGAGAACATGTTACAAACAGAGACATCTTGGACCAAC 1066
893 AAGAAAAGATGGAAGAGGGCTCACTGCTGCTGCGGCAACACTGTCAAGTTTCCG 952
1067 AAGAAAAGATGGAAGAGGGCTCACTGCTGCTGCGGCAACACTGTCAAGTTTCCG 1126
953 TGCCAGCCGGGGGGAACCCATGCGAATCCATGCGGTGCTGAAAAACGGGAAGATTT 1012
1127 TGCCAGCCGGGGGGAACCCATGCGAATCCATGCGGTGCTGAAAAACGGGAAGATTT 1186
1013 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1072
1187 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1246
1073 GAAAGTGTGCTCCATCTGCAAGAGAAATTTATCTGTGTAGTGAATGATGATGATGAT 1132
1247 GAAAGTGTGCTCCATCTGCAAGAGAAATTTATCTGTGTGTGAGATGATGATGATGAT 1306
1133 TCCATCATATCAACGATACCACTGATGTTGTGAGAGGATCGCTCAACGGCCCATCTTC 1192
1307 TCCATCATATCAACGATACCACTGATGTTGTGAGAGGATCGCTCAACGGCCCATCTTC 1366
1193 CAAGCCGAGTCCCGGCAATGCTCTCAAGTGTGAGAGAGATCGTATGATGATGATGAT 1252
1367 CAAGCCGAGTCCCGGCAATGCTCTCAAGTGTGAGAGAGATCGTATGATGATGATGAT 1426
1253 AAGGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
1427 AAGGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
1313 AGTAAATACGGGCTCCGACGGGCTGCTTACCTCAAGGTTCTACAGCATCTCGGGATTAAT 1372
1487 AGTAAATACGGGCTCCGACGGGCTGCTTACCTCAAGGTTCTCAAGGCTCTCGGGATTAAT 1546
1373 AGTTCATATGAGAGTGTGCTGCTTGTATGATGATGATGATGATGATGATGATGATGAT 1432
1547 AGTTCATATGAGAGTGTGCTGCTTGTATGATGATGATGATGATGATGATGATGATGAT 1606
1433 ATATGTAAGGCTTCAATATATATAGGAGAGGCAACAGTCTGCTGCTCACTGCTCTG 1492
1607 ATATGTAAGGCTTCAATATATATAGGAGAGGCAACAGTCTGCTGCTCACTGCTCTG 1666
1493 CCAAAACAGCAAGCGCTGGAAGAGAAAGAGATTAACAGCTTCCCAAGATCACTGAG 1552
1667 CCAAAACAGCAAGCGCTGGAAGAGAAAGAGATTAACAGCTTCCCAAGATCACTGAG 1726
1553 ATAGCCATTTATCTGATAGAGGCTTCTTATATGCTCTGTATGATGATGATGATGATGAT 1612
1727 ATAGCCATTTATCTGATAGAGGCTTCTTATATGCTCTGTATGATGATGATGATGATGAT 1786
1613 TGCCGAATGAGAACAGCAACAGCAACAGCAACAGCTTACAGAGCCGAGCGGCTGTGCAAG 1672
1787 TGCCGAATGAGAACAGCAACAGCAACAGCAACAGCTTACAGAGCCGAGCGGCTGTGCAAG 1846

1673 CTGACCAACCGATATCCCTGCGGAGACAGGTATCAAGTTTGCGCTGAGTCCAGTCTTCC 1732
1847 CTGACCAACCGATATCCCTGCGGAGACAGGTATCAAGTTTGCGCTGAGTCCAGTCTTCC 1906
1733 ATGAATCTCAACACCCCGCTGCTGAGATTAACACAGCTTCTTCTTCAACCGCAGACAC 1792
1907 ATGAATCTCAACACCCCGCTGCTGAGATTAACACAGCTTCTTCTTCAACCGCAGACAC 1966
1793 CCGATGCTGAGCGGGCTCTCCAGATATGATCTTCCAGAGAACCCAAATATGAGATTTCA 1852
1967 CCGATGCTGAGCGGGCTCTCCAGATATGATCTTCCAGAGAACCCAAATATGAGATTTCA 2026
1853 AAGATTAAGCTGATCACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGATGATG 1912
2027 AAGATTAAGCTGATCACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGATGATG 2086
1913 GCGGAAGCAGTGGGATTTGACAAAGCAACCCCAAGAGCGGTGACCCGTGCGCTGAAG 1972
2087 GCGGAAGCAGTGGGATTTGACAAAGCAACCCCAAGAGCGGTGACCCGTGCGCTGAAG 2146
1973 ATGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2032
2147 ATGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2206
2033 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
2207 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2266
2267 GGGCTCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
2093 GGGCTCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2152
2267 GGGCTCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
2153 GCCCGAGGCGCACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2212
2327 GCCCGAGGCGCACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2386
2213 ATGACCTTCAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2272
2387 ATGACCTTCAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2446
2273 GCTTCCCAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2332
2447 GCTTCCCAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2506
2333 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2392
2507 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2566
2393 AAAAAACAGCAATGGGAGGCTTCCAGTCAAGTGAATGATGATGATGATGATGATGATGAT 2452
2567 AAAAAACAGCAATGGGAGGCTTCCAGTCAAGTGAATGATGATGATGATGATGATGATGAT 2626
2453 AGAGTATACATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2512
2627 AGAGTATACATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2686
2513 ACTTTAGGGGAGCTGCGCTTACCAAGAGATTTCCGTGAGAGAACTTTTAACTGCTGAAG 2572
2687 ACTTTAGGGGAGCTGCGCTTACCAAGAGATTTCCGTGAGAGAACTTTTAACTGCTGAAG 2746
2573 GAAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
2747 GAAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2806
2633 GACTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2692
2807 GACTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2866
2693 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2752
2867 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2926
2753 GAGTATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2812

[illegible]

	PAT	05-OCT-2005
	Linear	
DNA	4574 bp	
LOCUS	CS173036	
DEFINITION	Sequence 25 from Patent WO2005085851.	
ACCESSION	CS173036	
VERSION	CS173036.1	
KEYWORDS	GI : 77157499	
SOURCE	Homo sapiens (human)	

SOURCE ORGANISM	REFERENCE
Homo sapiens (human)	Adra, C.N.
Homo sapiens	Granulocyte subtype-selective receptors and ion channels and uses thereof
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	Patent: WO 2005/085851-A 25 15-SEP-2005;

FEATURES	Adra, Chaker N. (US)
source	Location/Qualifiers 1..4574 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:3606"
CDS	593..3061

```

/note="unnamed protein product"
/codon_start=1
/protein_id="CAJ31699.1"
/db_xref="gi:77157500"
/translation="MWSGRPICLVVYTMATLSLRPSFLVEDTTLLEPSPPTKIQ
SQPEVYAAAPGESLEVRCLKDAQAVISTKQGVHGPNNRVLIGETVIGAIPTRDS
GLVYCTASRYADSETWYFMVAWDAISGDDDEDTDGAQVSVSNNNKRAPVYTNTE
KMERLHIAVPAANTYKFCRCPAGGNMPIMETLKNKGCEKQSHRIGGVYVRNQHSLI
BSVYSDKGNTPCVAMENEGYSINHTYHLMVDYERSPHRILQAGIPANSTYGVGIVE
VCKYKSDAPHIQNIKHVEKNGSKYGGPLGYLVYKLVKQVSSINSAEVLAPNTLAA
AGETICKSYNTIGQANQSAMLTVPKQAPRBRKIRTASPRYLEAICTGVPLACM
VVATILCRMKNTIKKPKDPSQPAVHKLTKPLRQVTVASBSSNMKSNTPVLRIT
RLSTADTPMLAGVSEYELPEDPKMEFPRDLTLGKPGBCFCQGVVAEAVGLDKQ
PKBAVTAIVKMLKDAETKDLSDVSEEMKMKMGKHNKINILNGACCTODPDLVYIK
YASGKNLEAYRARBPMEYSEYDINRPEEOMTFKDLASCTYGLARAMEYLAQSCYV
HRLDAARVLVTENNVMKTIADFGRLADINNIIDYKTKTNGLSPVKMAPEALFDRVY
HQSDVMSRGVLMKELFTLIGSGPYPIGELPYBELFKLLKBHRBMDKPAKCNTELMMMDRO
WHAQVSRQETPKQLVEDDRLILTLITLITNBEYDLSQPLEQISPTSDTSSCSGDDS
FSPDPMPEPCLPQYPHINGSVKT"

```

ORIGIN					
Query Match:	97.0%	Score 3013.2;	DB 2;	Length 4574;	
Best Local Similarity:	99.5%;	Pred No. 0;			
Matches 3097; Conservative	0;	Mismatches	8;	Indels	9;
				Gaps	7.

QY	1	CCCGACGAGCAAAAGTTTGGTGGTGAAGCAACG-CAAGCCGTAGCTCTTTCTTCTCTCGTTCC	59
Db	168	CTGCGAGGCAAAAGTTTGGTGGTGAAGCAACGCAAGCCTAGTCTTTCTTCTCTCGTTCC	227
QY	60	CCAAATCCGAGGCGAGCCCGCGGGCGGTCAATG---GCGCTTCTTCGCAAGCTCGGAGTACGC	116
Db	228	CCAAATCCGA-GGGAGCCCGCGGGCGGTCAATGCGCGCTCTCTCCGACAGCTCGGAGGTACGC	286
QY	117	G-TGAAGCCCGGGAGGCTTTGGCGCCGGCCAAAGACCCAAAGGACCACTCTTCTGGGTTTGA	175
Db	287	GCTGAAGCCCGGGAGGCTTTGGCGCCGGCCAAAGACCCAAAGGACCACTCTTCTGGGTTTGA	346
QY	176	GTTGTCCTCCCGCAACCCCGGGCTCGTGGCTTTCTCCATCCCGAACCCACGCGGAGGC-CCGG	234
Db	347	GTTGTCCTCCCAACCCCGGGCTCGTGGCTTTCTCCATCCCGAACCCACGCGGAGGC	406
QY	235	GACAAACAAGGTGCGCGAGAGAGGCTTGCATTCAAGTGACTGACGACGACG-GCAGCGC	293
Db	407	GACAAACAAGGTGCGCGAGAGAGGCTTGCATTCAAGTGACTGACGAGGACGCGCAGCGC	466
QY	294	CTCGGTTCTTGAGCCCAACGCA- GCTGAAGCAATTGCGCGTAACTCATGCCCCGTAGAAGA	352
Db	467	CTCGGTTCTTGAGCCCAACGCAAGGCTAAAGGCATTGCGCGTAACTCATGCCCCGTAGAAGA	526
QY	353	AGTGTGAGAGTGGGATTTAAGTCCACAATGAGATATGGAAGAGGACCGGGGATTTGTAAC	412
Db	527	AGTGTGAGAGTGGGATTTAAGTCCACAATGAGATATGGAAGAGGACCGGGGATTTGTAAC	586
QY	413	GTAAACAATGGTCAAGCTGGGCTCGTTTCATCTGCTCGTGGTCAACATGCAACCTTG	472
Db	587	GTAAACAATGGTCAAGCTGGGCTCGTTTCATCTGCTCGTGGTCAACATGCAACCTTG	646
QY	473	TCCCTGGACCCGCGCTCTCTTCAAGTTATGTTAGAGATACCAATTAGACCAAGAAAGCCA	532
Db	647	TCCCTGGACCCGCGCTCTCTTCAAGTTATGTTAGAGATACCAATTAGACCAAGAAAGCCA	706
QY	533	CCAAACAATAACCAAACTCTTCAACAAGAGATGTAAGTGGCTGGCGCAAGGGGAGTGGCTA	592
Db	707	CCAAACAATAACCAAACTCTTCAACAAGAGATGTAAGTGGCTGGCGCAAGGGGAGTGGCTA	766
QY	593	GAGGTGGCGTGCCTGTTGAAGAATGCGCGCGTGATCAAGTTGGACTAAGATGGGGTGCAC	652
Db	767	GAGGTGGCGTGCCTGTTGAAGAATGCGCGCGTGATCAAGTTGGACTAAGATGGGGTGCAC	826
QY	653	TTGGGGCCCAACATATAGACAGTGCCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAACA	712
Db	827	TTGGGGCCCAACATATAGACAGTGCCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAACA	886
QY	713	CTTAGAGACTTCGGGCTCTATGCTTGTATCTGCCAGTAGAGACTGTAAACAATGAAACTTTGG	772
Db	887	CTTAGAGACTTCGGGCTCTATGCTTGTATCTGCCAGTAGAGACTGTAAACAATGAAACTTTGG	946
QY	773	TACTTCATGGTGAATGTCACAGATGCCATTCATCCGGAATGATGAGATGACCCGAT	832
Db	947	TACTTCATGGTGAATGTCACAGATGCCATTCATCCGGAATGATGAGATGACCCGAT	1006
QY	833	GGTGCAGAAAGTTTGTCAGTAGAAACAGTAAACAACAAGAGACCACTATCTGACCAAC	892
Db	1007	GGTGCAGAAAGTTTGTCAGTAGAAACAGTAAACAACAAGAGACCACTATCTGACCAAC	1066
QY	893	ACAGAAAAAGTGAAGAAAGCGGCTCATGCTGTGTGCTTCGGCGCAACACTGTCAAGTTTGGC	952
Db	1067	ACAGAAAAAGTGAAGAAAGCGGCTCATGCTGTGTGCTTCGGCGCAACACTGTCAAGTTTGGC	1126
QY	953	TGCCCAACCGGGGGGGAACCAATGCAACAATGCGGTGGGTGAAGAAACGGGAAGAGATT	1012
Db	1127	TGCCCAACCGGGGGGGAACCAATGCAACAATGCGGTGGGTGAAGAAACGGGAAGAGATT	1186
QY	1013	AAGCAGAGAGATCGCATTTGAGAGGCTACAGAGTACGAACCAAGCACTGAGCGCTCATTAATG	1072
Db	1187	AAGCAGAGAGATCGCATTTGAGAGGCTACAGAGTACGAACCAAGCACTGAGCGCTCATTAATG	1246
QY	1073	GAAAGTGTGCTCCATCTGACAGAGGAAATTAATCTGTGTATGAGGAATGAATACGGG	1132

Db 1247 GAAAGGTGTCCCATCTGACAAAGGAAATTATCTGTGTGTGAGATGAATACG66 1306
 1133 TCCATCATCATCAGTACCACTGAGTGTGTGAGCGATCCGCTCACCGGCCATCTTC 1192
 Db 1307 TCCATCATCATCAGTACCACTGAGTGTGTGAGCGATCCGCTCACCGGCCATCTTC 1366
 1193 CAAGCGGAGCTGCGGCAAAATGCTTCCACAGTGTGTGAGAGAGCTGAGATTGTCTGC 1252
 Db 1367 CAAGCGGAGCTGCGGCAAAATGCTTCCACAGTGTGTGAGAGAGCTGAGATTGTCTGC 1426
 1253 AAGGTTTACAGTATATCCCAAGCCCAATCCAGTGTGTGAGAGAGCTGAGATTGTCTGC 1312
 Db 1427 AAGGTTTACAGTATATCCCAAGCCCAATCCAGTGTGTGAGAGAGCTGAGATTGTCTGC 1486
 1313 AAGTAAATAGGAGGCGGCGGAGCTGCTTCAAGTGTGTGAGAGAGCTGAGATTGTCTGC 1372
 Db 1487 AAGTAAATAGGAGGCGGCGGAGCTGCTTCAAGTGTGTGAGAGAGCTGAGATTGTCTGC 1546
 1373 AGTTCCATGACAGAGTGTGTCTGTTCATATGTGACCGAGGCGGAGTGTGTGAGATTGT 1432
 Db 1547 AGTTCCATGACAGAGTGTGTCTGTTCATATGTGACCGAGGCGGAGTGTGTGAGATTGT 1606
 1433 ATATGTAAGTCTTCAATTTATAGGCGAGGCCAACAGTGTGTGTGAGATTGTCTGC 1492
 Db 1607 ATATGTAAGTCTTCAATTTATAGGCGAGGCCAACAGTGTGTGTGAGATTGTCTGC 1666
 1493 CCAAAACAGCAGCGCTGAGAGAGAAAGAGATTACAGCTTCCCAAGTACTGAGAG 1552
 Db 1667 CCAAAACAGCAGCGCTGAGAGAGAAAGAGATTACAGCTTCCCAAGTACTGAGAG 1726
 1553 ATAGCAATTACTGCAATAGGGGTCTTCTTAATGCTGTATGTGTGTGATACAGTACTCTG 1612
 Db 1727 ATAGCAATTACTGCAATAGGGGTCTTCTTAATGCTGTATGTGTGTGATACAGTACTCTG 1786
 1613 TGGCGATGAAAGACAGACCAAGAGGCGAGCTTACAGCGAGCGGCTGTGACAG 1672
 Db 1787 TGGCGATGAAAGACAGACCAAGAGGCGAGCTTACAGCGAGCGGCTGTGACAG 1846
 1673 CTGACCAACGTAATCCCTGCGGAGAGCAGTAAAGTTCGCTGAGTCCAGCTCTCTC 1732
 Db 1847 CTGACCAACGTAATCCCTGCGGAGAGCAGTAAAGTTCGCTGAGTCCAGCTCTCTC 1906
 1733 ATGAATCCAAACACCCGCTGTGTGAGAGTAACAACAGCTCTCTTCAACGAGACACC 1792
 Db 1907 ATGAATCCAAACACCCGCTGTGTGAGAGTAACAACAGCTCTCTTCAACGAGACACC 1966
 1793 CCCATGCTGCGAGGGGTCTCCAGTATGAATCTTCCAGAGAGCCCAAAATGGAGTTTCA 1852
 Db 1967 CCCATGCTGCGAGGGGTCTCCAGTATGAATCTTCCAGAGAGCCCAAAATGGAGTTTCA 2026
 1853 AGAGATTAAGCTGACACTGCGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTCTAG 1912
 Db 2027 AGAGATTAAGCTGACACTGCGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTCTAG 2086
 2087 GCGGAGCAGTGGGAAATTGACAAAGCAAGCCCAAGGAGCGGTCAACCGTGGCCGTGAG 2146
 1913 GCGGAGCAGTGGGAAATTGACAAAGCAAGCCCAAGGAGCGGTCAACCGTGGCCGTGAG 1972
 Db 2087 GCGGAGCAGTGGGAAATTGACAAAGCAAGCCCAAGGAGCGGTCAACCGTGGCCGTGAG 2146
 1973 ATGTTGAAGATGATGCGACAGAGAAAGCTTTCTGATCTGAGTGTGAGATGAGAGAG 2032
 Db 2147 ATGTTGAAGATGATGCGACAGAGAAAGCTTTCTGATCTGAGTGTGAGATGAGAGAG 2206
 2033 ATGAAGATGATGCGGAGAAACAAAGATATCATTAATCTTCTTGGAGCTGACACAGAT 2092
 Db 2207 ATGAAGATGATGCGGAGAAACAAAGATATCATTAATCTTCTTGGAGCTGACACAGAT 2266
 2093 GGGGCTCTCTATGTCATAGTTAGTATGCTTAAAGCAACCTCGGAGAAATACCTCGA 2152
 Db 2267 GGGGCTCTCTATGTCATAGTTAGTATGCTTAAAGCAACCTCGGAGAAATACCTCGA 2326
 2153 GCCCGAGGCGCACCGGAGTGAAGTACTCTCTATGACTTAAACGCTGTCTGAGAGACAG 2212

Db 2327 GCCCGAGGCGCACCGGAGTGAAGTACTCTATGACATTAACCGTGTCTGAGAGCAG 2386
 2213 ATGACCTTCAAGAGATTGGTGTGATGACCTTACCGAGCTGTGACAGCGAGTGAAGTCTG 2272
 Db 2387 ATGACCTTCAAGAGATTGGTGTGATGACCTTACCGAGCTGTGACAGCGAGTGAAGTCTG 2446
 2273 GCTTCCAAAATGATTTATCATGAGATTTAGAGCCAGAAAATGTTTGTGTAACAGAAAAC 2332
 Db 2447 GCTTCCAAAATGATTTATCATGAGATTTAGAGCCAGAAAATGTTTGTGTAACAGAAAAC 2506
 2333 AATGTGATGAAATATGACAGACTTTGAGTCTGCGAGAGATATCAACATATGACTATTAAC 2392
 Db 2507 AATGTGATGAAATATGACAGACTTTGAGTCTGCGAGAGATATCAACATATGACTATTAAC 2566
 2393 AAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGTGATGAGTCTCCAGAGGCCCTGTGAT 2452
 Db 2567 AAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGTGATGAGTCTCCAGAGGCCCTGTGAT 2626
 2453 AAGATATACATCATCAGAGTATGATGATGCTTCCGAGGAGTATATGAGGAGATCTTC 2512
 Db 2627 AAGATATACATCATCAGAGTATGATGATGCTTCCGAGGAGTATATGAGGAGATCTTC 2686
 2513 ACTTTAGGGGCTGCGCCCTTACCCAGAGATTCCTGAGAGAACTTTTAAGCTGTGAAG 2572
 Db 2687 ACTTTAGGGGCTGCGCCCTTACCCAGAGATTCCTGAGAGAACTTTTAAGCTGTGAAG 2746
 2573 GAAGGACACAGATGATATGACAGCCCACTGACACCAACGATCTGATATGATGAGG 2632
 Db 2747 GAAGGACACAGATGATATGACAGCCCACTGACACCAACGATCTGATATGATGAGG 2806
 2633 GACTGTGAGCATGAGTGTGCTTCCAGAGACCAAGTTCACAGTGTGTGAGAACTTG 2692
 Db 2807 GACTGTGAGCATGAGTGTGCTTCCAGAGACCAAGTTCACAGTGTGTGAGAACTTG 2866
 2693 GATGCAATTCGACTCTCAACCAATGAGAAATCTTGGAGCTTCAACCTCTCGAA 2752
 Db 2867 GATGCAATTCGACTCTCAACCAATGAGAAATCTTGGAGCTTCAACCTCTCGAA 2926
 2753 CAGTATTCACCTTATGTTACCTTGAACACAAAGTTCCTTTCAGAGAGATGATCTGT 2812
 Db 2927 CAGTATTCACCTTATGTTACCTTGAACACAAAGTTCCTTTCAGAGAGATGATCTGT 2986
 2813 TTTTTCAGAGACCCCAATGCTTACAGAACCATGCTCTTCAATATCAACATTAACGCG 2872
 Db 2987 TTTTTCAGAGACCCCAATGCTTACAGAACCATGCTCTTCAATATCAACATTAACGCG 3046
 2873 AGTGTAAACATGATGACTGTGTGCTGTGCTGTCCCAACAGAGCAGCACTGGAACT 2932
 Db 3047 AGTGTAAACATGATGACTGTGTGCTGTGCTGTCCCAACAGAGCAGCACTGGAACT 3106
 2933 AGCTACATGAGAGGAGAGACATGCTTCCAGAGCTTGTGTCTTCCATTTGATATAG 2992
 Db 3107 AGCTACATGAGAGGAGAGACATGCTTCCAGAGCTTGTGTCTTCCATTTGATATAG 3166
 2993 GATCAGAGAGTAAATTTGAGAAAGTATGAGATATGATGATTAAGTTTAACTGTTG 3052
 Db 3167 GATCAGAGAGTAAATTTGAGAAAGTATGAGATATGATGATTAAGTTTAACTGTTG 3226
 3053 AAAACTTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGCAGTGTGACTGC 3106
 Db 3227 AAAACTTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGCAGTGTGACTGC 3280

RESULT 4
 DD187137 4574 bp DNA linear PAT 19-JAN-2006
 LOCUS DD187137 Novel targets for obesity from subcutaneous fat.
 DEFINITION DD187137.1 GI:85643346
 ACCESSION DD187137.1
 VERSION JP 2005176846-A/27.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1673 CTGACCAACGATATCCCCCTGGAGAGACAGTTTGGGCTGAGTCCAGCTCTCC 1732
 1847 CTGACCAACGATATCCCCCTGGAGAGAGGTAACAGTTTGGGCTGAGTCCAGCTCTCC 1906
 1733 ATGAATCTCAACACCCCGCTGGTGAAGTAACAACCCCTCTCTTCAACCGCAGACACC 1792
 1907 ATGAATCTCAACACCCCGCTGGTGAAGTAACAACCCCTCTCTTCAACCGCAGACACC 1966
 1793 CCCATGCTGGAGGGGCTCTCCAGTATGAATCTTCCAGAGAACCCAAATGGGAGTTTCCA 1852
 1967 CCCATGCTGGAGGGGCTCTCCAGTATGAATCTTCCAGAGAACCCAAATGGGAGTTTCCA 2026
 1853 AGAGATTAAGCTGACA CTGGGCAAGCCCTGGAGAAAGTTGCTTTGGGCAAGTGTCTATG 1912
 2027 AGAGATTAAGCTGACA CTGGGCAAGCCCTGGAGAAAGTTGCTTTGGGCAAGTGTCTATG 2086
 1913 GGGGAAGCAGTGGGAATTTGACAACAAGCCCAAGAGGGGGTCAACCGTGGCGGTGAAG 1972
 2087 GGGGAAGCAGTGGGAATTTGACAACAAGCCCAAGAGGGGGTCAACCGTGGCGGTGAAG 2146
 1973 ATGTTGAAGATGATGCTCCAGAGAAAGACTTTCTGATCTGATCTGATCTGATCTGATG 2032
 2147 ATGTTGAAGATGATGCTCCAGAGAAAGACTTTCTGATCTGATCTGATCTGATCTGATG 2206
 2033 ATGAAGATGATGAGGAAACAAGAAATATCATTAATCTTTGGAGCTTGCACACAGAT 2092
 2207 ATGAAGATGATGAGGAAACAAGAAATATCATTAATCTTTGGAGCTTGCACACAGAT 2266
 2093 GGGGCTCTTATGTCATAGTGAATGCTCTTAAAGGGAACCTCGAGAAATACCTCCGA 2152
 2267 GGGGCTCTTATGTCATAGTGAATGCTCTTAAAGGGAACCTCGAGAAATACCTCCGA 2326
 2153 GCCCGAGGCGCACCCGGAGTGAAGTACTCTTATGACATTAAACCGTCTTCTGAGAGCAG 2212
 2327 GCCCGAGGCGCACCCGGAGTGAAGTACTCTTATGACATTAAACCGTCTTCTGAGAGCAG 2386
 2213 ATGACCTTCAAGAGCTTGGTGTCAATGCACTTACAGCTGGCCAGACGATGAGTACTTG 2272
 2387 ATGACCTTCAAGAGCTTGGTGTCAATGCACTTACAGCTGGCCAGACGATGAGTACTTG 2446
 2273 GCTTCCCAAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAACAGAAAC 2332
 2447 GCTTCCCAAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAACAGAAAC 2506
 2333 AATGATGATAAATATGACAGACTTGGACTGCGCAGAGATATCAACATATAGACTATTAAC 2392
 2507 AATGATGATAAATATGACAGACTTGGACTGCGCAGAGATATCAACATATAGACTATTAAC 2566
 2393 AAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAAGTGGCTCCAGAAAGCCCTGTTGAT 2452
 2567 AAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAAGTGGCTCCAGAAAGCCCTGTTGAT 2626
 2453 AGAGTATTAACCTGATCAAGATGATGCTGGTCTCGGGGTGTTAATGTTGGAGATCTTC 2512
 2627 AGAGTATTAACCTGATCAAGATGATGCTGGTCTCGGGGTGTTAATGTTGGAGATCTTC 2686
 2513 ACTTTAGGGGGCTCGCCCTTACCCAGAGGATTCGCGTGAAGAACTTTTAAAGCTGTAAG 2572
 2687 ACTTTAGGGGGCTCGCCCTTACCCAGAGGATTCGCGTGAAGAACTTTTAAAGCTGTAAG 2746
 2573 GAAGGACACAGAAATGATTAAGCCAGCTGCAACAGAACTGTAACATGATGATGAGG 2632
 2747 GAAGGACACAGAAATGATTAAGCCAGCTGCAACAGAACTGTAACATGATGATGAGG 2806
 2633 GATGTTGGAGATGAGTGGCTCCAGAGACCAACGTTCAAGAGGTTGGTGAAGAACTTG 2692
 2807 GATGTTGGAGATGAGTGGCTCCAGAGACCAACGTTCAAGAGGTTGGTGAAGAACTTG 2866
 2693 GATGAAATTTCTCACTTCAACAACCAATGAGAAATTAATTGAGCTCAGCCCAACCTCTTGAA 2752
 2867 GATGAAATTTCTCACTTCAACAACCAATGAGAAATTAATTGAGCTCAGCCCAACCTCTTGAA 2926
 2753 CAGTATTCACCTAGTAACTCTGACCAAGAAAGTTCTTGTCTTCAAGAGATGATTTCTGTT 2812

Db 2227 CAGTATTCACCTAGTAACTCTGACACAAAGAGTTCTTGTCTTCAAGAGATGATTTCTGTT 2986
 Qy 2813 TTTTCTCCAGACCCCATGCTCTTACGAACCATGCTCTTCTCAATTCACACATTAAGGCG 2872
 Db 2987 TTTTCTCCAGACCCCATGCTCTTACGAACCATGCTCTTCTCAATTCACACATTAAGGCG 3046
 Qy 2873 AGTGTAAACATGAAATGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2932
 Db 3047 AGTGTAAACATGAAATGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3106
 Qy 2933 AGTAACTGAGACAGGAGACCATGCTCCAGAGACTTGTGTCTCACTTGTATATATG 2992
 Db 3107 AGCTAACTGAGACAGGAGACCATGCTCCAGAGACTTGTGTCTCACTTGTATATATG 3166
 Qy 2993 GATCAGAGAGTAAATTAATTTGAAAAGTATCATGATATGCTGTAAGATTTATACATTTG 3052
 Db 3167 GATCAGAGAGTAAATTAATTTGAAAAGTATCATGATATGCTGTAAGATTTATACATTTG 3226
 Qy 3053 AAAACTGTATATCTTCCCAAGAGAGAAAGGTTCTGAGAGAGTGAAGTGC 3106
 Db 3227 AAAACTGTATATCTTCCCAAGAGAGAAAGGTTCTGAGAGAGTGAAGTGC 3280

RESULT 5
 CS115081
 LOCUS CS115081 4587 bp DNA linear PAT 08-JUL-2005
 DEFINITION Sequence 38 from Patent EP1548445.
 ACCESSION CS115081
 VERSION CS115081.1 GI:7063752
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1
 AUTHORS Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mirzahi, J. and Ostenson, C.G.
 TITLE Novel targets for obesity from fat tissue
 JOURNAL Patent: EP 1548445-A 38 29-JUN-2005;
 F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)
 FEATURES
 source location/Qualifiers
 1..4587
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 93.5%; Score 2904.2; DB 2; Length 4587;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;
 Qy 1 CCCGAGCAAGTTGTTGTTGAGGACG-CAAGCTGATCTTCTTCTCTGTTCC 59
 Db 168 CTGCGAGCAAGTTGTTGTTGAGGACGCAAGCTGATCTTCTTCTCTGTTCC 227
 Qy 60 CCAATCCAGGAGCCCGCGGGGTCTATG--GGCTCTCCGAGGCTGGGATAGCG 116
 Db 228 CCAATCCAGGAGCCCGCGGGGTCTATG--GGCTCTCCGAGGCTGGGATAGCG 287
 Qy 117 GTGAAGCCCGGAGAGGTTGGCCCGCGGAGAACCCCAAGACCACTTCTGCTTTGAG 176
 Db 288 GTGAAGCCCGGAGAGGTTGGCCCGCGGAGAACCCCAAGACCACTTCTGCTTTGAG 347
 Qy 177 TTGCTCCCGCAACCCCGGGCTGTGCTTCTTCAATCCCAACCGCGGGGC-CGGG 235
 Db 348 TTGCTCCCGCAACCCCGGGCTGTGCTTCTTCAATCCCAACCGCGGGGC-CGGG 407
 Qy 236 ACAACAGAGTGGCGGAGAGAGGTTGCCATTCAAGTGAATGACAGCAGC-CCAGCGCC 294
 Db 408 ACAACAGAGTGGCGGAGAGAGGTTGCCATTCAAGTGAATGACAGCAGC-CCAGCGCC 467

QY	295	TGGTTCCTGAGACCCACCGCA - GCTGAAGCATTTGCCGTGATGCTATGCTCCCTGTAGAGAA	353
-Db	468	TGGTTCCTGAGACCCACCGCAGGCTGAAGGACATTGCCGTGTGTGCATGCCCCGTGTGAAGAA	527
QY	354	GTGTGCACAATGGGAATTAAAGTCACAATGGAAATATAGGAAGGACCGGGGATTGTATCCG	413
Db	528	GTGTGCACAATGGGAATTAAAGTCACAATGGAAATATAGGAAGGACCGGGGATTGTATCCG	587
QY	414	TAAACATGGTCAAGCTGGGGTGGTTTCATCTGCCTGTGTGTGTGTCACATGCGCAACTTGT	473
Db	588	TAAACATGGTCAAGCTGGGGTGGTTTCATCTGCCTGTGTGTGTGTCACATGCGCAACTTGT	647
QY	474	CCCTGGCCCGGCCTCTTCAAGTTTATGTTAGAGATACCAATTAGAGCCAGAGAGCCAC	533
Db	648	CCCTGGCCCGGCCTCTTCAAGTTTATGTTAGAGATACCAATTAGAGCCAGAGAGCCAC	707
QY	534	CAACCAATATCCAAATCTCTCAACCAAGAAATGTACTGGCTGCCCAAGGGGAGTCCGTAG	593
Db	708	CAACCAATATCCAAATCTCTCAACCAAGAAATGTACTGGCTGCCCAAGGGGAGTCCGTAG	767
QY	594	AGGTGCGCTGCTGTGTGAAGAATGCGCGCTGATCATGTTGGACTTAAGGATGGGGTGCCT	653
Db	768	AGGTGCGCTGCTGTGTGAAGAATGCGCGCTGATCATGTTGGACTTAAGGATGGGGTGCCT	827
QY	654	TGGGGCCCAACAAATAGGACAGTGCCTTATGGGAGATCTTGCAATAAAGGCGCCACAC	713
Db	828	TGGGGCCCAACAAATAGGACAGTGCCTTATGGGAGATCTTGCAATAAAGGCGCCACAC	887
QY	714	CTAAGACTCCGGGCTCTTATGCTTTGATCTGCCATGAGACTGTAGACAGTGAACCTTGT	773
Db	888	CTAAGACTCCGGGCTCTTATGCTTTGATCTGCCATGAGACTGTAGACAGTGAACCTTGT	947
QY	774	ACTTATGCTGAATGTCAACAATGCATCTCATCCGAGATGATAGGATGACACCGATG	833
Db	948	ACTTATGCTGAATGTCAACAATGCATCTCATCCGAGATGATAGGATGACACCGATG	1007
QY	834	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAACAGAGACCAATATCTGACCAACA	893
Db	1008	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAACAGAGACCAATATCTGACCAACA	1067
QY	894	CAGAAAAGATGGAAGAGGGGCTTCATGCTGTGCTGCGGCCAACACTGTCAAGTTTCCT	953
Db	1068	CAGAAAAGATGGAAGAGGGGCTTCATGCTGTGCTGCGGCCAACACTGTCAAGTTTCCT	1127
QY	954	GCCCAAGCGGGGGGAACCAATGCCAACATGCGGTGCTGAAGAAAAGGGAAGGTTTA	1013
Db	1128	GCCCAAGCGGGGGGAACCAATGCCAACATGCGGTGCTGAAGAAAAGGGAAGGTTTA	1187
QY	1014	AGCAGAGCATGCAATTGGAGGCTTCAAGAGTACGAAACACAGACTGAGGCTCATTTATGG	1073
Db	1188	AGCAGAGCATGCAATTGGAGGCTTCAAGAGTACGAAACACAGACTGAGGCTCATTTATGG	1247
QY	1074	AAAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTATGAGAAATATACGGGT	1133
Db	1248	AAAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTATGAGAAATATACGGGT	1307
QY	1134	CCATTAATCAACAGTACCACTGTGATGTTGTGAGAGCATGCGCTCACCGGCCCATCTCC	1193
Db	1308	CCATTAATCAACAGTACCACTGTGATGTTGTGAGAGCATGCGCTCACCGGCCCATCTCC	1367
QY	1194	AAGCCGCACTGCCGCAATATGCTTCAACAGTGTGTGAGAGAGCTTAAATGTTGTCTGCA	1253
Db	1368	AAGCCGCACTGCCGCAATATGCTTCAACAGTGTGTGAGAGAGCTTAAATGTTGTCTGCA	1427
QY	1254	AGGTTTACATGATGCTCCACGCCCCATCTCACTGATGATCAAGCACTGTGAAGAAACGCGCA	1313
Db	1428	AGGTTTACATGATGCTCCACGCCCCATCTCACTGATGATCAAGCACTGTGAAGAAACGCGCA	1487
QY	1314	GTAAATATGCGGGCCGACGCGGCTGCTTACCTCAAGGTTCTCAAGCACTCCGGGATTAATA	1373
Db	1488	GTAAATATGCGGGCCGACGCGGCTGCTTACCTCAAGGTTCTCAAGGTTCTCAAGGTTTAATA	1547
QY	1374	GTTCACATGCAAGATGCTGCTGT-----TCATGTGACCGAGGCGGATGCTGGGG	1427

Db	1548	CCACGGACAAAGAGATTGAGGTTCTCTATATATGCGAATGTAACTTTTGAGAACGCTGGG	1607
Qy	1428	AATATATATGTAGAGTCTCCAAATTATATAGGGCAGGCCAACAGCTTGGCTGCTCACTG	1487
Db	1608	AATATATGCTGTTGGCGGGATATTCTATTTGGGAATATCTTTCACTGCACTGGTTGACAG	1667
Qy	1488	TCCTGCCAAAACAGCAAGCGCTGTGAAAGAAAAAGAGATTACAGCTTTCCCGACATACC	1547
Db	1668	TTCTGGCC-----AGCGCTGGAAAGAAAAAGGAATTACAGCTTTCCCGACATACC	1718
Qy	1548	TGAGATATAGCCATTACGATATAGGGGCTTTAACTCGACTGATATGGTGTAAACATCA	1607
Db	1719	TGGAGATATAGCATTACTGCAATAGGGGCTTTCTTAATGGCTGTATATGTGTAAACATCA	1778
Qy	1608	TCCTGTGCCGAATAGAAACAGAACCAAGAACCCAGACTTCAGCAGCCAGCCGGCTGTGC	1667
Db	1779	TCCTGTGCCGAATAGAAACAGAACCAAGAACCCAGACTTCAGCAGCCAGCCGGCTGTGC	1838
Qy	1668	ACAAGCTGACCAAAAGTATCCCTCTGGGAGACAGGTAAACAGTTTCGGCTGAGTCCAGCT	1898
Db	1839	ACAAGCTGACCAAAAGTATCCCTCTGGGAGACAGGTAAACAGTTTCGGCTGAGTCCAGCT	1958
Qy	1728	CCTCATGTAACTTCCAAACACCCCGCTGGTGTAGAGTAACAACAACGCTCTCTTCAACGGCAG	1787
Db	1899	CCTCATGTAACTTCCAAACACCCCGCTGGTGTAGAGTAACAACAACGCTCTCTTCAACGGCAG	1958
Qy	1788	ACACCCCATCTGTGGCAGGGGTCTCCGAGTATGTAACTTCCAGAGAACCCCAAAATGGAGT	1847
Db	1959	ACACCCCATCTGTGGCAGGGGTCTCCGAGTATGTAACTTCCAGAGAACCCCAAAATGGAGT	2018
Qy	1848	TTCCAAAGATATAGCTGAACACTGTGGCAAGCCCTCTGGAGAAAGTGTCTTTGGCAATGG	1907
Db	2019	TTCCAAAGATATAGCTGAACACTGTGGCAAGCCCTCTGGAGAAAGTGTCTTTGGCAATGG	2078
Qy	1908	TCAATGGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGGGCGGTCAACGCTGGCCG	1967
Db	2079	TCAATGGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGGGCGGTCAACGCTGGCCG	2138
Qy	1968	TGAAGATTTTAAAGATGATGCCACAGAGAAAGACTTTCTGATCTGGTGTACAGATATGG	2027
Db	2139	TGAAGATTTTAAAGATGATGCCACAGAGAAAGACTTTCTGATCTGGTGTACAGATATGG	2198
Qy	2028	AGATGATGAAAGATTTGGGAAACAAAGATATCATTAATCTTCTTGGACCCTGCACAC	2087
Db	2199	AGATGATGAAAGATTTGGGAAACAAAGATATCATTAATCTTCTTGGACCCTGCACAC	2258
Qy	2088	AGATGGGCTCTCTATGTCAATGTTGATATGCTCTTAAAGGCACCTCCGAGAAATACC	2147
Db	2259	AGATGGGCTCTCTATGTCAATGTTGATATGCTCTTAAAGGCACCTCCGAGAAATACC	2318
Qy	2148	TCCCAAGCCCGGAGCCACCCCGGGAATGAGTATCTCTATGACATTAACCGTGTCTGAGG	2207
Db	2319	TCCCAAGCCCGGAGCCACCCCGGGAATGAGTATCTCTATGACATTAACCGTGTCTGAGG	2378
Qy	2208	AGCAGATGACCTTCAAGGACTTGTGTCTATGCACTTACACAGCTGGCCGACAGCGATGAGT	2267
Db	2379	AGCAGATGACCTTCAAGGACTTGTGTGTCTATGCACTTACACAGCTGGCCGACAGCGATGAGT	2438
Qy	2268	ACTTGGCTTCCCAAAATATGATTCATGAGATTTAGCAGCCGAAATGTTTGGTAAACAG	2327
Db	2439	ACTTGGCTTCCCAAAATATGATTCATGAGATTTAGCAGCCGAAATGTTTGGTAAACAG	2498
Qy	2328	AAAACAATGTGATGAAAATATGACAACTTTGGAATCTCCGCAAGATATCAAACTATAGCT	2387
Db	2499	AAAACAATGTGATGAAAATATGACAACTTTGGAATCTCCGCAAGATATCAAACTATAGCT	2558
Qy	2388	ATTACAAAAGACCAACCAATGGGGGCTTCCAGTCAAGTGGATGGCTCCAGAACCCGTGT	2447
Db	2559	ATTACAAAAGACCAACCAATGGGGGCTTCCAGTCAAGTGGATGGCTCCAGAACCCGTGT	2618
Qy	2448	TTGATAGATATACATCATGAGATGATGTCTGGTCTTTGGGGGTGTAATGTGGAGAA	2507

Db	2619	TTGATAGAGTATACACTATCAAGATGATGTCGGTCTCTCGGGGTGTAAATGAGGAGA	2678
Qy	2508	TCTTCACTTTTAGGGGGCTCGCCCTTACCAGGGATTCCTCGTGAAGAACTTTTAAAGTCGC	2567
Db	2679	TCTTCACTTTTAGGGGGCTCGCCCTTACCAGGGATTCCTCGTGAAGAACTTTTAAAGTCGC	2738
Qy	2568	TGAAGGAAGGACACAGAAATGGAATGAGCCAGGCCAATGACCAAGAACTGTACATGATGA	2627
Db	2739	TGAAGGAAGGACACAGAAATGGAATGAGCCAGGCCAATGACCAAGAACTGTACATGATGA	2798
Qy	2628	TGAGGGACTGTGTGCGATGCAAGTGCCTTCCAGAGACCAACGTTACAGCACTTGTAGAAAG	2687
Db	2799	TGAGGGACTGTGTGCGATGCAAGTGCCTTCCAGAGACCAACGTTACAGCACTTGTAGAAAG	2858
Qy	2688	ACTTGATTCGAATTTCTCACTCTCACACCAATGAGGAATACTTGGACCTCAGCCAACTTC	2747
Db	2859	ACTTGATTCGAATTTCTCACTCTCACACCAATGAGGAATACTTGGACCTCAGCCAACTTC	2918
Qy	2748	TGGAACAGTATTCACCTGATTAACCTTGACACAAAGAAATCTTGTTCTTCAGAGATGAT	2807
Db	2919	TGGAACAGTATTCACCTGATTAACCTTGACACAAAGAAATCTTGTTCTTCAGAGATGAT	2978
Qy	2808	CTGTTTTTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTCAGATTCACACATAA	2867
Db	2979	CTGTTTTTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTCAGATTCACACATAA	3038
Qy	2868	ACGGCAGTGTAAAACATGAATGACTGTGTCTGCTGTGCCCAACAGACAGCACTGGG	2927
Db	3039	ACGGCAGTGTAAAACATGAATGACTGTGTCTGCTGTGCCCAACAGACAGCACTGGG	3098
Qy	2928	AACCTAGCTACACATGAGAGGGAGACATGCTCCAGAGCTGTGTCTCACTGAT	2987
Db	3099	AACCTAGCTACACATGAGAGGGAGACATGCTCCAGAGCTGTGTCTCACTGAT	3158
Qy	2988	ATATGATCAGAGAGTAAATTAATTTGAAAAAGTATCAGCATATGTGTAAGATTATATAC	3047
Db	3159	ATATGATCAGAGAGTAAATTAATTTGAAAAAGTATCAGCATATGTGTAAGATTATATAC	3218
Qy	3048	AGTTGAAAACTTGTATATCTTCCCGACAGAGAGAGAAGGTTTCTGGACGATGAGCTGC	3106
Db	3219	AGTTGAAAACTTGTATATCTTCCCGACAGAGAGAGAAGGTTTCTGGACGATGAGCTGC	3277
RESULT 6			
CS237527		4587 bp	DNA
LOCUS	CS237527		linear
DEFINITION	Sequence 242 from Patent WO2005113596.		PAT 04-JAN-2006
ACCESSION	CS237527		
VERSION	CS237527.1	GI:84364558	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
ORGANISM	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini;		
ORGANISM	Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Jin, P.		
JOURNAL	Patent: WO 2005113596-A 242 01-DEC-2005;		
FEATURES	Receptor Biologix, Inc. (US)		
FEATURES	location/Qualifiers		
FEATURES	1..4587		
FEATURES	/organism="Homo sapiens"		
FEATURES	/mol_type="unassigned DNA"		
FEATURES	/db_xref="taxon:9606"		
ORIGIN			
Query Match	93.5%;	Score 2904.2;	DB 2; Length 4587;
Best Local Similarity	97.3%;	Pred. No. 0;	
Matches 3034; Conservative	0; Mismatches	63; Indels	22; Gaps 7;
Qy	1	CCCGGAGGCAAGTTTGTGTGAGGCAAG-CAAGCTGATGTCCTTCTCTCGTTC	59
Db	168	CTCGCAGCAAGATTGTGTGAGGCAAGCCCAAGCTGATGTCCTTCTCTCGTTC	227

QY	6	CCAAATCCGAGGGGACGCGCGGGCCGTCAG---GGCCTCTCCGAGCGCTGGGGTACGC	116
Db	228	CCAAATCCGAGGGGACGCGCGGGCCGTCATGCCCGGCTCTCCGAGCGCTGGGGTACGC	287
QY	117	GTGAGGCCCGGGAGGCTTGGCGCGCGGGAGAGCCCAAGACACTCTTCTGCGTTTGGAG	176
QY	288	GTGAGGCCCGGGAGGCTTGGCGCGCGGGAGAGCCCAAGAGCACTCTTCTGCGTTTGGAG	347
QY	177	TTTGCTCCCGGCACACCCCGGGCTGGTGGCTTTCTCCATCCCGACCCACGCGGGGGC-CGGGG	235
Db	348	TTTGCTCCCGGCACACCCCGGGCTGGTGGCTTTCTCCATCCCGACCCACGCGGGGGC-CGGGG	407
QY	236	ACAAACACAGGTCGCGAGAGCGCTTGCATTCAAGTACCTGCAGCAGCAGC-GCAGCGCC	294
Db	408	ACAAACACAGGTCGCGAGAGCGCTTGCATTCAAGTACCTGCAGCAGCAGCAGCGCAGCGCC	467
QY	295	TCGGTTCCTGAGCCCAACCGCA-GCTGAAGGCAATTGGCGGTATGTCATGCCCCGTATGAGGAA	353
Db	468	TCGGTTCCTGAGCCCAACCGCAGCGCTGAAGGCAATTGGCGGTATGTCATGCCCCGTATGAGGAA	527
QY	354	GTGAGCAGATGGGATTTAAGTCACATGAGAGATATGGAAGAGACCGGGATTTGTTACG	413
Db	528	GTGAGCAGATGGGATTTAAGTCACATGAGAGATATGGAAGAGACCGGGATTTGTTACG	587
QY	414	TAAACATGTCAGCTGGGGTCTGTTTCATCTGCTGTGCTGTCACCATGGCAACTTGT	473
Db	588	TAAACATGTCAGCTGGGGTCTGTTTCATCTGCTGTGCTGTCACCATGCAACTTGT	647
QY	474	CCCTGGCCCGGGCCCTCCCTTCAGTTTATGTTGAGATACCAATTATGAGCCAGAAAGGCAAC	533
Db	648	CCCTGGCCCGGGCCCTCCCTTCAGTTTATGTTGAGATACCAATTATGAGCCAGAAAGGCAAC	707
QY	534	CAACCAATACCAATCTCTCAACAGAGTGTACGTGGCTGCGCAAGGGAGTCTGCTAG	593
Db	708	CAACCAATACCAATCTCTCAACAGAGTGTACGTGGCTGCGCAAGGGAGTCTGCTAG	767
QY	594	AGTGCGCTGCTGTTGAAAGATGCCCGCCGTGATCACTTGGACTTAAGATGGGGTGGACT	653
Db	768	AGTGCGCTGCTGTTGAAAGATGCCCGCCGTGATCACTTGGACTTAAGATGGGGTGGACT	827
QY	654	TGGGGCCCAACATAGGACAGTGTCTTATGCGGAGTACTTGCAGATTAAGGGCCGCACAC	713
Db	828	TGGGGCCCAACATAGGACAGTGTCTTATGCGGAGTACTTGCAGATTAAGGGCCGCACAC	887
QY	714	CTAGAGCTCGGCTCTATGCTTGTATCTGCCAGTAGAGCTGTAGACAGTGAACCTTGT	773
Db	888	CTAGAGCTCGGCTCTATGCTTGTATCTGCCAGTAGAGCTGTAGACAGTGAACCTTGT	947
QY	774	ACTTCATGTTAATGTCAAGATGCATCTCATCCGAGATGATGAGGATGACACCGATG	833
Db	948	ACTTCATGTTAATGTCAAGATGCATCTCATCCGAGATGATGAGGATGACACCGATG	1007
QY	834	GTGCGGAAGATTTTGTCAGTAGAGACAGTAAACAAGAGAGCACATCTGACCAACA	893
Db	1008	GTGCGGAAGATTTTGTCAGTAGAGACAGTAAACAAGAGAGCACATCTGACCAACA	1067
QY	894	CAGAAAAATGAAAAAGCGGCTCCATGCTGTGCGGCCCAACAAGTGAAGTTGGCT	953
Db	1068	CAGAAAAATGAAAAAGCGGCTCCATGCTGTGCGGCCCAACAAGTGAAGTTGGCT	1127
QY	954	GCCCAAGCGGGGGGAAACCAATGCAACCAATGCGGTGGCTGAAAAACGGAGAGAGTTTA	1013
Db	1128	GCCCAAGCGGGGGGAAACCAATGCAACCAATGCGGTGGCTGAAAAACGGAGAGAGTTTA	1187
QY	1014	AGCAGAGCATGCAATTGGAGGCTTACAAAGTTACGAACCAAGCACTGGAGCTCATTTATGG	1073
Db	1188	AGCAGAGCATGCAATTGGAGGCTTACAAAGTTACGAACCAAGCACTGGAGCTCATTTATGG	1247
QY	1074	AAAGTGTGTCCTCATCTGACAAAGGAAATTATACCTGTGTGTGGAGAAATGAATACGGGT	1133
Db	1248	AAAGTGTGTCCTCATCTGACAAAGGAAATTATACCTGTGTGTGGAGAAATGAATACGGGT	1307

1134 CCATCAATGACAGGATACCTGGATGTGTGAGAGCATGCTCCACCGGCGCCATCTCC 1193
1308 CCAATCAATGACAGGATACCTGGATGTGTGAGAGCATGCTCCACCGGCGCCATCTCC 1367
1194 AAGCGGAGCTGCGGCAATATGCTCCAGATGTGTGAGAGAGATGATGTTGTCTGA 1253
1368 AAGCGGAGCTGCGGCAATATGCTCCAGATGTGTGAGAGAGATGATGTTGTCTGA 1427
1254 AGGTTTCAAGTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1313
1428 AGGTTTCAAGTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1487
1314 GTAAATGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1373
1488 GTAAATGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1547
1374 GTTTCATGAGAGAGTGTGCTGTCTGT-----TCAATGTGAGAGAGAGAGAGAG 1427
1548 CCAAGGAG 1607
1428 AATATATATGTATAGGTTTCAATATATATATATATATATATATATATATATAT 1487
1608 AATATATATGTATAGGTTTCAATATATATATATATATATATATATATATATAT 1667
1488 TCTTGCCAAAAG 1547
1668 TCTTGCC-----AGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1718
1548 TGAAGATAGGAT 1607
1719 TGAAGATAGGAT 1778
1608 TCTTGCTGCGAGATAG 1667
1779 TCTTGCTGCGAGATAG 1838
1668 ACAAGCTGACCAAGAT 1727
1839 ACAAGCTGACCAAGAT 1898
1728 CTTTCATGAGAT 1787
1899 CTTTCATGAGAT 1958
1788 ACAAGCTGACCAAGAT 1847
1959 ACAAGCTGACCAAGAT 2018
1848 TTTCCAAAGAT 1907
2019 TTTCCAAAGAT 2078
1908 TCAATGAGAGAGAGAT 1967
2079 TCAATGAGAGAGAGAT 2138
1968 TGAAGATGTGAAAGAT 2027
2139 TGAAGATGTGAAAGAT 2198
2028 AGATGATGAGAGAGAT 2087
2199 AGATGATGAGAGAGAT 2258
2088 AGATGAGAGAGAT 2147
2259 AGATGAGAGAGAT 2318
2148 TCCGAG 2207
2319 TCCGAG 2378
2208 AGCAGATGAG 2267

2379 AGCAGATGAG 2438
2268 ACTTGAGCTTCCCAAAAT 2327
2439 ACTTGAGCTTCCCAAAAT 2498
2328 AAAAAGATGATGAG 2387
2499 AAAAAGATGATGAG 2558
2388 ATTACAAAAG 2447
2559 ATTACAAAAG 2618
2448 TTGATGATGAT 2507
2619 TTGATGATGAT 2678
2508 TCTTGCACTTAAAG 2567
2679 TCTTGCACTTAAAG 2738
2568 TGAAG 2627
2739 TGAAG 2798
2628 TGAAG 2687
2799 TGAAG 2858
2688 ACTTGATGATGAT 2747
2859 ACTTGATGATGAT 2818
2748 TCGAAGATGATGAT 2807
2919 TCGAAGATGATGAT 2978
2808 CTGTTTTTCTCGAG 2867
2979 CTGTTTTTCTCGAG 3038
2868 ACGGAGAT 2927
3039 ACGGAGAT 3098
2928 AACCTAGCTACCTGAG 2987
3099 AACCTAGCTACCTGAG 3158
2988 ATATGAT 3047
3159 ATATGAT 3218
3048 AGTTGAAAAGCTGAT 3106
3219 AGTTGAAAAGCTGAT 3277
RESULT 7
DD187136 4587 bp DNA linear PAT 19-JAN-2006
LOCUS DD187136
DEFINITION Novel targets for obesity from subcutaneous fat.
ACCESSION DD187136.1 GI:85643345
VERSION JP 2005176846-A/26.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 4587)

AUTHORS Ostenson,C., Clarc,R.G., DuchateauNguyen,G., Gardes,C. and Mizrahi,J.
TITLE Novel targets for obesity from subcutaneous fat
JOURNAL Patent: JP 2005176846-A 26 07-JUL-2005;
F Hoffmann-lia Roche AG
COMMENT OS Homo sapiens
PN JP 2005176846-A/26
PD 07-JUL-2005
PR 22-DEC-2004 JP 2004370470
PI 22-DEC-2003 EP 03104902.6
PI claes-goran ostenson,roger g clarc,gullemette duchateau- pi
nguyen,
PI christophe gardes,jacques mizrahi
CC fibroblast growth factor receptor 2 transcript variant 1 FH
Key Location/Qualifiers
FT misc_feature (1)..(4587)
FT /note='LocusID: 2263; NM 000141' FT
/note='The feature key is missing in the FT
original data. It is automatically supplemented by the JPO'.
FEATURES
source Location/Qualifiers
1..4587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 93.5%; Score 2904.2; DB 2; Length 4587;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3044; Conservative 0; Mismatches 63; Indels 22; Gaps 7;
QY 1 CCCGCGAGCAAAAGTTTGTGTGAGGCAACG-CAAGCTGAGTCTTTTCTTCTGTTCC 59
DB 168 CTGCGAGCAAAATTGTTGTGTGAGGCAACGCAAGCTGAGTCTTTTCTTCTGTTCC 227
QY 60 CCAAAATCCAGGCGACCCCGGGCGTCANG---GGGCTCTCCGAGAGCTGGGGTAAACG 116
DB 228 CCAAAATCCAGGCGACCCCGGGCGTCANG---GGGCTCTCCGAGAGCTGGGGTAAACG 287
QY 117 GTGAACCCCGGAGAGCTTGGCGCGCGGAGAACCCAGAGACACTCTTCTGCGTTTGGAG 176
DB 288 GTGAACCCCGGAGAGCTTGGCGCGCGGAGAACCCAGAGACACTCTTCTGCGTTTGGAG 347
QY 177 TTGCTCCCGCAACCCCGGGCTCTGTGCTTTCTTCATCCCGACCAACGCGGGGCG-CGGG 235
DB 348 TTGCTCCCGCAACCCCGGGCTCTGTGCTTTCTTCATCCCGACCAACGCGGGGCGGGG 407
QY 236 ACAACACAGGTCCCGAGAGAGCGTTGCAATTCAGAGTCACTGACAGCGAGCG-ACAAGCGC 284
DB 408 ACAACACAGGTCCCGAGAGAGCGTTGCAATTCAGAGTCACTGACAGCGAGCGAGCGCG 467
QY 295 TCGGTTCTGAGGCCCAACCGCA-GCTGAGAGCAATTGCGCTAGTCAATGCCCCGTAGAGAA 353
DB 468 TCGGTTCTGAGGCCCAACCGCAAGGCTGAGGCAATTGCGCGTGAATGCCGTAGAGAGAA 527
QY 354 GTGTGAGATGGAGATTAACTTCAATGAGATATGAGAGAGAACCGGGGATTTGTAACG 413
DB 528 GTGTGAGATGGAGATTAACTTCAATGAGATATGAGAGAGAACCGGGGATTTGTAACG 587
QY 414 TAAACATGTGTCAGTGGGGTCTGTTTCACTGCGCTGTGCTGATCAACATGGCAACCTGT 473
DB 588 TAAACATGTGTCAGTGGGGTCTGTTTCACTGCGCTGTGCTGATCAACATGGCAACCTGT 647
QY 474 CCCGCGCGGAGCCCTCTTCAAGTTAGTTAGAGATACCACTTAAAGCCAGAGAGCCAC 533
DB 648 CCCGCGCGGAGCCCTCTTCAAGTTAGTTAGAGATACCACTTAAAGCCAGAGAGCCAC 707
QY 534 CAACCAATAACCAATCTTCAACAGAGATGTAAGTGGCTGCGCGAGGGAGTGTAG 553
DB 708 CAACCAATAACCAATCTTCAACAGAGATGTAAGTGGCTGCGCGAGGGAGTGTAG 767
QY 594 AGGTGCGCTGCTGTTGAAGAATGCCCGCTGATCAATTGATCTTAAGATGGGTTGACT 653

DB 768 AGGTGCGCTGCTGTTGAAGAATGCCCGCTGATCAATTGATCTTAAGATGGGTTGACT 827
QY 654 TGGGGCCCAACATATGAGACAGTGTCTTATTTGGGAGTACTTTCAGATTAAGGGCCGACAC 713
DB 828 TGGGGCCCAACATATGAGACAGTGTCTTATTTGGGAGTACTTTCAGATTAAGGGCCGACAC 887
QY 714 CTAGAGACTCCGGCCCTCTATGCTTGTATCTGCAAGTGAAGTGTAGACATGAACTTGGT 773
DB 888 CTAGAGACTCCGGCCCTCTATGCTTGTACTGCAAGTGAAGTGTAGACATGAACTTGGT 947
QY 774 ACTTCATGTGATGTCAAGATGTCATCTCAATCCGAGATGATGAGATGACACCGATG 833
DB 948 ACTTCATGTGATGTCAAGATGTCATCTCAATCCGAGATGATGAGATGACACCGATG 1007
QY 834 GTGCGGAAGATTTTGTCTAGTGAAGACATTAACAAAGAGACCAATCTGACCAACA 893
DB 1008 GTGCGGAAGATTTTGTCTAGTGAAGACATTAACAAAGAGACCAATCTGACCAACA 1067
QY 894 CAGAAAGATGGAAGAGGCGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT 953
DB 1068 CAGAAAGATGGAAGAGGCGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT 1127
QY 954 GCCCAGCCGGGGGGAACCCCAATGCCAATGCGGTGCTGAAAAACGGAAAGATTTA 1013
DB 1128 GCCCAGCCGGGGGGAACCCCAATGCCAATGCGGTGCTGAAAAACGGAAAGATTTA 1187
QY 1014 AGCAGAGCATGTGCTATTTGAGGCTTCAAGGTTCGAACCAAGCATCTGAGCCCTATTATG 1073
DB 1188 AGCAGAGCATGTGCTATTTGAGGCTTCAAGGTTCGAACCAAGCATCTGAGCCCTATTATG 1247
QY 1074 AAAAGTGTGTCATCTGCAAGAGGAATTAATCCTGTGTAGTGAAGATGAATCGGAT 1133
DB 1248 AAAAGTGTGTCATCTGCAAGAGGAATTAATCCTGTGTAGTGAAGATGAATCGGAT 1307
QY 1134 CCATCAATCAACGTAACCACTGATGTTGTGAGCGATGCTTCAACGCGCCCATCTCC 1193
DB 1308 CCATCAATCAACGTAACCACTGATGTTGTGAGCGATGCTTCAACGCGCCCATCTCC 1367
QY 1194 AAGCGGACTGCGCGGAATGCTTCAAGTGTGTGAGAGACGTAAGATTGTCTGCA 1253
DB 1368 AAGCGGACTGCGCGGAATGCTTCAAGTGTGTGAGAGACGTAAGATTGTCTGCA 1427
QY 1254 AGGTTTACAGTATGCCAGCCCAATCACTGATCAAGATCAAGACGTTGAAAAAGACGCA 1313
DB 1428 AGGTTTACAGTATGCCAGCCCAATCACTGATCAAGATCAAGACGTTGAAAAAGACGCA 1487
QY 1314 GTAATATACGGGCGCGAGCGGCTGCTTCAAGGTTCTCAAGCATCTGCGGGAATTAATA 1373
DB 1488 GTAATATACGGGCGCGAGCGGCTGCTTCAAGGTTCTCAAGCATCTGCGGGAATTAATA 1547
QY 1374 GTTCAATGCAAGTGTGCTGTGT-----TCAATGTGACCGAGCGGATGCTGGG 1427
DB 1548 CCAACGACAAAGAGATGGAAGTCTCTATATTCGAAATGTAATTTTGAAGACGCTGGGG 1607
QY 1428 AATATATATGTAAGTCTCAATTAATATAGGCGCAACCAAGTCTGCTGCTCACTG 1487
DB 1608 AATATATGCTTGGCGGGAATTTCTATTTGGAATATCTTTCATCTGATGTTGACAG 1667
QY 1488 TCCTGCAAAAGACGAAAGCGCTGGAAGAGAAAGAGATTAACGTTTCCCAACTACC 1547
DB 1668 TTCCTG-----AGCGCTGGAAGAGAAAGAGATTAACGTTTCCCAACTACC 1718
QY 1548 TGAAGATAGCCATTATCTGCAATAGGGGCTTCTTAAATGCCCTGTATGTGTGTAACGTCA 1607
DB 1719 TGAAGATAGCCATTATCTGCAATAGGGGCTTCTTAAATGCCCTGTATGTGTGTAACGTCA 1778
QY 1608 TCCTGCGCAATGAAGAACAGAACCAAGACGACTTTCAGACGCGGCGGCTGTGC 1667
DB 1779 TCCTGCGCAATGAAGAACAGAACCAAGACGACTTTCAGACGCGGCGGCTGTGC 1838
QY 1668 ACAAGCTGACCAAACTATTCCTCTGCGGAGACAGGTAAACGTTTGGGTGAGTCAAGCT 1727
DB 1839 ACAAGCTGACCAAACTATTCCTCTGCGGAGACAGGTAAACGTTTGGGTGAGTCAAGCT 1898

QY 1728 CCTCCATGAATCTCCAAACCCCGCTGGTGAAGAAATACAGACGCTCTCTTCAACGGCAG 1787
 DB 1899 CCTCCATGAATCTCCAAACCCCGCTGGTGAAGAAATACAGACGCTCTCTTCAACGGCAG 1958
 QY 1788 ACAACCCCATGCTGGCAGGGGTCTCCGAGTATGAATCTTCCAGAGAACCCAAATGGAGT 1847
 DB 1959 ACAACCCCATGCTGGCAGGGGTCTCCGAGTATGAATCTTCCAGAGAACCCAAATGGAGT 2018
 QY 1848 TTCCAGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGG 1907
 DB 2019 TTCCAGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGG 2078
 QY 1908 TCATGGGGAGAGAGCTGGGAAATTTGACAAAGCAAGCCCAAGAGGGCGGTCAACGGTGGCCG 1967
 DB 2079 TCATGGGGAGAGAGCTGGGAAATTTGACAAAGCAAGCCCAAGAGGGCGGTCAACGGTGGCCG 2138
 QY 1968 TGAAGATGTTGAAGATGATGCAAGAGAAAGACCTTCTGATCTGGTGCAGAGATGG 2027
 DB 2139 TGAAGATGTTGAAGATGATGCAAGAGAAAGACCTTCTGATCTGGTGCAGAGATGG 2198
 QY 2028 AGATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTTGAGGCTGCACAC 2087
 DB 2199 AGATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTTGAGGCTGCACAC 2258
 QY 2088 AGATGGGGCTCTCTATATGCTCATAGTGAATGCTCTTAAAGGCAACCTCCGAGAAATACC 2147
 DB 2259 AGATGGGGCTCTCTATATGCTCATAGTGAATGCTCTTAAAGGCAACCTCCGAGAAATACC 2318
 QY 2148 TCCGAGCCCGGAGGCAACCCGGAGATGAGTACTCTTAATGACATTAACCGTGTCTGAGG 2207
 DB 2319 TCCGAGCCCGGAGGCAACCCGGAGATGAGTACTCTTAATGACATTAACCGTGTCTGAGG 2378
 QY 2208 AGCAGATGACCTTCAAGAGACTTGTGTATGATGACCTTACAGCTGGCCAGACGATGAGT 2267
 DB 2379 AGCAGATGACCTTCAAGAGACTTGTGTATGATGACCTTACAGCTGGCCAGACGATGAGT 2438
 QY 2268 ACTTGGCTTCCCAAAATATGATTTATGAGATTTAGAGCAAGAAATGTTTGGTAAACAG 2327
 DB 2439 ACTTGGCTTCCCAAAATATGATTTATGAGATTTAGAGCAAGAAATGTTTGGTAAACAG 2498
 QY 2328 AAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2387
 DB 2499 AAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2558
 QY 2388 ATTACAAAAGAGACCAACATGAGGCGCTTCCAGTCAAGTGGATGCTCCAGAAAGCCCTGT 2447
 DB 2559 ATTACAAAAGAGACCAACATGAGGCGCTTCCAGTCAAGTGGATGCTCCAGAAAGCCCTGT 2618
 QY 2448 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2507
 DB 2619 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2678
 QY 2508 TCTTCACTTTAAGGGGGGCTGCGCTTACCAGGAGATTTCCGATGAGAGAACTTTTAAAGCTGC 2567
 DB 2679 TCTTCACTTTAAGGGGGGCTGCGCTTACCAGGAGATTTCCGATGAGAGAACTTTTAAAGCTGC 2738
 QY 2568 TGAAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2627
 DB 2739 TGAAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2798
 QY 2628 TGAAGAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2687
 DB 2799 TGAAGAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2858
 QY 2688 ACTTGGATGCAATTTCTCATCTCTCAACACATGAGAGATTTGAGACTCAGCCAACTC 2747
 DB 2859 ACTTGGATGCAATTTCTCATCTCTCAACACATGAGAGATTTGAGACTCAGCCAACTC 2918
 QY 2748 TCGAAGATATTCACCTAGTACCCTGACACAGAAAGTTCTTGTCTTCAAGAGATGAT 2807
 DB 2919 TCGAAGATATTCACCTAGTACCCTGACACAGAAAGTTCTTGTCTTCAAGAGATGAT 2978

QY 2808 CTGTTTTTCTCCAGACCCCATGCTTACGAAACATGCTTCTCTAGATACACATTA 2867
 DB 2979 CTGTTTTTCTCCAGACCCCATGCTTACGAAACATGCTTCTCTAGATACACATTA 3038
 QY 2868 ACCGAGCTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2927
 DB 3039 ACCGAGCTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3098
 QY 2928 AACCTAGCTACCTGAGAGAGAGACATGCTTCCAGAGCTTGTGTCTCACTTGTAT 2987
 DB 3099 AACCTAGCTACCTGAGAGAGACATGCTTCCAGAGCTTGTGTCTCACTTGTAT 3158
 QY 2988 ATATGATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3047
 DB 3159 ATATGATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3218
 QY 3048 AGTTGAAAACCTGTAATCTTCCACAGAGAGAGAAAGTTTGTGAGAGCTGCTGC 3106
 DB 3219 AGTTGAAAACCTGTAATCTTCCACAGAGAGAGAAAGTTTGTGAGAGCTGCTGC 3277
 RESULT 8
 CS031438
 LOCUS CS031438 4575 bp DNA linear PAT 10-MAR-2005
 DEFINITION Sequence 944 from Patent WO2005016962.
 ACCESSION CS031438
 VERSION CS031438.1 GI:60731480
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 AUTHORS Abbas, A.; Clark, H.; Ouyang, W.; Williams, M. P.; Wood, W. I. and Wu, T. D.
 TITL Composition and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 944 24-FEB-2005;
 FEATURES
 source
 1..4575
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 91.7%; Score 2849.4; DB 2; Length 4575;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;
 QY 1 CCCGCCAGCAAAAGTTGGTGAAGGCAAG-CAAGCTGAGTCTTCTTCTCTGCTCC 59
 DB 168 CTCGCGAGCAAAATTTGGTGAAGGCAAGCGCAAGCTGAGTCTTCTTCTCTGCTCC 227
 QY 60 CCAATCCGAGGCGAGCGCGGGCGTCAATG---GGGCTCTCCGAGAGCTTGGGGTAAACG 116
 DB 228 CCAATCCGAGGCGAGCGCGGGCGTCAATG---GGGCTCTCCGAGAGCTTGGGGTAAACG 287
 QY 117 G-TGAAGCCCGGAGGCTTGGCGCGCGGAGACCAAGAGACCACTTCTGCGTTTGA 175
 DB 288 GCTGAAGCCCGGAGGCTTGGCGCGCGGAGACCAAGAGACCACTTCTGCGTTTGA 347
 QY 176 GTTGTCTCCCGCAACCCCGGGCTGTGCTTCTTCCATCCGAGCCAGCGGGGGG-0GGG 224
 DB 348 GTTGTCTCCCGCAACCCCGGGCTGTGCTTCTTCCATCCGAGCCAGCGGGGGG-0GGG 407
 QY 235 GACAAACAGAGTGGCGGAGAGAGGTTGCAATCAAGTGAAGTGAAGAGCAGC-GCAGCG 293
 DB 408 GACAAACAGAGTGGCGGAGAGAGGTTGCAATCAAGTGAAGTGAAGAGCAGC-GCAGCG 467
 QY 294 CTCGGTTCCTGAGCCCAACCGCA-GCTGAAGGCAATGCGGCTAGTCAATGCGCTTAAGAG 352
 DB 468 CTCGGTTCCTGAGCCCAACCGCA-GCTGAAGGCAATGCGGCTAGTCAATGCGCTTAAGAG 527

QY 353 AGTGTGCAGATGGATTAAAGTCCACATGAGATATGAAAGAGACCGGGGATTGGTACC 412
 Db 528 AGTGTGCAGATGGATTAAAGTCCACATGAGATATGAAAGAGACCGGGGATTGGTACC 587
 QY 413 GTTAACTATGTCAGCTGGGGTGGTTTCACTGCTGGTGTGTGTGCAACATGCAACCTTG 472
 Db 588 GTTAACTATGTCAGCTGGGGTGGTTTCACTGCTGGTGTGTGTGCAACATGCAACCTTG 647
 QY 473 TCCCTGGCCCGGCGCTCTCTAGTGTAGTTAGAGATACCAATTAGAGCCAGAAAGGCCA 532
 Db 648 TCCCTGGCCCGGCGCTCTCTAGTGTAGTTAGAGATACCAATTAGAGCCAGAAAGGCCA 707
 QY 533 CCAACCAAAATACCAAAATCTCTCAACCAAGATGTACGTGGCTGCGCCAGGGAGTGGCTA 592
 Db 708 CCAACCAAAATACCAAAATCTCTCAACCAAGATGTACGTGGCTGCGCCAGGGAGTGGCTA 767
 QY 593 GAGGTGCGCTGCTCTGTGAAAGATGCGCCCTGTATCAATTTGATCTTAAGATGGGGTGCAC 652
 Db 768 GAGGTGCGCTGCTCTGTGAAAGATGCGCCCTGTATCAATTTGATCTTAAGATGGGGTGCAC 827
 QY 653 TTGGGGCCCAACCAATAGACACAGTCTTAATTGGGGAGTACTTGGAGATTAAGGGCGCCACA 712
 Db 828 TTGGGGCCCAACCAATAGACACAGTCTTAATTGGGGAGTACTTGGAGATTAAGGGCGCCACA 887
 QY 713 CCTAGAGACTCGGCGCTCTATGCTTGTACTGCGAGTACGATGAGACAGTGAACCTTGG 772
 Db 888 CCTAGAGACTCGGCGCTCTATGCTTGTACTGCGAGTACGATGAGACAGTGAACCTTGG 947
 QY 773 TACTTCAATGATGAATGTCAACAGTGCATCTCAATCCGGAGATGATAGAGATGACACGAT 832
 Db 948 TACTTCAATGATGAATGTCAACAGTGCATCTCAATCCGGAGATGATAGAGATGACACGAT 1007
 QY 833 GGTGCGGAAGATTTTGTGAGTGAAGAACATGACCAACAGAGACACATTACTGGAACCAAC 892
 Db 1008 GGTGCGGAAGATTTTGTGAGTGAAGAACATGACCAACAGAGACACATTACTGGAACCAAC 1067
 QY 893 ACAGAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGGCGCAACCTGTCAAAGTTTCCG 952
 Db 1068 ACAGAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGGCGCAACCTGTCAAAGTTTCCG 1127
 QY 953 TGGCCAGCCGGGGGGAACCCCAATGCCCAACCATGCGGTGTGAAGAAACGGGAAGGAGTTT 1012
 Db 1128 TGGCCAGCCGGGGGGAACCCCAATGCCCAACCATGCGGTGTGAAGAAACGGGAAGGAGTTT 1187
 QY 1013 AAGCAGAGATGCAATGAGGCTCAAGAGTACGAACCAAGACACTGAGCTCAATTATG 1072
 Db 1188 AAGCAGAGATGCAATGAGGCTCAAGAGTACGAACCAAGACACTGAGCTCAATTATG 1247
 QY 1073 GAAAGTGTGTCTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGG 1132
 Db 1248 GAAAGTGTGTCTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGG 1307
 QY 1133 TCCATCAATCAACATACCACTGTGATGTTGTGAAGGATCGCTCAACCGGCCCATCTC 1192
 Db 1308 TCCATCAATCAACATACCACTGTGATGTTGTGAAGGATCGCTCAACCGGCCCATCTC 1367
 QY 1193 CAAGCCGAGCTGCGGCAAAATGCTTCCACAGTGGTGGAGAGACGTAAGATTGTCTCG 1252
 Db 1368 CAAGCCGAGCTGCGGCAAAATGCTTCCACAGTGGTGGAGAGACGTAAGATTGTCTCG 1427
 QY 1253 AAGGTTTACATGATGCTCCAGCCCAATCATCATGATGATCAACGACGTGGAAGAACGCGC 1312
 Db 1428 AAGGTTTACATGATGCTCCAGCCCAATCATCATGATGATCAACGACGTGGAAGAACGCGC 1487
 QY 1313 AATTAATACGAGCGCGGACGCGGCTTACCTCAAGGTTTCTCAAGGTTTCTCAAGGCGCGC 1372
 Db 1488 AATTAATACGAGCGCGGACGCGGCTTACCTCAAGGTTTCTCAAGGTTTCTCAAGGCGCGC 1547
 QY 1373 AGTTTCAATGC-----AGAGTGTGCTGTGTTCATTAATGATGACGAGCGC 1417
 Db 1548 GGTGTTAACACACGAGCAAAAGATTTGAGGTTCTTAATTCGGAATGTAACTTTTGAG 1607

QY 1418 GATGCTGGGGAATATATATATATAGGTCTCAATTTATAGGCAAGCCACAGCTTCC 1477
 Db 1608 GACGCTGGGGAATATATATATATAGGTCTTGGCGGTTATTTCTATTGGGAATATCTTTCACTTGC 1667
 QY 1478 TGGCTCACTGTCTCTGCCAAAACAGCAAGCGCTGGAAAGAAAAGAGATTACAGCTTCC 1537
 Db 1668 TGGTTGACAGTTCTTCC-----AGCGCTGGAAAGAAAAGAGATTACAGCTTCC 1718
 QY 1538 CCAAGCTACTCGAGATATGCCATTTATCTGCATATAGGGGCTCTTAAATGCGCTGTATGGTG 1597
 Db 1719 CCAAGCTACTCGAGATATGCCATTTATCTGCATATAGGGGCTCTTAAATGCGCTGTATGGTG 1778
 QY 1598 GTTAACTATCTGTGCGGATGGAAGAACAGCAACCAAGAACGAGCTTACAGCGCAG 1657
 Db 1779 GTTAACTATCTGTGCGGATGGAAGAACAGCAACCAAGAACGAGCTTACAGCGCAG 1838
 QY 1658 CCGGCTGTGCACAAGCTGACCAAAAGTATCCCTGTGCGGAGACAGTTACAGTTTCCGCT 1717
 Db 1839 CCGGCTGTGCACAAGCTGACCAAAAGTATCCCTGTGCGGAGACAG-----GTTTCCGCT 1892
 QY 1718 GAGTCAAGCTCTCTCATGAACTCCAAACCCCGCTGTGTGAGATTAACAACGCTCTCT 1777
 Db 1893 GAGTCAAGCTCTCTCATGAACTCCAAACCCCGCTGTGTGAGATTAACAACGCTCTCT 1952
 QY 1778 TCAAGGGAGACACCCCATGCTGGCAGGGGTCTCCAGTATGAACCTTCCAGAGGACCA 1837
 Db 1953 TCAAGGGAGACACCCCATGCTGGCAGGGGTCTCCAGTATGAACCTTCCAGAGGACCA 2012
 QY 1838 AATGCGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTT 1897
 Db 2013 AATGCGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTT 2072
 QY 1898 GGGCAAGTGTCTATGGCGGAGACAGTGGGAATTGACAAAGACAGCCCAAGAGGCGGTC 1957
 Db 2073 GGGCAAGTGTCTATGGCGGAGACAGTGGGAATTGACAAAGACAGCCCAAGAGGCGGTC 2132
 QY 1958 ACCGTGGCCGTGAAGATGTTGAAGATGATGCAAGAAAGACCTTGTGATCTGGTG 2017
 Db 2133 ACCGTGGCCGTGAAGATGTTGAAGATGATGCAAGAAAGACCTTGTGATCTGGTG 2192
 QY 2193 TCAAGATGGAATATGATGAAGATGATGGAAGAACCAAGAAATATCAATAATCTTCTGGA 2252
 Db 2078 GCTTGCACACAGATGAGGCTCTCTATGTCAATGTTGAGTATGCTCTTAAAGGCAACCTC 2137
 QY 2253 GCTTGCACACAGATGAGGCTCTCTATGTCAATGTTGAGTATGCTCTTAAAGGCAACCTC 2312
 Db 2138 CGAGAAATACCTCGAGCCCGGAGGCAACCGGGAATGAGTACTCTATGACATTAACGCT 2197
 QY 2198 GTTCTGAGAGACAGATGACTTTCAGAGACTTGTGTCAATGCACTTACAGCTGAGCCAGA 2257
 Db 2373 GTTCTGAGAGACAGATGACTTTCAGAGACTTGTGTCAATGCACTTACAGCTGAGCCAGA 2432
 QY 2258 CGAGTGAATCTTGGCTTCCAAAATATATATCAAGATTTAGAGCCGGAATGTT 2317
 Db 2433 GGCATGAGTACTTGGCTTCCAAAATATATATCAAGATTTAGAGCCGGAATGTT 2492
 QY 2318 TTGTATACGAAACCAATGATGAAATATGAGACCTTGTGACTGCGCAGAGATATCAAC 2377
 Db 2493 TTGTATACGAAACCAATGATGAAATATGAGACCTTGTGACTGCGCAGAGATATCAAC 2552
 QY 2553 AATATGACTATTAACAAAAGACCAATGAGGCGCTTCCAGTCAAGGTGATGCTCCA 2612
 Db 2438 GAAAGCTGTGTTGATGAGTATACATCACTACAGATGATGTGTGTCTTCCGGGGTGA 2497
 QY 2613 GAAAGCTGTGTTGATGAGTATACATCACTACAGATGATGTGTGTCTTCCGGGGTGA 2672
 Db 2498 ATGTGGAATCTTCACTTTAGGGGCTGCGCCTACCCAGGATTCCTCGTGAAGAACCTT 2557

Db 2673 ATGGGAGAGATCTTCACTTTAGGGGGCTCCGCCCTACCCAGGAGTTCCCGTGGAGAACTT 2732
Qy 2558 TTTAAGCTGTGAAGGAAGACACAGATGATTAAGCCAACTGCAACCAAGAACTG 2617
Db 2733 TTTAAGCTGTGAAGGAAGACACAGATGATTAAGCCAACTGCAACCAAGAACTG 2792
Qy 2618 TACATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGCTTCAACAG 2677
Db 2793 TACATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGCTTCAACAG 2852
Qy 2678 TTGGTAGAAGACTTGAATCGAATTCGACTCTCAACCAATGAGAACTTGGAACTC 2737
Db 2853 TTGGTAGAAGACTTGAATCGAATTCGACTCTCAACCAATGAGAACTTGGAACTC 2912
Qy 2738 AGCCAACTCTCGAAGCAAGTATTCAGTTACCTTGAACAGAAAGTTCTTGTCTTCA 2797
Db 2913 AGCCAACTCTCGAAGCAAGTATTCAGTTACCTTGAACAGAAAGTTCTTGTCTTCA 2972
Qy 2798 GGAATGATTTCTGTTTTTTTCTCCAGACCCCATGCTTACAGAACATGCTTCCAGTAT 2857
Db 2973 GGAATGATTTCTGTTTTTTTCTCCAGACCCCATGCTTACAGAACATGCTTCCAGTAT 3032
Qy 2858 CCACACATTAACGGCAGGTTTAAACATGATGACTGCTGCTGCTGCTGCTGCTGCTGCT 2917
Db 3033 CCACACATTAACGGCAGGTTTAAACATGATGACTGCTGCTGCTGCTGCTGCTGCTGCT 3092
Qy 2918 CAGCATGAGAACCTAGCTACCTAGAGAGAGAACCAATGCTCCAGAGCTTGTCT 2977
Db 3093 CAGCATGAGAACCTAGCTACCTAGAGAGAGAACCAATGCTCCAGAGCTTGTCT 3152
Qy 2978 CCACTTGTATATGATGATCAGAGAGATTAATTTGAAAAATGATCAGCATATGTGTA 3037
Db 3153 CCACTTGTATATGATGATCAGAGAGATTAATTTGAAAAATGATCAGCATATGTGTA 3212
Qy 3038 AGATTTATACGTTGAAACCTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGCA 3097
Db 3213 AGATTTATACGTTGAAACCTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGCA 3272
Qy 3098 GTGAGCTGC 3106
Db 3273 GTGAGCTGC 3281

RESULT 9
CS040390 4575 bp DNA linear PAT 22-MAR-2005
LOCUS Sequence 944 from Patent WO2005019258.
DEFINITION CS040390
VERSION CS040390.1 GI:61848163
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.
AUTHORS Compositions and methods for the treatment of immune related
TITLE diseases
JOURNAL Patent: WO 2005019258-A 944 03-MAR-2005;
GENEID Genentech, Inc. (US)
FEATURES
source 1..4575
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 91.7%; Score 2849.4; DB 2; Length 4575;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;

Qy 1 CCCGCGAGCAAAATTGTTGATGAGCAACG-CAAGCCTAGTCTCTTCTCTCTGTTCC 59
Db 168 CTGGCAGAGCAAAATTGTTGATGAGCAACGCAAGCCTAGTCTCTTCTCTCTGTTCC 227
Qy 60 CCAATTCGAGGCAAGCCCGGCGGTATG---GGCTCTCCGACGCTGGGATACG 116
Db 228 CCAATTCGAGGCAAGCCCGGCGGTATG---GGCTCTCCGACGCTGGGATACG 287
Qy 117 G-TGAAGCCCGGAGGCTTGGCGCCCGCAAGACCAAGGACCACTCTTCTGGGTTTGA 175
Db 288 GCTGAAGCCCGGAGGCTTGGCGCCCGCAAGACCAAGGACCACTCTTCTGGGTTTGA 347
Qy 176 GTTGCTCCCGCAACCCCGGCTCGTGGCTTCTCCATCCGACCGAGCGGAGC-CGG 234
Db 348 GTTGCTCCCGCAACCCCGGCTCGTGGCTTCTCCATCCGACCGAGCGGAGC 407
Qy 235 GACACACAGGTGCGGAGGAGGCTTGCATTCAAGTGAAGTGAAGCAAGC-GCAGCG 293
Db 408 GACACACAGGTGCGGAGGAGGCTTGCATTCAAGTGAAGTGAAGCAAGC 467
Qy 294 CTGGGTTCTGAGCCCAAGCGCA-CTGAAGCAATGGCGGTAGTCAATGCGGTAGAGA 352
Db 468 CTGGGTTCTGAGCCCAAGCGCTGAAGCAATGGCGGTAGTCAATGCGGTAGAGA 527
Qy 353 AGTGTGAGATGGGATTTAAGTCCACATGAGATTAAGAGAGACCGGGAATTGTACC 412
Db 528 AGTGTGAGATGGGATTTAAGTCCACATGAGATTAAGAGAGACCGGGAATTGTACC 587
Qy 413 GTAACATGATGAGGAGGAGGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 472
Db 588 GTAACATGATGAGGAGGAGGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
Qy 473 TCCCTGCGCGCGCGCTCTTCAATTAATGAGATACCAATTAAGCCAGAAAGCCA 532
Db 648 TCCCTGCGCGCGCGCTCTTCAATTAATGAGATACCAATTAAGCCAGAAAGCCA 707
Qy 533 CCAACCAATTAACCAATCTCTCAACGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 592
Db 708 CCAACCAATTAACCAATCTCTCAACGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 767
Qy 593 GAGTGTGCTGCTGTTGAAAGATGCGCGGTATGCTGAAGTGAAGTGAAGTGAAGTGA 652
Db 768 GAGTGTGCTGCTGTTGAAAGATGCGCGGTATGCTGAAGTGAAGTGAAGTGAAGTGA 827
Qy 653 TTGGGCGCCCAACATAGAGACATGCTTATTTGGGAGATCTTGAAGTGAAGTGAAGTGA 712
Db 828 TTGGGCGCCCAACATAGAGACATGCTTATTTGGGAGATCTTGAAGTGAAGTGAAGTGA 887
Qy 713 CTTAGAGACTCGGCGCTTATGCTTGTATGCGAGTGAAGTGAAGTGAAGTGAAGTGA 772
Db 888 CTTAGAGACTCGGCGCTTATGCTTGTATGCGAGTGAAGTGAAGTGAAGTGAAGTGA 947
Qy 773 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
Db 948 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1007
Qy 833 GGTGCGGAGATTTTGTCAATGAGACAGTAAACAAAGAGACCACTATCTGAGCAAC 892
Db 1008 GGTGCGGAGATTTTGTCAATGAGACAGTAAACAAAGAGACCACTATCTGAGCAAC 1067
Qy 893 ACAGAAAAGATGAGAAAAGCGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
Db 1068 ACAGAAAAGATGAGAAAAGCGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
Qy 953 TGCCAGCCCGGGGAGAACCAATGCAACCATGCGGTGCTGAAAACGGGAAAGAGATT 1012
Db 1128 TGCCAGCCCGGGGAGAACCAATGCAACCATGCGGTGCTGAAAACGGGAAAGAGATT 1187
Qy 1013 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1072
Db 1188 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1247
Qy 1073 GAAAGTGTGATCCATGTCAGAAAGGAAATTATACCTGTGTAGTGAAGATGAATACGGG 1132

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mizrahi, J. and
Ostenson, C.G.
Novel targets for obesity from fat tissue
Patent: EP 1548445-A 42 29-JUN-2005;
F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)
location/Qualifiers
source 1..4575
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 91.7%; Score 2849.4; DB 2; Length 4575;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;
QY 1 CCGCGAGCAAAAGTTGGTGGAGGCAAG--CAAGCTGAGTCTTCTCTCTCTCTCC 59
168 CTCGCGCAAAAGTTGGTGGAGGCAAGCCCAAGCTGAGTCTTCTCTCTCTCTCC 227
QY 60 CCAATCCGAGGAGCGCCGCGGCGTCAATG---GCGCTCTCCGCAAGCTGAGGATACG 116
228 CCAATCCGAGGAGCGCCGCGGCGTCAATGCGCGCTCTCTCTCTCTCTCTCTCTCC 287
QY 117 G-TAAGCCGCGGAGGCTTGGCGCGCGGAAAGCCCAAGACCACTTCTCTCTCTTGA 175
288 GCTAAGCCGCGGAGGCTTGGCGCGCGGAAAGCCCAAGACCACTTCTCTCTCTTGA 347
QY 176 GTTGTCTCCCGCAACCCCGGCGTGTGCTTCTCAATCCGAGCCAGCGGAGGCG 234
348 GTTGTCTCCCGCAACCCCGGCGTGTGCTTCTCAATCCGAGCCAGCGGAGGCGG 407
QY 235 GACAACAAGGTCCGAGGAGCGGTTCATTAAGTGAATGTCAGACAGACAGC--GCAAGCG 293
408 GACAACAAGGTCCGAGGAGCGGTTCATTAAGTGAATGTCAGACAGACAGCAGCG 467
QY 294 CTGCGTCTGAGCCACCGCA--GCTAAGGCAATGGCGGTATGTCATGCCGATAGAGA 352
468 CTGCGTCTGAGCCACCGCAAGGCTGAGGCAATGGCGGTATGTCATGCCGATAGAGA 527
QY 353 AGTGTGAGAGGAGATTAAGTTCACATGAGATATGGAAGAGGACGCGGAGATTGTAC 412
528 AGTGTGAGAGGAGATTAAGTTCACATGAGATATGGAAGAGGACGCGGAGATTGTAC 587
QY 413 GTAACATGATGATGAGGTGATTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
588 GTAACATGATGATGAGGTGATTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647
QY 473 TCCTGTGCGCGGCTCTCTCTCAATTAGTGAAGATACCAATTAAGGCCAAGAGGCA 532
648 TCCTGTGCGCGGCTCTCTCTCAATTAGTGAAGATACCAATTAAGGCCAAGAGGCA 707
QY 533 CCAACCAAAATTCAAATCTCTCAACCAAGATATGAGTGTGCGGCAAGGAGGATTCGTA 592
708 CCAACCAAAATTCAAATCTCTCAACCAAGATATGAGTGTGCGGCAAGGAGGATTCGTA 767
QY 593 GAGGTGCGCTGCTGTTGAAGATGCGCGGTGATCAGTTGAGCTAAGAGATGAGGATGAC 652
768 GAGGTGCGCTGCTGTTGAAGATGCGCGGTGATCAGTTGAGCTAAGAGATGAGGATGAC 827
QY 653 TTGGGAGCCCAACATAGAGCAGTGTATTGGGAGATCTTTCAGATTAAGGAGGCCACA 712
828 TTGGGAGCCCAACATAGAGCAGTGTATTGGGAGATCTTTCAGATTAAGGAGGCCACA 887
QY 713 CTTGAGAGCTCGGCTCTATGCTTGTATCTGCAAGTATAGACATGATGAAGAACTTGG 772

DB 888 CTAGAGACTCCGCGCTTATGCTGTACTCCAGATAGACATGTAACAGTGAACCTTGG 947
QY 773 TACTTCATGTGAATGTCACAGATGCTCATCTCATCCGAGATGATGATGATGACCGAT 832
948 TACTTCATGTGAATGTCACAGATGCTCATCTCATCCGAGATGATGATGATGACCGAT 1007
QY 833 GGTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAAGAGACACATATCTGACCAAC 892
1008 GGTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAAGAGACACATATCTGACCAAC 1067
QY 893 ACAGAAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCAACCTGCAAGTTTCCG 952
1068 ACAGAAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCAACCTGCAAGTTTCCG 1127
QY 953 TGCCGAGCGCGGGGGAACCAATGCAACATGCGGTGCTGAAAACGGGAGAGTTT 1012
1128 TGCCGAGCGCGGGGGAACCAATGCAACATGCGGTGCTGAAAACGGGAGAGTTT 1187
QY 1013 AAGCAGAGCATGCAATGAGGCTCAAGATACGAACCAAGCACTGAGCTCATTTATG 1072
1188 AAGCAGAGCATGCAATGAGGCTCAAGATACGAACCAAGCACTGAGCTCATTTATG 1247
QY 1073 GAAAGTGTGTCCCATCTGACAAAGGAATTAATCTGTGTAGTGAATGAATACGG 1132
1248 GAAAGTGTGTCCCATCTGACAAAGGAATTAATCTGTGTAGTGAATGAATACGG 1307
QY 1133 TCCATCAATACACGTCACCTGATATGTTGTGACGATGCGCTCACCGGCCATCTTC 1192
1308 TCCATCAATACACGTCACCTGATATGTTGTGACGATGCGCTCACCGGCCATCTTC 1367
QY 1193 CAAGCCGAGCTGCGGCAATGCTCCACAGTGTGAGAGACATGAGTTGTCTG 1252
1368 CAAGCCGAGCTGCGGCAATGCTCCACAGTGTGAGAGACATGAGTTGTCTG 1427
QY 1253 AAGTTTACAGTATGATCCAGCCCAATCACTGATGATCAAGCACTGGAAGAAACGCG 1312
1428 AAGTTTACAGTATGATCCAGCCCAATCACTGATGATCAAGCACTGGAAGAAACGCG 1487
QY 1313 AGTAAATACGAGGCGGAGCGGCTGCTTCACTCAAGTTCTCAAGGATTCGAGGATTAAT 1372
1488 AGTAAATACGAGGCGGAGCGGCTGCTTCACTCAAGGATTCGAGGATTAAT 1547
QY 1373 AGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1417
1548 GGTGTTTACACCAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1607
QY 1418 GATGCTGAGGAT 1477
1608 GATGCTGAGGAT 1667
QY 1478 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1537
1668 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1718
QY 1538 CCAAGCTACCTGAGATGAGCAATTTATCTGATGAGGCTCTTCTTAATCGCTGATGCTG 1597
1719 CCAAGCTACCTGAGATGAGCAATTTATCTGATGAGGCTCTTCTTAATCGCTGATGCTG 1778
QY 1598 GTAACAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1657
1779 GTAACAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1838
QY 1658 CCGGCTGTGCAAAAGTGAACCAAGTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1717
1839 CCGGCTGTGCAAAAGTGAACCAAGTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1892
QY 1718 GAGTCCAGCTCTCTCAATGAATCCAAACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1777
1893 GAGTCCAGCTCTCTCAATGAATCCAAACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952
QY 1778 TCAACGCGACAGACCCCATGCTGCAAGGAGCTCCGAGATGAATCTTCCAGAGACCA 1837
1953 TCAACGCGACAGACCCCATGCTGCAAGGAGCTCCGAGATGAATCTTCCAGAGACCA 2012

QY 1838 AATGGAAGTTTCAGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAGAGTTCTTT 1897
 DB 2013 AATGGAGATTTCCAGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAGAGTTCTTT 2072
 QY 1898 GGGCAAGTGTCAATGCGGAGAGAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1957
 DB 2073 GGGCAAGTGTCAATGCGGAGAGAGAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2132
 QY 1958 ACCGTGGCGTGAAGATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2017
 DB 2133 ACCGTGGCGTGAAGATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2192
 QY 2018 TCAGAGATGAGATGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2077
 DB 2193 TCAGAGATGAGATGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2252
 QY 2078 GCGTGAACAGAGATGGGCTCTCTATGATGATGATGATGATGATGATGATGATGATG 2137
 DB 2253 GCGTGAACAGAGATGGGCTCTCTATGATGATGATGATGATGATGATGATGATGATG 2312
 QY 2138 CGAGAAATACCTCCGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2197
 DB 2313 CGAGAAATACCTCCGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372
 QY 2198 GTTCTGAGAGAGAGATGACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2257
 DB 2373 GTTCTGAGAGAGAGATGACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2432
 QY 2258 CGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2317
 DB 2433 CGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2492
 QY 2318 TTGGTAAACAGAAAACATGATGATGATGATGATGATGATGATGATGATGATGAT 2377
 DB 2493 TTGGTAAACAGAAAACATGATGATGATGATGATGATGATGATGATGATGATGAT 2552
 QY 2378 AATATATGATTAACAAAACATGATGATGATGATGATGATGATGATGATGATGATG 2437
 DB 2553 AATATATGATTAACAAAACATGATGATGATGATGATGATGATGATGATGATGATG 2612
 QY 2438 GAAGCCCTGTTTATGAGATGATGATGATGATGATGATGATGATGATGATGATG 2497
 DB 2613 GAAGCCCTGTTTATGAGATGATGATGATGATGATGATGATGATGATGATGATG 2672
 QY 2498 ATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGAGATTCCTCGTGAAGA 2557
 DB 2673 ATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGAGATTCCTCGTGAAGA 2732
 QY 2558 TTTAAGCTGCTGAAG 2617
 DB 2733 TTTAAGCTGCTGAAG 2792
 QY 2618 TACATGATGATGAG 2677
 DB 2793 TACATGATGATGAG 2852
 QY 2678 TTGGTAAAG 2737
 DB 2853 TTGGTAAAG 2912
 QY 2738 AGCCAACTCTCGAAGAGATTAACCTGATGATGATGATGATGATGATGATGATGAT 2797
 DB 2913 AGCCAACTCTCGAAGAGATTAACCTGATGATGATGATGATGATGATGATGATGAT 2972
 QY 2798 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2857
 DB 2973 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3032
 QY 2858 CCAACATTAACAG 2917
 DB 3033 CCAACATTAACAG 3092

QY 2918 CAGCACTGGGAACCTAGCTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2977
 DB 3093 CAGCACTGGGAACCTAGCTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3152
 QY 2978 CCACCTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3037
 DB 3153 CCACCTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3212
 QY 3038 AGATTTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3097
 DB 3213 AGATTTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3272
 QY 3098 GTGACCTGC 3106
 DB 3273 GTGACCTGC 3281

RESULT 11
 DD187140
 LOCUS DD187140 4575 bp DNA linear PAT 19-JAN-2006
 DEFINITION Novel targets for obesity from subcutaneous fat.
 ACCESSION DD187140
 VERSION DD187140.1 GI:85643349
 KEYWORDS JP 2005176846-A/30.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 4575)
 Otsenon,C., Clarc,R.G., DuchateauMnguyen,G., Gardes,C. and Mizrahi,J.
 Novel targets for obesity from subcutaneous fat
 Patent: JP 2005176846-A 30 07-JUL-2005;
 JOURNAL P Hoffmann-La Roche AG
 COMMENT OS Homo sapiens
 PN JP 2005176846-A/30
 PD 07-JUL-2005
 PF 22-DEC-2004 JP 2004370470
 PR 22-DEC-2003 EP 03104902.6
 PI claes-goran otsenon,roger g clarc,gullemette duchateau- pi nguyen,
 PI christophe gardes,jacques mizrahi
 CC fibroblast growth factor receptor 2 transcript variant 5 FH
 Key Location/Qualifiers
 FT misc_feature (1)..(4575)
 FT /note='The feature key is missing in the FT original data. It is automatically supplemented by the JPO'.
 FEATURES
 source Location/Qualifiers
 1..4575
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 91.7%; Score 2849.4; DB 2; Length 4575;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;
 QY 1 CCGGAGAGAAAGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 59
 DB 168 CTGGCAGAGAAAGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
 QY 60 CCAAAATCCAG 116
 DB 228 CCAAAATCCAG 287
 QY 117 G-TGAAGCCCGAG 175
 DB 288 GCTGAAGCCCGAG 347

Db 2493 TTGTTACGAAAAAATGATGATGAAATAGACAGACTTTGAGCTGCCAGATATCAAC 2552
2378 AATATAGACTATTTACAAAAAGACCAATGGCGGCTTCACTCAAGTGAATGGCTCCA 2437
2553 AATATAGACTATTTACAAAAAGACCAATGGCGGCTTCACTCAAGTGAATGGCTCCA 2612
2438 GAAGCCCTGTTGATGAGTATACATCTACAGAGTATGTCGTCTTCCGGGGTTA 2497
2613 GAAGCCCTGTTGATGAGTATACATCTACAGAGTATGTCGTCTTCCGGGGTTA 2672
2498 ATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGGATTCCTCCGAGAACTT 2557
2673 ATGTGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGGATTCCTCCGAGAACTT 2732
2558 TTTAAGCTCTGAAGAGACACAGAAATGATTAAGCCAGCCAACTGACCAAGAACTG 2617
2733 TTTAAGCTCTGAAGAGACACAGAAATGATTAAGCCAGCCAACTGACCAAGAACTG 2792
2618 TACATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGTTCAAGCAG 2677
2793 TACATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAGACCAAGTTCAAGCAG 2852
2678 TTGGTGAAGACTTGTGATGATTTCTCACTCTCAACCAATGAGGAATATCTGACCTC 2737
2853 TTGGTGAAGACTTGTGATGATTTCTCACTCTCAACCAATGAGGAATATCTGACCTC 2912
2738 AGCCAACTCTCGAAGAGTAATTCACCTAGTTACCTGACACAAAGATTCTGTCTTCA 2797
2913 AGCCAACTCTCGAAGAGTAATTCACCTAGTTACCTGACACAAAGATTCTGTCTTCA 2972
2798 GGAAGATGATTTCTTTTCTCCAGACCCCATGCTTACGAAACAGCCCTTCTCAAGTAT 2857
2973 GGAAGATGATTTCTTTTCTCCAGACCCCATGCTTACGAAACAGCCCTTCTCAAGTAT 3032
2858 CCACACATTAACCGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGAT 2917
3033 CCACACATTAACCGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGAT 3092
2918 CAGCACTGGGAACTTACCTGACCTGAGCAGAGAGACCATGCTCCAGAGCTGTGTCT 2977
3093 CAGCACTGGGAACTTACCTGACCTGAGCAGAGAGACCATGCTCCAGAGCTGTGTCT 3152
2978 CCACTTGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3037
3153 CCACTTGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3212
2498 AGATTATATACAGTTGAAACCTTGTATCTTCCAGAGAGAGAAAGTTCTGAGACA 3097
3213 AGATTATATACAGTTGAAACCTTGTATCTTCCAGAGAGAGAAAGTTCTGAGACA 3272
2498 GTGAGCTGC 3106
3273 GTGAGCTGC 3281

RESULT 12
AR669941 3080 bp DNA linear PAT 13-JUN-2005
LOCUS AR669941 Sequence 25 from patent US 6900053.
DEFINITION AR669941
ACCESSION AR669941
VERSION AR669941.1 GI:67608232
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 3080)
AUTHORS Freiler,S.M.
TITLES Antisense modulation of fibroblast growth factor receptor 2
expression
JOURNAL Patent: US 6900053-A 25 31-MAY-2005;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
Source 1..3080
Location/Qualifiers

ORIGIN /organism="unknown"
/mol_type="genomic DNA"
Query Match 90.3%; Score 2806.2; DB 2; Length 3080;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2879; Conservative 0; Mismatches 8; Indels 8; Gaps 6;
1 CCCGAGACAAAGTTGGTGGAGGCAAG -CAAGCTGAGTCCCTTCTCTCTGTTCC 59
186 CTGGGAGCAAAAGTTGGTGGAGGCAAGCCAAAGCTGAGTCTTCTCTCTGTTCC 245
60 CCAATCCGAGGAGCCGCGGCGGTGATG--GCGCTCTCCGACAGCTGGGATACG 116
246 CCAATCCGAGGAGCCGCGGCGGTGATG--GCGCTCTCCGACAGCTGGGATACG 305
117 G-TGAAGCCGAGGAGCTTGGCGCCGAGAAACCAAGACCACTCTTCTGCTTTGA 175
306 GCTGAAGCCGAGGAGCTTGGCGCCGAGAAACCAAGACCACTCTTCTGCTTTGA 365
176 GTTGTCTCCCGCAACCCCGGCGTGTGCTTCTTCATCTCCGACCCAGCGGCGG 234
366 GTTGTCTCCCGCAACCCCGGCGTGTGCTTCTTCATCTCCGACCCAGCGGCGG 425
225 GACAAACAGAGTGGGAGGAGCGTTGCAATTAAGTACTGACAGCAGCAGC -GAGCGC 293
426 GACAAACAGAGTGGGAGGAGCGTTGCAATTAAGTACTGACAGCAGCAGCAGC 485
294 CTGGTCTCTGAGCCACCGCA -GCTGAAGGCAATGCGGTATGTCATGCTCCGTAAG 352
486 CTGGTCTCTGAGCCACCGCAAGGCTGAAGGCTGAGGCTGATGTCATGCTCCGTAAG 545
353 AGTGTGCAATGAGGATTAACCTTCAATGAGATGATGAAAGAGCCGGGGATGGTATC 412
546 AGTGTGCAATGAGGATTAACCTTCAATGAGATGATGAAAGAGCCGGGGATGGTATC 605
413 GTAACATGATGATGAGGATTAACCTTCAATGAGATGATGAAAGAGCCGGGGATGGTATC 472
606 GTAACATGATGATGAGGATTAACCTTCAATGAGATGATGAAAGAGCCGGGGATGGTATC 665
472 TCCCTGGCCGCGCCCTCTCTTCAATTAAGTGAATGATGATGATGATGATGATGATGAT 532
666 TCCCTGGCCGCGCCCTCTCTTCAATTAAGTGAATGATGATGATGATGATGATGATGAT 725
533 CCAACCAATTAACCAATCTTCAACCAAGATGATGATGATGATGATGATGATGATGATGAT 592
726 CCAACCAATTAACCAATCTTCAACCAAGATGATGATGATGATGATGATGATGATGATGAT 785
593 GAGGTGCGCTGCTGTTGAAGATGCGCGCGTATCAATGATGATGATGATGATGATGATGAT 652
786 GAGGTGCGCTGCTGTTGAAGATGCGCGCGTATCAATGATGATGATGATGATGATGATGAT 845
653 TTGGGAGCCCAACATAGACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 712
846 TTGGGAGCCCAACATAGACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 905
713 CCAAGAGATCCGCGCTCTATGCTTGTATGCTGCAATTAAGATGATGATGATGATGATGAT 772
906 CCAAGAGATCCGCGCTCTATGCTTGTATGCTGCAATTAAGATGATGATGATGATGATGAT 965
773 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
966 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025
833 GGTGCGAAGATTTTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
1026 GGTGCGAAGATTTTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
893 ACGAAGAGATGAAAGAGCGCTCCATGCTGCTGCGGCGCAACACTGTCAAGTTTCCG 952
1086 ACGAAGAGATGAAAGAGCGCTCCATGCTGCTGCGGCGCAACACTGTCAAGTTTCCG 1145
953 TGCACAGCGGGGGGAAACCAATGCAACATGCGGTGGCTGAAAAACGGGAAGAGTTT 1012

Db 1146 TGCCACCGGGGGAAACCAATGCCAATCGGCTGCGAAGGAGAGATTT 1205
 Qy 1013 AAGCAGAGCATGCGATTGAGGCTACAGGTACGAAACCAAGCATGAGCTCATTTATG 1072
 Db 1206 AAGCAGAGCATGCGATTGAGGCTACAGGTACGAAACCAAGCATGAGCTCATTTATG 1265
 Qy 1073 GAAAGTGTGCTCCATCTGACAGAGGAAATTAATCTGTGTATGTGGAATTAATAGGG 1132
 Db 1266 GAAAGTGTGCTCCATCTGACAGAGGAAATTAATCTGTGTGTGGAATTAATAGGG 1325
 Qy 1133 TCCATCAATCAACAGTACCACTGATGTTGTGAGAGGATCGCTCAACGGCCATCTC 1192
 Db 1326 TCCATCAATCAACAGTACCACTGATGTTGTGAGAGGATCGCTCAACGGCCATCTC 1385
 Qy 1193 CAAGCCGAGCTGCGGCAAAATGCTTCCACAGTGTGCGAGAGAGCTGAGATTGTCTGC 1252
 Db 1386 CAAGCCGAGCTGCGGCAAAATGCTTCCACAGTGTGCGAGAGAGCTGAGATTGTCTGC 1445
 Qy 1253 AAGTTTACAGTATGCTCCAGCCCAATCCAGTGTGATCAAGCAACGTGGAAGAAAGAGG 1312
 Db 1446 AAGTTTACAGTATGCTCCAGCCCAATCCAGTGTGATCAAGCAACGTGGAAGAAAGAGG 1505
 Qy 1313 AGTAATATCGGGGCGGAGCGGCTGCTCACTCAAGGTTCTCAAGCATCGGGGATTAAT 1372
 Db 1506 AGTAATATCGGGGCGGAGCGGCTGCTCACTCAAGGTTCTCAAGCATCGGGGATTAAT 1565
 Qy 1373 AGTTCAATGAGAGTGTGCTGCTCTGTCAATGTGACGAGCGGAGTGTGGGAAAT 1432
 Db 1566 AGTTCAATGAGAGTGTGCTGCTCTGTCAATGTGACGAGCGGAGTGTGGGAAAT 1625
 Qy 1433 ATATGTAAAGTCTTCAATTAATATGAGGAGGAGCAAGCTGTGCTGCTCACTGTCTG 1492
 Db 1626 ATATGTAAAGTCTTCAATTAATATGAGGAGGAGCAAGCTGTGCTGCTCACTGTCTG 1685
 Qy 1493 CCAAAACAGAGAGGCGCTGGAAGAAAGAGATTAAGCTTCCCGAGCTACCTGAG 1552
 Db 1686 CCAAAACAGAGAGGCGCTGGAAGAAAGAGATTAAGCTTCCCGAGCTACCTGAG 1745
 Qy 1553 ATAGCCATTTAATCTGATAGAGGCTTCTTATTCGCTGTATGTGTAAAGTATCTG 1612
 Db 1746 ATAGCCATTTAATCTGATAGAGGCTTCTTATTCGCTGTATGTGTAAAGTATCTG 1805
 Qy 1613 TGCCGAATGAAGAACAGACCAAGAGCCAGACTTCAAGCCGAGCGGCTGTGACAAAG 1672
 Db 1806 TGCCGAATGAAGAACAGACCAAGAGCCAGACTTCAAGCCGAGCGGCTGTGACAAAG 1865
 Qy 1673 CTGACCAAAAGGTATCCCTGCGGAGACAGGTAAAGTTTCCGCTGAGTCCAGCTCTCC 1732
 Db 1866 CTGACCAAAAGGTATCCCTGCGGAGACAGGTAAAGTTTCCGCTGAGTCCAGCTCTCC 1925
 Qy 1733 ATGAATCTCAACACCCGCTGTGTAGATTAACAAGCCCTCTTCAACGGCAGACACC 1792
 Db 1926 ATGAATCTCAACACCCGCTGTGTAGATTAACAAGCCCTCTTCAACGGCAGACACC 1985
 Qy 1793 CCAATGCTGCGAGGGGTCTCCGAGTATGAATTTCAAGAGACCAAAATGGAGTTTCCA 1852
 Db 1986 CCAATGCTGCGAGGGGTCTCCGAGTATGAATTTCAAGAGACCAAAATGGAGTTTCCA 2045
 Qy 1853 AGAATTAAGCTGACACTGCGGCAAGCCCTGCGGAGAAAGTTGCTTGGGCAAGTGTATG 1912
 Db 2046 AGAATTAAGCTGACACTGCGGCAAGCCCTGCGGAGAAAGTTGCTTGGGCAAGTGTATG 2105
 Qy 1913 GCGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGGCGGTCAACGCTGTGAGAG 1972
 Db 2106 GCGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGGCGGTCAACGCTGTGAGAG 2165
 Qy 1973 ATGTTGAAGATGATGCTCAAGAGAAAGCTTTCTGATCTGTGTCAAGATGAGATG 2032
 Db 2166 ATGTTGAAGATGATGCTCAAGAGAAAGCTTTCTGATCTGTGTCAAGATGAGATG 2225
 Qy 2033 ATGAAGATGATGTTGGGAACCAAGAAATTAATTAATCTTGTGAGCTGACACAGAT 2092

Db 2226 ATGAAGATGATGTTGGGAACCAAGAAATATCAATTAATCTTGTGAGCTGTGACAGAGAT 2285
 Qy 2093 GGGCTCTCTATGTCATATGATGATGCTCTTAAAGGCACTCCGAAATACCTCGCA 2152
 Db 2286 GGGCTCTCTATGTCATATGATGATGCTCTTAAAGGCACTCCGAAATACCTCGCA 2345
 Qy 2153 GCGGAGAGCCACCCGAGATGAGTACTCTTATGACATTAACGTTGCTGAGAGAGAG 2212
 Db 2346 GCGGAGAGCCACCCGAGATGAGTACTCTTATGACATTAACGTTGCTGAGAGAGAG 2405
 Qy 2213 ATGACCTTCAAGACTTGTGTATGACACTTCAACAGCTGCGCAGACGATGATCTTG 2272
 Db 2406 ATGACCTTCAAGACTTGTGTATGACACTTCAACAGCTGCGCAGACGATGATCTTG 2465
 Qy 2273 GCTTCCCAAAAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2332
 Db 2466 GCTTCCCAAAAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2525
 Qy 2333 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2392
 Db 2526 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2585
 Qy 2393 AAAAAGACCAACCAATGAGGCGGCTTCCAGTCAAGTGTGATGATGATGATGATGATG 2452
 Db 2586 AAAAAGACCAACCAATGAGGCGGCTTCCAGTCAAGTGTGATGATGATGATGATGATGATG 2645
 Qy 2453 AAGATATCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2512
 Db 2646 AAGATATCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2705
 Qy 2513 ACTTTAGGGGGGCTGGCTTACCAAGGATGATGATGATGATGATGATGATGATGATGATG 2572
 Db 2706 ACTTTAGGGGGGCTGGCTTACCAAGGATGATGATGATGATGATGATGATGATGATGATG 2765
 Qy 2573 GAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
 Db 2766 GAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2825
 Qy 2633 GATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2692
 Db 2826 GATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2885
 Qy 2693 GATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2752
 Db 2886 GATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2945
 Qy 2753 CAGTATTCACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2812
 Db 2946 CAGTATTCACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3005
 Qy 2813 TTTTCTCAGACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2872
 Db 3006 TTTTCTCAGACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3065
 Qy 2873 AGTGTAAACATGA 2887
 Db 3066 AGTGTAAACATGA 3080

RESULT 13
 HUMFPR2A 3080 bp mRNA linear PRI 08-NOV-1994
 LOCUS Homo sapiens fibroblast growth factor receptor 2 IIIB (FGR2) mRNA,
 DEFINITION complete cds.
 ACCESSION M97193
 VERSION M97193.1 GI:182566
 KEYWORDS fibroblast growth factor receptor 2; ligand binding.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 3080)

Db 1686 CCAAAACAGACAGCCCTGAGAGAGAAAAGAGATTACAGCTTCCCAAGATCCTGGAG 1745
 Qy 1553 ATAGCAATTTATCTGCATAGGGGTCTTTAATGCGCTGTATGCTGTAAACATCATCTG 1612
 Db 1746 ATAGCAATTTATCTGCATAGGGGTCTTTAATGCGCTGTATGCTGTAAACATCATCTG 1805
 Qy 1613 TGCAGATGAAACACACAGACCAAGAGCCAGATTCAGCAGCCAGCCGCTGTGCAAG 1672
 Db 1806 TGCAGATGAAACACACAGACCAAGAGCCAGATTCAGCAGCCAGCCGCTGTGCAAG 1865
 Qy 1673 CTGACCAAAAGTATCCCTGCGGAGAGCAGTAAAGTTTGGCTGAGTCACTCTCC 1732
 Db 1866 CTGACCAAAAGTATCCCTGCGGAGAGCAGTAAAGTTTGGCTGAGTCACTCTCC 1925
 Qy 1733 ATGACATCCCAACACCCGCTGTGAGGATTAACAACGCTCTCTTCAACGAGACACC 1792
 Db 1926 ATGACATCCCAACACCCGCTGTGAGGATTAACAACGCTCTCTTCAACGAGACACC 1985
 Qy 1793 CCCATGCTGACAGGGGTCTTCCAGATTAACCTTCAGAGGACCCAAATGGAGTTCCA 1852
 Db 1986 CCCATGCTGACAGGGGTCTTCCAGATTAACCTTCAGAGGACCCAAATGGAGTTCCA 2045
 Qy 1853 AGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTGGGCAAGTGTGATG 1912
 Db 2046 AGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTGGGCAAGTGTGATG 2105
 Qy 1913 GCGAAGCAGTGGGAATTGACAAAGACCCAGAGAGCGGTCAACCTGCGGTGAG 1972
 Db 2106 GCGAAGCAGTGGGAATTGACAAAGACCCAGAGAGCGGTCAACCTGCGGTGAG 2165
 Qy 1973 ATGTTGAAGATGATGTCACAGAGAAAGACCTTCTGATCTGCTGTGATGATGAGATG 2032
 Db 2166 ATGTTGAAGATGATGTCACAGAGAAAGACCTTCTGATCTGCTGTGATGATGAGATG 2225
 Qy 2033 ATGAAAGTATGTTGGGAACCAAGATATCAATAATCTTGGAGCTGCACACAGAT 2092
 Db 2226 ATGAAAGTATGTTGGGAACCAAGATATCAATAATCTTGGAGCTGCACACAGAT 2285
 Qy 2093 GGGCCTCTATGTCATAGTGTAGTATGCTTAAAGCAACCTCCAGATATCTCCGA 2152
 Db 2286 GGGCCTCTCTATGTCATAGTGTAGTATGCTTAAAGCAACCTCCAGATATCTCCGA 2345
 Qy 2153 GCCCGAGGCAACCCGAGATGAGTACTCTATGACATTAACCTGTCTGAGAGACAG 2212
 Db 2346 GCCCGAGGCAACCCGAGATGAGTACTCTATGACATTAACCTGTCTGAGAGACAG 2405
 Qy 2213 ATGACCTTCAAGACTTGTGTCTATGACCACTGAGCGTGCAGAGGATGAGTACTTG 2272
 Db 2406 ATGACCTTCAAGACTTGTGTCTATGACCACTGAGCGTGCAGAGGATGAGTACTTG 2465
 Qy 2273 GCTTCCCAAAAATGTATTCATCGAGATTAGCAGCCAGAAATGTTTGTAAAGAAAAC 2332
 Db 2466 GCTTCCCAAAAATGTATTCATCGAGATTAGCAGCCAGAAATGTTTGTAAAGAAAAC 2525
 Qy 2333 AATGTGATGAATAATAGCAGACTTGTGACTGCGCAGAGATATCAACAATATAGCTATTAAC 2392
 Db 2526 AATGTGATGAATAATAGCAGACTTGTGACTGCGCAGAGATATCAACAATATAGCTATTAAC 2585
 Qy 2393 AAAAAAGCAACATGAGGCGGCTTCCAGTCAAGTGAAGTGTCCAGAAAGCCCTGTGAT 2452
 Db 2586 AAAAAAGCAACATGAGGCGGCTTCCAGTCAAGTGAAGTGTCCAGAAAGCCCTGTGAT 2645
 Qy 2453 AGAGTATACACTCATCAGAGTATGCTGCTTCCGAGGTGTTAATGTGAGATCTTC 2512
 Db 2646 AGAGTATACACTCATCAGAGTATGCTGCTTCCGAGGTGTTAATGTGAGATCTTC 2705
 Qy 2513 ACTTTAGGGGCTGCGCTTACCCAGAGATTCCTGAGAGAACTTTTAACTGCTGAG 2572
 Db 2706 ACTTTAGGGGCTGCGCTTACCCAGAGATTCCTGAGAGAACTTTTAACTGCTGAG 2765
 Qy 2573 GAAAGACACAAATGATTAAGCAGCACTGACCAAGCAACTGATCATGATGAGG 2632

Db 2766 GAAAGACACAGATGATTAAGCAGCACTGACCAACAACTGATCATGATGAGG 2825
 Qy 2633 GACTGTGGCATGACAGTGGCCCTCCAGAGACCAAGTTTCAAGCATGTGTAGAAAGCTTG 2692
 Db 2826 GACTGTGGCATGACAGTGGCCCTCCAGAGACCAAGTTTCAAGCATGTGTAGAAAGCTTG 2885
 Qy 2693 GATCGAATTTCACTCTCAACAACAAATGAGAAATCTTGAACCTCAGCAACTCTCGAA 2752
 Db 2886 GATCGAATTTCACTCTCAACAACAAATGAGAAATCTTGAACCTCAGCAACTCTCGAA 2945
 Qy 2753 CAGTATTCACCTTACCTTCAACACAGAAAGTTCTTGTCTTCAAGAAATGATTTCTGT 2812
 Db 2946 CAGTATTCACCTTACCTTCAACACAGAAAGTTCTTGTCTTCAAGAAATGATTTCTGT 3005
 Qy 2813 TTTTCTCCAGACCCCATGCTTACAGAACATGCTTCTCAGTATCACAATPAACGGC 2872
 Db 3006 TTTTCTCCAGACCCCATGCTTACAGAACATGCTTCTCAGTATCACAATPAACGGC 3065
 Qy 2873 AGGTAAACATGA 2887
 Db 3066 AGGTAAACATGA 3080

RESULT 14

AR669919 4268 bp DNA linear PAT 13-JUN-2005
 LOCUS AR669919
 DEFINITION Sequence 3 from patent US 6900053.
 ACCESSION AR669919
 VERSION AR669919.1 GI:67608210
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 4268)
 AUTHORS Freiler,S.M.
 TITLE Antisense modulation of fibroblast growth factor receptor 2 expression
 JOURNAL Patent: US 6900053-A 3 31-MAY-2005;
 ISIS Pharmaceuticals, Inc.; Carlsbad, CA
 FEATURES
 source 1..4268
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 89.6%; Score 2781.8; DB 2; Length 4268;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

Qy 149 CCCAAGACACACTCTGCGGTTTGGAGTGTCTCCCGCAACCCCGGCTGTCGCTTTC 208
 Db 1 CCCAAGACACACTCTGCGGTTTGGAGTGTCTCCCGCAACCCCGGCTGTCGCTTTC 60
 Qy 209 TCCATCCCGACCCACGCGGGGC-CGGGACACACAGGTGCGAGAGAGCGTTGCCATTTC 267
 Db 61 TCCATCCCGACCCACGCGGGGCAGGAGCAACAGGTGCGAGAGAGCGTTGCCATTTC 120
 Qy 268 AAGTACTGACAGACAC-GCAGCGCTTGGTTCTGAGCCCAACGCA-GCTGAAGGCA 325
 Db 121 AAGTACTGACAGACAGCGCGAGCGCTGCTGCTGAGCCCAACGCAAGGCA 180
 Qy 326 TTGCGGTATTCATGCGCGGTAGAGAGAGTGCAGATGAGATTAAGTCCACATGAGAG 385
 Db 181 TTGCGGTATTCATGCGCGGTAGAGAGAGTGCAGATGAGATTAAGTCCACATGAGAG 240
 Qy 386 TATGAAGAGACCGGGGATTTGTACCGTAAACATGCTGAGGTGCTTTCATCTGC 445
 Db 241 TATGAAGAGACCGGGGATTTGTACCGTAAACATGCTGAGGTGCTTTCATCTGC 300
 Qy 446 CTGGTCTGTGTACCATGAGCACTTGTCTCTGGCCCGGCTTCACTTATGAGTGAAG 505
 Db 301 CTGGTCTGTGTACCATGAGCACTTGTCTCTGGCCCGGCTTCACTTATGAGTGAAG 360

QY	506	GATACCACTTAGACCGAAGAGCCAAACCAATTCCTCAACCAAGTGT	565
Db	361	GATACCACTTAGAGCCGAAGAGCCAAACCAATTCCTCAACCAAGTGT	420
QY	566	TACGCGCTGGCGCCAGGGGAGTCGTAGAGTGGCGCTGCTGGAAAGATGCCGCGTGT	625
Db	421	TACGCGCTGGCGCCAGGGGAGTCGTAGAGTGGCGCTGCTGGAAAGATGCCGCGTGT	480
QY	626	ATCAGTTGAGCTAAGAGATGGGGTGTCACTTGGGGCCAAACAATAGAACAGTCTTATTTGGG	685
Db	481	ATCAGTTGAGCTAAGAGATGGGGTGTCACTTGGGGCCAAACAATAGAACAGTCTTATTTGGG	540
QY	686	GAGTACTTGGACGATTAAGGGGCGCCACGCTTAGAGACTTCGGCCCTTATGTCTTGACTGGC	745
Db	541	GAGTACTTGGACGATTAAGGGGCGCCACGCTTAGAGACTTCGGCCCTTATGTCTTGACTGGC	600
QY	746	AGTAGGACTGTAGAACGTGAACCTTGTGATCTTCAATGGTAATGTCAAGATGGCATCTCA	805
Db	601	AGTAGGACTGTAGAACGTGAACCTTGTGATCTTCAATGGTAATGTCAAGATGGCATCTCA	660
QY	806	TCCGGAGATGATGAGAGTGAACCGATGGTGGGAAATTTTGTCAGTAGAACATTAAC	865
Db	661	TCCGGAGATGATGAGAGTGAACCGATGGTGGGAAATTTTGTCAGTAGAACATTAAC	720
QY	866	AACAAGAGAGCACTACTGTGACCAACAACAAGAAAGATGAAAGCGGCTTCATGCTGTGT	925
Db	721	AACAAGAGAGCACTACTGTGACCAACAACAAGAAAGATGAAAGCGGCTTCATGCTGTGT	780
QY	926	CCTGGCGGCCAACATGTCAAGTTTGTGCTGCCACGCGGGGGGAAACCAATGCCAACATGT	985
Db	781	CCTGGCGGCCAACATGTCAAGTTTGTGCTGCCACGCGGGGGGAAACCAATGCCAACATGT	840
QY	986	CGGTGGCTGAAAAACGGAGAGAGTTTAAAGCAGAGACATGCAATTGAGGCTCAAGATTA	1045
Db	841	CGGTGGCTGAAAAACGGAGAGAGTTTAAAGCAGAGACATGCAATTGAGGCTCAAGATTA	900
QY	1046	CGAAACCAAGCACTGAGAGCTCTTATGAAAGTGTGTGCCATCTGACAAAGGAAATTTAT	1105
Db	901	CGAAACCAAGCACTGAGAGCTCTTATGAAAGTGTGTGCCATCTGACAAAGGAAATTTAT	960
QY	1106	ACCTGTGATGTGGAGAAATGAATAGGGGTGCATCAATCAACGTACCACTGAGATGTTGTGT	1165
Db	961	ACCTGTGATGTGGAGAAATGAATAGGGGTGCATCAATCAACGTACCACTGAGATGTTGTGT	1020
QY	1166	GAGCAGTCGCTCACCGGCGCATCTCTCAAGCGGACCTGCGGCAATATGCTCTCAAGTGT	1225
Db	1021	GAGCAGTCGCTCACCGGCGCATCTCTCAAGCGGACCTGCGGCAATATGCTCTCAAGTGT	1080
QY	1226	GTCCGAGAGAGCGTAGAGTTTGTCTGCAAGGTTTACAGTATGCCAGCCCAATCCAG	1285
Db	1081	GTCCGAGAGAGCGTAGAGTTTGTCTGCAAGGTTTACAGTATGCCAGCCCAATCCAG	1140
QY	1286	TGGATTCACACAGTGGAAAGAACCGGCACTAAATACGGGCGCCAGGGGCTGCCATCCTC	1345
Db	1141	TGGATTCACACAGTGGAAAGAACCGGCACTAAATACGGGCGCCAGGGGCTGCCATCCTC	1200
QY	1346	AAGGTTCTCAAGCACTCGGGAGTAAATAGTTTCCAAATGCAAGAGTCTGGCTCTGT-----	1400
Db	1201	AAGGTTCTCAAGCACTCGGGAGTAAATAGTTTCCAAATGCAAGAGTCTGGCTCTGT-----	1260
QY	1401	-TCAATGTGACCGAGCGGATGCTGGGAAATATATATGTAGGTTCTCAATTAATATAGG	1455
Db	1261	-TCAATGTGACCGAGCGGATGCTGGGAAATATATATGTAGGTTCTCAATTAATATAGG	1320
QY	1460	CAGGCGCAACAGTGTGCTGCGCTCACTGTCTCGGCCAAAAACAGCAAGCGCTGGAGAGAA	1519
Db	1321	CAGGCGCAACAGTGTGCTGCGCTCACTGTCTCGGCCAAAAACAGCAAGCGCTGGAGAGAA	1371
QY	1520	AAGGAGATTAACAGCTTCCCAAGATTAACCTGAGATTAAGCAATTAATTAAGGAGGCTTTC	1579
Db	1372	AAGGAGATTAACAGCTTCCCAAGATTAACCTGAGATTAAGCAATTAATTAAGGAGGCTTTC	1431
QY	1580	TTAATGCGCTGTATGTGTGTAAACAGTCACTCTGTGCGAATGAGAAACAGCAAGAG	1639

Db	1432	TTAATCGCCTGTATGTGTGTGAACATCATCTCTGTGCCGATTAAGAAACAGACCAAGAAAG	1491
QY	1640	CCAGACTTTCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAACGTAATCCCCCTTGCAGACA	1699
Db	1492	CCAGACTTTCAGCAGCCAGCCGGCTGTGCACAACCTGACCAAGTAATCCCCCTTGCAGACA	1551
QY	1700	CAGGTAAACAGTTTCGGGTGTAGTCCAGTCTCCATGAACCTCCAAACACCCCGCTGTGAGG	1759
Db	1552	CAGGTAAACAGTTTCGGGTGTAGTCCAGTCTCCATGAACCTCCAAACACCCCGCTGTGAGG	1611
QY	1760	ATTAACAACAGCCCTCTTTCAACGGCAGACACCCCATGTGTGCAAGGGGTCTCCAGTAT	1819
Db	1612	ATTAACAACAGCCCTCTTTCAACGGCAGACACCCCATGTGTGCAAGGGGTCTCCAGTAT	1671
QY	1820	GAACCTTCCAGAGACCCCAAAATGGAGTTTCCAGAGATTAAGCTGACCTTGGCAGACCC	1879
Db	1672	GAACCTTCCAGAGACCCCAAAATGGAGTTTCCAGAGATTAAGCTGACCTTGGCAGACCC	1731
QY	1880	CTGGGAGAAAGTTGCTTTGGGCAAGTGTGATGAGCCGGAACACATGGGGAATTTGACAAAGAC	1939
Db	1732	CTGGGAGAAAGTTGCTTTGGGCAAGTGTGATGAGCCGGAACACATGGGGAATTTGACAAAGAC	1791
QY	1940	AAGCCCAAGAGGGGGGTCAACCGTGGCCGTGAAGATGTTGAAAAGTATGATGCAAGAGAA	1999
Db	1792	AAGCCCAAGAGGGGGGTCAACCGTGGCCGTGAAGATGTTGAAAAGTATGATGCAAGAGAA	1851
QY	2000	GACCTTTCGTATCTGTGTCTCAGAGATGGAATGATGAAGATGATTTGGAGAAACACAGAAAT	2059
Db	1852	GACCTTTCGTATCTGTGTCTCAGAGATGGAATGATGAAGATGATTTGGAGAAACACAGAAAT	1911
QY	2060	ATCATTAATCTCTTCTTGAGCCTGCAACACAGATAGGGCCTCTCATATGTCATATGTTGAATAT	2119
Db	1912	ATCATTAATCTCTTCTTGAGCCTGCAACACAGATAGGGCCTCTCATATGTCATATGTTGAATAT	1971
QY	2120	GCCCTTAAAGGCAACTCCGAGAAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAATAC	2179
Db	1972	GCCCTTAAAGGCAACTCCGAGAAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAATAC	2031
QY	2180	TCTATATGACATTAACCGTGTCTTGAGAGCAGATGACCTTCAAGGACTTGTGTCTATGC	2239
Db	2032	TCTATATGACATTAACCGTGTCTTGAGAGCAGATGACCTTCAAGGACTTGTGTCTATGC	2091
QY	2240	AACCTAACAGCTGGGCAACACGATAGGATGATCTTGGCCTCCCAAAAATGATTTCAATCGAGAT	2299
Db	2092	AACCTAACAGCTGGGCAACACGATAGGATGATCTTGGCCTCCCAAAAATGATTTCAATCGAGAT	2151
QY	2300	TTAGCAGCCAGAAAATGTTTGTGTAAACAGAAAACAATGTGATGAAAATAGCAGACTTTTGA	2359
Db	2152	TTAGCAGCCAGAAAATGTTTGTGTGTAAACAGAAAACAATGTGATGAAAATAGCAGACTTTTGA	2211
QY	2360	CTCGCCAGAGATATCAACATATATAGACTTATTACAAAAAGCACACCAATGGCGGCTTCCA	2419
Db	2212	CTCGCCAGAGATATCAACATATATAGACTTATTACAAAAAGCACCAATGGCGGCTTCCA	2271
QY	2420	GTCAAATGTGATGTGCTCCAGAAAGCCCTGTTTATATGAGATATCACTCATCAGAGATGATC	2479
Db	2272	GTCAAATGTGATGTGCTCCAGAAAGCCCTGTTTATATGAGATATCACTCATCAGAGATGATC	2331
QY	2480	TGTGCTCTCGGGGTGTAAATGTGGGAGATCTTCACTTTAGGGGGCTGCGCCTTACCAGGG	2539
Db	2332	TGTGCTCTCGGGGTGTAAATGTGGGAGATCTTCACTTTAGGGGGCTGCGCCTTACCAGGG	2391
QY	2540	ATTCCCGTGAAGAACTTTTTAAGCTGTGTAAGAGAGACACAGATATGATTAAGCCAGCC	2599
Db	2392	ATTCCCGTGAAGAACTTTTTAAGCTGTGTAAGAGAGACACAGATATGATTAAGCCAGCC	2451
QY	2600	AACTGACCAACAGAACTGTATACATGATATGAGGACCTTTGGCATATGATGTCCTCCAG	2659
Db	2452	AACTGACCAACAGAACTGTATACATGATATGAGGACCTTTGGCATATGATGTCCTCCAG	2511
QY	2660	AGACCAAGTTCAAGCAGTGTGTGAAACCTTGGATGCAATTTCTCACTCTACAAACCAAT	2719

Db	2512	AGACCAACGTTTCAGCAGCGTGTGTAGAAAGCTTGATGGAATTTCTCAGTCCACAAACAAAT	2571
QY	2720	GAGGAATACCTTGGACCTCAAGCAAACCTCTCGAA CAGATTCACTTAAGTACCTTGACACA	2779
Db	2572	GAGGAATACCTTGGACCTCAAGCAAACCTCTGAA CAGATTCACTTAAGTACCTTGACACA	2631
QY	2780	AGAACTTCTGTCTTTCAGAGATGATTCGTCTTTTCTCCAGACCCCAATGCTTACGAA	2839
Db	2632	AGAACTTCTGTCTTTCAGAGATGATTCGTCTTTTCTCCAGACCCCAATGCTTACGAA	2691
QY	2840	CCATGCTCTTCTCAGTATCCACACATTAACGGCAGTGTATAAACATGATATGACTGTCTCT	2899
Db	2692	CCATGCTCTTCTCAGTATCCACACATTAACGGCAGTGTATAAACATGATATGACTGTCTCT	2751
QY	2900	GCTGTCTCCCAACAGGACAGCACTGGGAACCTTAGCTACACTGAGCAGGGAGACCAATGCC	2959
Db	2752	GCTGTCTCCCAACAGGACAGCACTGGGAACCTTAGCTACACTGAGCAGGGAGACCAATGCC	2811
QY	2960	TCCCAAGACTTGTGTCTCCCACTTGATATATATGATCAGAGGAGTAATATTTGAAAAG	3019
Db	2812	TCCCAAGACTTGTGTCTCCCACTTGATATATATGATCAGAGGAGTAATATTTGAAAAG	2871
QY	3020	TAAACAGATATGTGTAAAGATTTATCAGTGTGAAAACCTGTAACTCTCCACAGAGAG	3079
Db	2872	TAAACAGATATGTGTAAAGATTTATCAGTGTGAAAACCTGTAACTCTCCACAGAGAG	2931
QY	3080	AAGAAAGTTCTGAGCAGTGGAATGC	3106
Db	2932	AAGAAAGTTCTGAGCAGTGGAATGC	2958

LOCUS	AX332811	4268 bp	DNA	linear	PAT 09-JAN-2002
DEFINITION	Sequence 3320 from Patent WO0194629.				
ACCESSION	AX332811				
VERSION	AX332811.1 GI:18123445				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horriagan, S., Soppet, D.R. and Weaver, Z.				
TITLE	Cancer gene detemination and therapeutic screening using signature gene sets				
JOURNAL	Patent: WO 0194629-A 3320 13-DEC-2001;				
FEATURES	Avalon Pharmaceuticals (US)				
source	location/Qualifiers				
	1..4268				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	89.6%	Score 2781.8;	DB 2;	Length 4268;	
Best Local Similarity	97.3%;	Fred. No. 0;			
Matches 2887;	Conservative	0;	Mismatches 62;	Indels 18;	Gaps 5;
Dy	149	CCGAAGGACCACTCTTCGCGTTTGAGATGTCCTCCCGCAACCCCGGCGCTGTCGCTTTC	208		
Dd	1	CCCAAGGACCACTCTTCGCGTTTGAGATGTCCTCCCGCAACCCCGGCGCTGTCGCTTTC	60		
Dy	209	TCCATCCCGAACCCAGCGGGGC-CGGGAGCAACAAGGTCGCGAGAGCGTTGCATTTC	267		
Dd	61	TCCATCCCGAACCCAGCGGGGC-CGGGAGCAACAAGGTCGCGAGAGCGTTGCATTTC	120		
Dy	268	AAGTACATGACGACGACGACAC-GCAGGCGCTCGCTTCCTGAGCCCAACCGGA-GCTGAAGGCA	325		
Dd	121	AAGTACATGACGACGACGACGAGGCGCTCGCTTCCTGAGCCCAACCGGAGCTGAAGGCA	180		

OY	326	TTGGCGCTAGTCCATGCGCCCTAGAGAAAGTGTGAGATGGGATTAACGTCAACATGGAGA	385
Db	181	TTGGCGCTAGTCCATGCGCCCTAGAGAAAGTGTGAGATGGGATTAACGTCAACATGGAGA	240
OY	386	TATGGAAGAGAACCGGGGATTTGGTACCGTAAACCATGGTCACTGGGGTGGTTTCATCTGC	445
Db	241	TATGGAAGAGAACCGGGGATTTGGTACCGTAAACCATGGTCACTGGGGTGGTTTCATCTGC	300
OY	446	CTGTGCTGTGTCAACCATGGCAACCTTGTCCCTGGCCCGGCGCTTCCTTCACTTATGTTAG	505
Db	301	CTGTGCTGTGTCAACCATGGCAACCTTGTCCCTGGCCCGGCGCTTCCTTCACTTATGTTAG	360
OY	506	GATACCAATTAGAGCCAGAAAGCCCAACCAATATCTTCAACCAAGAAAGTG	565
Db	361	GATACCAATTAGAGCCAGAAAGCCCAACCAATATCTTCAACCAAGAAAGTG	420
OY	566	TACGTGGCTGGCCAGAGGGAGTGCCTAGAGGTGCGTGCCTGTGAAAGATGCCGCCGTG	625
Db	421	TACGTGGCTGGCCAGAGGGAGTGCCTAGAGGTGCGTGCCTGTGAAAGATGCCGCCGTG	480
OY	626	ATCAGTTGGACTTAAGATGGGGGTGCACTTTGGGGCCCAACAATAGACAAGTGCTTATTTGGG	685
Db	481	ATCAGTTGGACTTAAGATGGGGGTGCACTTTGGGGCCCAACAATAGACAAGTGCTTATTTGGG	540
OY	686	GAGTACTTTGCAGATTAAGAGGGCGCCCAACCTAGAGACTCCGGCCCTATAGCTGTGACTGCC	745
Db	541	GAGTACTTTGCAGATTAAGAGGGCGCCCAACCTAGAGACTCCGGCCCTATAGCTGTGACTGCC	600
OY	746	AGTAGACTGTGAGCAAGTAAACTTTGGTACTTCACTGGTGAATGTCAAGATGCCATCTCA	805

QY	806	TCGCGAGATGATGAGATGACACCGATGCTGCGGAGATTYYTGTCACTGAGAAACGTAAAC	865
Db	661	TCGCGAGATGATGAGATGACACCGATGCTGCGGAGATTYYTGTCACTGAGAAACGTAAAC	720
QY	866	AACAAAGAGACCACTACTGGAACCAACACGAAAAGATGAAAAAGCGCTCCAGCTGTG	925
Db	721	AACAAAGAGACCACTACTGGAACCAACACGAAAAGATGAAAAAGCGCTCCAGCTGTG	780
QY	926	CCTGCGGCAACACTGCTCAAGTTTCGCTGCCAGCCGCGGGGAAACCCATATGCCAACATG	985
Db	781	CCTGCGGCAACACTGCTCAAGTTTCGCTGCCAGCCGCGGGGAAACCCATATGCCAACATG	840
QY	986	CGGTGCTGAAAAACGGAGAGATTAAAGCAGAGCATGCGCATTTGAGAGCTCAAGAGTA	1045
Db	841	CGGTGCTGAAAAACGGAGAGATTAAAGCAGAGCATGCGCATTTGAGAGCTCAAGAGTA	900
QY	1046	CGAAACCAAGCATCTGAGAGCTCATTAATGAGAAAGTGTGCCATCTGCAAGAGGAAATTAAT	1105
Db	901	CGAAACCAAGCATCTGAGAGCTCATTAATGAGAAAGTGTGCCATCTGCAAGAGGAAATTAAT	960
QY	1106	ACCTGTGATGAGAAATGAAATACGGGTCCATCATCAACGTAACCACTTGATGTTGTG	1165
Db	961	ACCTGTGATGAGAAATGAAATACGGGTCCATCATCAACGTAACCACTTGATGTTGTG	1020
QY	1166	GAGGATATGCTTCAACCGGCCCATCTCTCAACCGCGGATCGCGCGGAATATGCTTCCACAGTG	1225
Db	1021	GAGGATATGCTTCAACCGGCCCATCTCTCAACCGCGGATCGCGCGGAATATGCTTCCACAGTG	1080
QY	1226	GTCGAGAGACGTAGATTTGTCTGCAAGGTTTATCAGTAGTGTCCAGGCCCATCATCCAG	1285
Db	1081	GTCGAGAGACGTAGATTTGTCTGCAAGGTTTATCAGTAGTGTCCAGGCCCATCATCCAG	1140
QY	1286	TGATCAAGCATGTGAAAAAGAACGGCAGTAAATACGGGCCCGGACGGGCTGCCCTTAATCTC	1345
Db	1141	TGATCAAGCATGTGAAAAAGAACGGCAGTAAATACGGGCCCGGACGGGCTGCCCTTAATCTC	1200
QY	1346	AAGGTTTCAAGCACTCGGGGATTAATATAGTTCCATCAAGATGCTGAGCTGTG-----	1400
Db	1201	AAGGTTTCAAGCGCCCGGCTGTATACCAACGGAACAAAGATTTGAGGTTCTGTAAATTT	1260
QY	1401	-TCAATGTGACCGAGCGGATGCTGGGGAATATATATGTAAGTCTCCAAATTAATATAGG	1459

Db	1261	CGAAGTGAACCTTTTGAAGACCGCTGGGGAATACGTGCTTGGGGGTAATCTATGGG	1320
OY	1460	CAGGCGAACCAAGTCGCTGCGCTCACTGTCTCTGCCMAAACAGCAAGCGCTGGAAAGAA	1519
Db	1321	ATATCTCTTCACTGTGCAATGGTTGACAGTTCTGCG-----AGCGCTGGAAAGAA	1371
OY	1520	AAGAGATTACAGCTTCCCCAGACTACTGAGATAGCAATTATCTCATPAGGGGTCTTC	1579
Db	1372	AAGGAGATTACAGCTTCCCAAGACTACTCTGAGATAGCAATTATCTCATPAGGGGTCTTC	1431
OY	1580	TTAATCGCTGTATGTGTGTAAAGTCAAGTCACTCCGAGCCGATGAAGAACAGCAAGAA	1639
Db	1432	TTAATCGCTGTATGTGTGTAAAGTCAAGTCACTCTGTGCCAATGAAAGAACAGCAAGAA	1491
OY	1640	CCAGACTTCAGCAGCCAGCCGCGCTGTGCAAGCTGACCAACGATCCCTCGGAGA	1699
Db	1492	CCAGACTTCAGCAGCCAGCCGCGCTGTGCAAGCTGACCAACGATCCCTCGGAGA	1551
OY	1700	CAGGTAACAGTTTCGGCTGAGTCCAGCTCTCTCAGTAACTCCAAACCCCGCTGTAGG	1759
Db	1552	CAGGTAACAGTTTCGGCTGAGTCCAGCTCTCTCAGTAACTCCAAACCCCGCTGTAGG	1611
OY	1760	ATTAACAACGCTCTCTTCAACGGCAGACACCCCAAGCTGGCGAGGGGTCTCGAGTAT	1819
Db	1612	ATTAACAACGCTCTCTTCAACGGCAGACACCCCAAGCTGGCGAGGGGTCTCGAGTAT	1671
OY	1820	GAACCTTCAGAGAGACCCAAATGGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCC	1879
Db	1672	GAACCTTCAGAGAGACCCAAATGGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCC	1731
OY	1880	CTGGAGAAAGTTCCTTTGGGCAAGTGTCAATGCGGAAAGCATGTGGGAATTTGACAAAGAC	1939
Db	1732	CTGGAGAAAGTTCCTTTGGGCAAGTGTCAATGCGGAAAGCATGTGGGAATTTGACAAAGAC	1791
OY	1940	AAGCCCAAGAGGCGGTCAACGCTGCGCGTGAAGATGTTGAAGATGATGCCACAGAGAA	1999
Db	1792	AAGCCCAAGAGGCGGTCAACGCTGCGCGTGAAGATGTTGAAGATGATGCCACAGAGAA	1851
OY	2000	GACCTTTCGATCTGTGATGTCAGAGATGAGATGATGAAGATGATTTGGGAAACACAGAAAT	2059
Db	1852	GACCTTTCGATCTGTGATGTCAGAGATGAGATGATGAAGATGATTTGGGAAACACAGAAAT	1911
OY	2060	ATCATTAATCTTCTTGAGACCTGCAACACAGATGGGCTCTCTATGTCAATGTTGAGTAT	2119
Db	1912	ATCATTAATCTTCTTGAGACCTGCAACACAGATGGGCTCTCTATGTCAATGTTGAGTAT	1971
OY	2120	GCTCTTAAAGGGAACCTCCGAAATATACCTCCGAGCCGGAAGGCCACCCGGGATGGAGTAC	2179
Db	1972	GCTCTTAAAGGGAACCTCCGAAATATACCTCCGAGCCGGAAGGCCACCCGGGATGGAGTAC	2031
OY	2180	TCTTATGACATTAACCGTGTCTTGAGAGCAGATGACCTTCAAGAGCTTGGTGTCAATGC	2239
Db	2032	TCTTATGACATTAACCGTGTCTTGAGAGCAGATGACCTTCAAGAGCTTGGTGTCAATGC	2091
OY	2240	ACCTTACAGCTGCGCCAGCGATGAGTACTTGGCTTCCCAAAAATGATTTCAATGAGAT	2299
Db	2092	ACCTTACAGCTGCGCCAGCGATGAGTACTTGGCTTCCCAAAAATGATTTCAATGAGAT	2151
OY	2300	TTAGCAGCCAGAAATCTTTTGGTAAACAGAAACAAATGTATGAATAATGACACTTGGGA	2359
Db	2152	TTAGCAGCCAGAAATCTTTTGGTAAACAGAAACAAATGTATGAATAATGACACTTGGGA	2211
OY	2360	CTGCGCAGAGATATCAACAATATAGACTTATCAAAAAGACCAACAAATGGCGGCTTCCA	2419
Db	2212	CTGCGCAGAGATATCAACAATATAGACTTATCAAAAAGACCAACAAATGGCGGCTTCCA	2271
OY	2420	GTCAAGTGAATGGCTTCAGAAAGCCCTGTTGATAGATTAACATCAAGTGAATGC	2479
Db	2272	GTCAAGTGAATGGCTTCAGAAAGCCCTGTTGATAGATTAACATCAAGTGAATGC	2331
OY	2480	TGGTCTTGGGGTGTAAATGTGGAGATCTTCACTTAAGGGGGCTGGCCCTAACCAAGG	2539

Db	2332	TGTCCTTCGGGGGAGTTAAAGTGGAGACCTTCACCTTAAAGGGGCGCTCGCCCTACCCAGGG	2391
OY	2540	ATTCCCGTGGAGGAACTTTTAACTCTGTGAAGGAAGAACAACAATAGGATTAACCGACGC	2599
Db	2392	ATTCCCGTGGAGGAACTTTTAACTCTGTGAAGGAAGAACAACAATAGGATTAACCGACGC	2451
OY	2600	AACGTGCACAACGAACTGTACATGATGATGAGGAGACTGTGGCAATGACAGTGCCTCCAG	2659
Db	2452	AACGTGCACAACGAACTGTACATGATGATGAGGAGACTGTGGCAATGACAGTGCCTCCAG	2511
OY	2660	AGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATGGAATTCTCACTTCAACAACCAAT	2719
Db	2512	AGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATGGAATTCTCACTTCAACAACCAAT	2571
OY	2720	GAGGAATTCCTGGACCTCAAGCCAACCTCTGGAAGAATTCACACCTAGTTAACCTGACACA	2779
Db	2572	GAGGAATTCCTGGACCTCAAGCCAACCTCTGGAAGAATTCACACCTAGTTAACCTGACACA	2631
OY	2780	AGAAGTCTGTCTTCAGAGAGATGATCTGTTTTCTCCAGACCCCATGCCCTTAACGA	2839
Db	2632	AGAAGTCTGTCTTCAGAGAGATGATCTGTTTTCTCCAGACCCCATGCCCTTAACGA	2691
OY	2840	CCATGCTCTCTCAAGTATCCACAATTAACGGCAGTGTAAACATGAAATGACTGTGCT	2899
Db	2692	CCATGCTCTCTCTCAAGTATCCACAATTAACGGCAGTGTAAACATGAAATGACTGTGCT	2751
OY	2900	GCGTGTCCCAACAGGACAGACACTGGGAACTTAGCTACACTGACAGGAGAGACATATCC	2959
Db	2752	GCGTGTCCCAACAGGACAGACACTGGGAACTTAGCTACACTGACAGGAGAGACATATCC	2811
OY	2960	TCCCAAGACTGTGTCTCCACTTGTATATATGATCAGAGAGATTAATTAATTGGAAAAG	3019
Db	2812	TCCCAAGACTGTGTCTCCACTTGTATATATGATCAGAGAGATTAATTAATTGGAAAAG	2874
OY	3020	TAAATCAGATATGTGTAAAGATTTATACAGTTGAAAATCTGTAAATCTTCCCAAGAGAG	3079
Db	2872	TAAATCAGATATGTGTAAAGATTTATACAGTTGAAAATCTGTAAATCTTCCCAAGAGAG	2931
OY	3080	AAGAAAGTTTTCTGAGCAGTGGACCTGC	3106
Db	2932	AAGAAAGTTTTCTGAGCAGTGGACCTGC	2998

Search completed: October 2, 2006, 21:52:09
Job time : 17277 secs

Job time : 17277 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 16:41:08 ; Search time 1747 Seconds
(without alignments)
12395.995 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106
1 cccgcgagcaaaatttcgtg.....ttcttgagcagtgactgc 3106

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 348612431 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3106	100.0	3106	14	AEC02075
2	3025.4	97.4	4612	14	ADZ13046
3	3025.4	97.4	5003	14	ADZ13052
4	3013.2	97.0	4574	12	ADL61208
5	3013.2	97.0	4574	13	AD080247
6	3013.2	97.0	4574	13	ADP81631
7	3013.2	97.0	4574	14	AE81172
8	3013.2	97.0	4574	15	AEF06407
9	2967.4	95.5	4485	14	ADZ13094
10	2904.2	93.5	4587	13	ACF91630
11	2904.2	93.5	4587	14	AE81171
12	2904.2	93.5	4587	14	AE81171
13	2890.2	93.1	4609	14	ADZ13056
14	2890.2	93.1	5000	14	ADZ13044
15	2882.2	92.8	4990	14	ADZ13114
16	2867.8	92.3	4607	14	ADZ13088
17	2867.8	92.3	4998	14	ADZ13108
18	2849.4	91.7	4575	12	ADN03975

19	2849.4	91.7	4575	13	ACF91634	ACF91634 Human SIR
20	2849.4	91.7	4575	14	ADY15138	ADY15138 DNA encod
21	2849.4	91.7	4575	14	AE81175	AE81175 Human fib
22	2824.2	90.9	4472	14	ADZ13070	ADZ13070 Human can
23	2806.2	90.3	3080	10	ADH63071	ADH63071 Human fib
24	2781.8	89.6	4268	6	ABL64983	ABL64983 Lung canc
25	2781.8	89.6	4268	6	ABL66289	ABL66289 Lung canc
26	2781.8	89.6	4268	6	ABL68594	ABL68594 Kidney ca
27	2781.8	89.6	4268	10	ADH63049	ADH63049 Human fib
28	2780.2	89.5	5080	14	ADZ13078	ADZ13078 Human can
29	2765.8	89.0	4697	14	ADZ13080	ADZ13080 Human can
30	2765.8	89.0	5088	14	ADZ13062	ADZ13062 Human can
31	2747.4	88.5	4667	6	ABV94024	ABV94024 Breast ca
32	2747.4	88.5	4667	13	ACF91639	ACF91639 Human SIR
33	2747.4	88.5	4667	14	AE81180	AE81180 Human fib
34	2747.4	88.5	4696	12	ADQ24133	ADQ24133 Human sof
35	2728.6	87.8	2923	10	ADH63066	ADH63066 Human fib
36	2723.4	87.7	2826	10	ADH63067	ADH63067 Human fib
37	2722	87.6	2868	10	ADH63065	ADH63065 Human fib
38	2722	87.6	2941	10	ADH63064	ADH63064 Human fib
39	2709.4	87.2	3416	2	AAQ21004	AAQ21004 bek recep
40	2641.4	85.0	3241	14	ADZ13082	ADZ13082 Human can
41	2641.4	85.0	3632	14	ADZ13106	ADZ13106 Human can
42	2639.6	85.0	3219	13	ACF91636	ACF91636 Human SIR
43	2639.6	85.0	3219	14	AE81177	AE81177 Human fib
44	2556.8	82.3	3248	12	ADQ49088	ADQ49088 Human ded
45	2506.2	80.7	3238	14	ADZ13050	ADZ13050 Human can

ALIGNMENTS

RESULT 1	
AEC02075	
ID	AEC02075 standard; mRNA; 3106 BP.
AC	AEC02075;
XX	
DT	20-OCT-2005 (first entry)
XX	
DE	Nucleotide sequence of keratinocyte growth factor receptor.
XX	
KW	gene expression profile; metanephric mesenchyme cell;
KW	renal progenitor cell; cell therapy; tissue regeneration; nephrotropic;
KW	genitourinary disease; renal failure; genetic marker; ss;
KW	keratinocyte growth factor receptor.
XX	
OS	Homo sapiens.
XX	
PN	WO2005075636-A1.
XX	
PD	18-AUG-2005.
XX	
PF	09-FEB-2005; 2005WO-AU000162.
XX	
PR	09-FEB-2004; 2004AU-00900600.
XX	
PA	(UYOU) UNIV QUEENSLAND.
PA	(MONU) UNIV MONASH.
XX	
PI	Little M, Challen G;
XX	
DR	WPI; 2005-564566/57.
XX	
PT	Identifying gene expression profile associated with metanephric
PT	mesenchyme development, comprises identifying genes e.g. sca-1 that are
PT	differentially expressed in metanephric mesenchyme cells at particular
PT	stage of embryonic development.
XX	
XX	
PS	Example 2; Fig 8; 15pp; English.
XX	
CC	The specification describes a method of identifying a gene expression
CC	profile associated with metanephric mesenchyme development, e.g. in renal

CC progenitor cells. The method comprises identifying one or more genes that
CC are differentially expressed at least 1.8 fold by one or more metanephric
CC mesenchyme cells at a particular stage of embryonic development compared
CC to one or more intermediate mesoderm cells. The method of the invention
CC is useful for identifying a metanephric mesenchyme cell. These cells are
CC useful for in vitro and in vivo generation of renal tissue, and are
CC useful for treating disease such as acute renal failure, kidney
CC transplant dysfunction and/or chronic renal failure. ABC02045-ABC02126
CC represent human genetic markers of metanephric mesenchyme/renal
CC progenitor cells.

XX Sequence 3106 BP; 825 A; 785 C; 843 G; 653 T; 0 U; 0 Other;

Query Match 100.0%; Score 3106; DB 14; Length 3106;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGCGAAGAAAGTTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTGTTCC 60
DB 1 CCGGCGAAGAAAGTTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTGTTCC 60
QY 61 CAAATCCGAGGAGCGCCGCGGCGTCAATGCGCTCTCCGACGCTGGGATACGGGTGA 120
DB 61 CAAATCCGAGGAGCGCCGCGGCGTCAATGCGCTCTCCGACGCTGGGATACGGGTGA 120
QY 121 AGCCCGGAGGCTTGTGCGCGCGGAGAACCAAGAACCACTTCTTGTGAGTTGC 180
DB 121 AGCCCGGAGGCTTGTGCGCGCGGAGAACCAAGAACCACTTCTTGTGAGTTGC 180
QY 181 TCCCGCGAACCCCGGCGTGTGCTTCTTCATCCGACCCAGCGGGGCGGAGAAC 240
DB 181 TCCCGCGAACCCCGGCGTGTGCTTCTTCATCCGACCCAGCGGGGCGGAGAAC 240
QY 241 ACAGGTGCGGAGAGCGTTGCAATCAAGTGACTGACGACGACGCGCTCGTT 300
DB 241 ACAGGTGCGGAGAGCGTTGCAATCAAGTGACTGACGACGACGCGCTCGTT 300
QY 301 CCTGAGCCCAACCGGAGTGAAGGCAATTCGCGTATGTCATGCCGTGAGAGAAAGTGTGA 360
DB 301 CCTGAGCCCAACCGGAGTGAAGGCAATTCGCGTATGTCATGCCGTGAGAGAAAGTGTGA 360
QY 361 GATGGAATTAAAGTTCACATGAGATATGGAAGGACGCGGGAATGTACCGTTAACAT 420
DB 361 GATGGAATTAAAGTTCACATGAGATATGGAAGGACGCGGGAATGTACCGTTAACAT 420
QY 421 GGTCACTGGGAGTCTGTTTCATCTGCGTGTCTGTGATCCATGCAACCTTGTCCCTGCG 480
DB 421 GGTCACTGGGAGTCTGTTTCATCTGCGTGTCTGTGATCCATGCAACCTTGTCCCTGCG 480
QY 481 CCGGCGCTCTTCAATGTTAGTGAATACCACTTGAAGCCAGAAAGGCAACCAACCA 540
DB 481 CCGGCGCTCTTCAATGTTAGTGAATACCACTTGAAGCCAGAAAGGCAACCAACCA 540
QY 541 ATACCAAAATCTCAACCAAGATGATGCGTGGCGCCAGGGGAAGTCCGTAGAAGGTGCG 600
DB 541 ATACCAAAATCTCAACCAAGATGATGCGTGGCGCCAGGGGAAGTCCGTAGAAGGTGCG 600
QY 601 CTGCTGTTGAAAGATGCGCGCTGATCACTTGAAGTGAAGTGGGTGCACTTTGGGGCC 660
DB 601 CTGCTGTTGAAAGATGCGCGCTGATCACTTGAAGTGAAGTGGGTGCACTTTGGGGCC 660
QY 661 CAAACAATAGGACAGTGTCTTATTTGGGAGTACTTGACAGATTAAGGGCCCAACCTAGAGA 720
DB 661 CAAACAATAGGACAGTGTCTTATTTGGGAGTACTTGACAGATTAAGGGCCCAACCTAGAGA 720
QY 721 CTGCGGCTCTATGCTTGTACTGCACTAGAGCTGTGAAGTGAAGCTTGTGATCTTCAAT 780
DB 721 CTGCGGCTCTATGCTTGTACTGCACTAGAGCTGTGAAGTGAAGCTTGTGATCTTCAAT 780
QY 781 GGTGAATGTCAAGATGCACTTCATCCGAGATGATGAGGATGACACCGATGGTGGGA 840
DB 781 GGTGAATGTCAAGATGCACTTCATCCGAGATGATGAGGATGACACCGATGGTGGGA 840

QY 841 AGATTTGTGAGTGGAACAGTAAACAAGAGACCACTATGAGCAACACAGAAA 900
DB 841 AGATTTGTGAGTGGAACAGTAAACAAGAGACCACTATGAGCAACACAGAAA 900
QY 901 GATGAAAAAGCGCTCACTGCTGTGCTGCGGCAACCTGTCAAGTTTGGTCCGACG 960
DB 901 GATGAAAAAGCGCTCACTGCTGTGCTGCGGCAACCTGTCAAGTTTGGTCCGACG 960
QY 961 CCGGGGAAACCAATGCCAACATGCGGTGTGAAAAACGGGAAGGATTTAAACAGA 1020
DB 961 CCGGGGAAACCAATGCCAACATGCGGTGTGAAAAACGGGAAGGATTTAAACAGA 1020
QY 1021 GCATGCAATTTGAGGCTACAGGTACGAACAGCACTGAGCTCATTTATGAAAGTGT 1080
DB 1021 GCATGCAATTTGAGGCTACAGGTACGAACAGCACTGAGCTCATTTATGAAAGTGT 1080
QY 1081 GGTCCATCTGACAAAGGAAATTAATCTGTATGAGAAATGATACGGGTTCATCA 1140
DB 1081 GGTCCATCTGACAAAGGAAATTAATCTGTATGAGAAATGATACGGGTTCATCA 1140
QY 1141 TCAACAGTACCACTGATGTTGTGAGAGATGCTTCAACCGGCTCTTCAAGCGG 1200
DB 1141 TCAACAGTACCACTGATGTTGTGAGAGATGCTTCAACCGGCTCTTCAAGCGG 1200
QY 1201 ACTGCGGAAATGCTTCCACAGTGTGAGAGACGTAAGATTTGTCTGCAAGTTTA 1260
DB 1201 ACTGCGGAAATGCTTCCACAGTGTGAGAGACGTAAGATTTGTCTGCAAGTTTA 1260
QY 1261 CAGTATGCCAGCCCAATCAGTGTATCAAGCACTGTGAAAAAAGCGAGTAAATA 1320
DB 1261 CAGTATGCCAGCCCAATCAGTGTATCAAGCACTGTGAAAAAAGCGAGTAAATA 1320
QY 1321 CCGGCGCCAGCGGCTGCTTACTTCAAGTTTCAAGCACTGGGATTAATGTTCCAA 1380
DB 1321 CCGGCGCCAGCGGCTGCTTACTTCAAGTTTCAAGCACTGGGATTAATGTTCCAA 1380
QY 1381 TGCAGAAAGTGTGCTGTCTGTCAATGTGACCGAGCGGATGTGGGAAATATATATGTA 1440
DB 1381 TGCAGAAAGTGTGCTGTCTGTCAATGTGACCGAGCGGATGTGGGAAATATATATGTA 1440
QY 1441 GGTCTCCAAATTATAGGCGAGGCCAACCAAGTCTGCTGCTCACTGTCTGCCAAACA 1500
DB 1441 GGTCTCCAAATTATAGGCGAGGCCAACCAAGTCTGCTGCTCACTGTCTGCCAAACA 1500
QY 1501 GCAAGCGCTGGAAGAAAAAGAGATTACGCTTCCCAAGCTACCTGGAATGCCAT 1560
DB 1501 GCAAGCGCTGGAAGAAAAAGAGATTACGCTTCCCAAGCTACCTGGAATGCCAT 1560
QY 1561 TTACTGCAATAGGAGTCTTATATGCGCTGTATGAGTGAAGTCACTCTGTGCGAAT 1620
DB 1561 TTACTGCAATAGGAGTCTTATATGCGCTGTATGAGTGAAGTCACTCTGTGCGAAT 1620
QY 1621 GAAAGACAGACCAAGAACCAAGCTTCAAGACCAAGCGGCTGTGCAACAGCTGACAA 1680
DB 1621 GAAAGACAGACCAAGAACCAAGCTTCAAGACCAAGCGGCTGTGCAACAGCTGACAA 1680
QY 1681 AGGTATCCCTCTGCGAGACAGGTAAACATTTGCGTGAAGTCAAGTCTTCAAGAAC 1740
DB 1681 AGGTATCCCTCTGCGAGACAGGTAAACATTTGCGTGAAGTCAAGTCTTCAAGAAC 1740
QY 1741 CAAACACCGGCTGTGAGATTAACAACAGCGCTTCTTCAAGGAGCAACCCCATGCT 1800
DB 1741 CAAACACCGGCTGTGAGATTAACAACAGCGCTTCTTCAAGGAGCAACCCCATGCT 1800
QY 1801 GGTGAGGAGTCTGAGTATGAATTTCAAGGACCAAAATGGAGATTCCAAGAGATTA 1860
DB 1801 GGTGAGGAGTCTGAGTATGAATTTCAAGGACCAAAATGGAGATTCCAAGAGATTA 1860
QY 1861 GCTGACACTGGGAGAGCCCTGAGAGAGAGTGTCTTTGGCAAGTGTATATGGCGGAAC 1920
DB 1861 GCTGACACTGGGAGAGCCCTGAGAGAGAGTGTCTTTGGCAAGTGTATATGGCGGAAC 1920
QY 1921 AGTGGAAATTGAACAAGACCAAGGAGGCGGTCAAGTGTGAGTGTGA 1980

```

Db      1921  AGTGGGATTTGACAAAGACGAGCCGAGAGGCGGTGACCGGTGGAGATGTTGAA 1980
Qy      1981  AGATGATGCCACAGAGAAAGACCTTTCTGATCTGCTGTGACAGATGAGATGATGAAGAT 2040
Db      1981  AGATGATGCCACAGAGAAAGACCTTTCTGATCTGCTGTGACAGATGAGATGATGAAGAT 2040
Qy      2041  GATTGGGAAACAGAAATATCATTAATCTTTGAGGCTTGCACACAGATGGGCTCTT 2100
Db      2041  GATTGGGAAACAGAAATATCATTAATCTTTGAGGCTTGCACACAGATGGGCTCTT 2100
Qy      2101  CTATGTCATAGTATGATGCTCTTAAAGCACTCCGAGAAATCTCCAGGCCGAG 2160
Db      2101  CTATGTCATAGTATGATGCTCTTAAAGCACTCCGAGAAATCTCCAGGCCGAG 2160
Qy      2161  GCCACCCGGAGTAGTACTCTTATGACATTAACCGTGTCTTGAGAGACGATGACTT 2220
Db      2161  GCCACCCGGAGTAGTACTCTTATGACATTAACCGTGTCTTGAGAGACGATGACTT 2220
Qy      2221  CAAGACTTGGTGTCAATGACCTTACAGCTGGCCAGACGATGAGATCTTGGCTTCCA 2280
Db      2221  CAAGACTTGGTGTCAATGACCTTACAGCTGGCCAGACGATGAGATCTTGGCTTCCA 2280
Qy      2281  AAAATGATTTATGAGATTTAGACGACGAAATGTTTGGTAAACAGAAACATGTGAT 2340
Db      2281  AAAATGATTTATGAGATTTAGACGACGAAATGTTTGGTAAACAGAAACATGTGAT 2340
Qy      2341  GAAATATGACAGACTTTGACTCGCCAGAGATATCAACATATGACTATTAACAAAAGAC 2400
Db      2341  GAAATATGACAGACTTTGACTCGCCAGAGATATCAACATATGACTATTAACAAAAGAC 2400
Qy      2401  CACCAATGGGGGGCTTCCAGTCAAGTGAATGCTCCAGAGCCCTGTTTGAATAGATTA 2460
Db      2401  CACCAATGGGGGGCTTCCAGTCAAGTGAATGCTCCAGAGCCCTGTTTGAATAGATTA 2460
Qy      2461  CACTCATCAGAGTATGCTGTGCTCTTGGGGTGTATATGAGGAGATCTTCACTTTAGG 2520
Db      2461  CACTCATCAGAGTATGCTGTGCTCTTGGGGTGTATATGAGGAGATCTTCACTTTAGG 2520
Qy      2521  GGGGCTCGCTTACCAGGAGATTCGCTGAGAGAACTTTTAAAGTGTCTGAAGAGACA 2580
Db      2521  GGGGCTCGCTTACCAGGAGATTCGCTGAGAGAACTTTTAAAGTGTCTGAAGAGACA 2580
Qy      2581  CAGATGATTAAGCCAGCCACTGCAACCAAGTGAATGATGAGAGAGCTGTG 2640
Db      2581  CAGATGATTAAGCCAGCCACTGCAACCAAGTGAATGATGAGAGAGCTGTG 2640
Qy      2641  GCATGAGTGGCTCCGAGAGACCAAGTTCAGAGATGATGAGAGAGCTTGGATCGAAT 2700
Db      2641  GCATGAGTGGCTCCGAGAGACCAAGTTCAGAGATGATGAGAGAGCTTGGATCGAAT 2700
Qy      2701  TCTGACTCTCAACCAATGAGAAATCTTGAAGCTTGAAGAGCTTGAAGAGATTC 2760
Db      2701  TCTGACTCTCAACCAATGAGAAATCTTGAAGCTTGAAGAGCTTGAAGAGATTC 2760
Qy      2761  ACCATGTTACCTTCAACCAAGTTCCTTGAAGAGATGATGATGATGATGATGATGAT 2820
Db      2761  ACCATGTTACCTTCAACCAAGTTCCTTGAAGAGATGATGATGATGATGATGATGAT 2820
Qy      2821  AGACCCCATGCTTACCAAGTTCCTTGAAGAGATGATGATGATGATGATGATGATGAT 2880
Db      2821  AGACCCCATGCTTACCAAGTTCCTTGAAGAGATGATGATGATGATGATGATGATGAT 2880
Qy      2881  AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
Db      2881  AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
Qy      2941  TGACAGGAGAGACATGCTTCCAGAGCTTGTGCTTCACTTGTATATATGATGATGAT 3000
Db      2941  TGACAGGAGAGACATGCTTCCAGAGCTTGTGCTTCACTTGTATATATGATGATGAT 3000
Qy      3001  GAGTAAATTAATGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3060

```

```

Db      3001  GAGTAAATTAATGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
Qy      3061  TAATCTTCCGAGAGAGAGAAAGTTCGTGAGACAGTGAATTC 3106
Db      3061  TAATCTTCCGAGAGAGAGAAAGTTCGTGAGACAGTGAATTC 3106
Qy      3061  TAATCTTCCGAGAGAGAGAAAGTTCGTGAGACAGTGAATTC 3106

RESULT 2
ADZ13046
ID ADZ13046 standard; cDNA; 4612 BP.
XX
XX ADZ13046;
AC
XX
XX 16-JUN-2005 (first entry)
DT
XX
XX Human cancer-associated cDNA #164.
DE
XX
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KM cytostatic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX NC02005031001-A2.
PN
XX
XX 07-APR-2005.
PD
XX
XX 23-SEP-2004; 2004MO-US031617.
PF
XX
XX 23-SEP-2003; 2003US-00669920.
PR
XX
XX (CHIR ) CHIRON CORP.
PA
XX
XX Morris DM, Malandro MS;
PI
XX
XX WPI; 2005-273395/28.
DR
XX
XX P-PSDB; ADZ13047.
DR
XX
XX
XX
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
PT
XX
XX Disclosure; SEQ ID NO 566; 198bp; English.
PS
XX
XX
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated cDNA of the
CC invention.
XX
XX
XX Sequence 4612 BP; 1238 A; 1090 C; 1165 G; 1119 T; 0 U; 0 Other;
SQ
Query Match 97.4%; Score 3025.4; DB 14; Length 4612;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

```


QY 1 CCCGCGAGCAAAAGTTTGTGTGAGGCAACG-CAAGCTGAGTCTTCTCTCTGTTCC 59
DB 187 CTCGCGAGCAAAAGTTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTCTGTTCC 246
QY 60 CCAAAATCCGAGGGCAACCCCGGGGCGTCAATG---GGGCTCTCCGAGCGTGGGGATACGC 116
DB 247 CCAAAATCCGAGGGCAACCCCGGGGCGTCAATGCCCCGCTCTCCGAGGCTGGGGATACGC 306
QY 117 GTGAAGCCCGGAGAGGCTGGCGCCGGGGAAGAACCCAAAGGACACTCTCTGTGCGTTTGGAG 176
DB 307 GTGAAGCCCGGAGAGGCTGGCGCCGGGGAAGAACCCAAAGGACACTCTCTGTGCGTTTGGAG 366
QY 177 TTGCTCCCCGCAACCCCGGGCTGTGCTGCTTCTTCATCCCGAACCCAGCGGGGC -CGGG 235
DB 367 TTGCTCCCCCAACCCCGGGCTGTGCTGCTTCTTCATCCCGAACCCAGCGGGGC -CGGG 426
QY 236 ACAAACAAGTTCGCGAGAGGCGTTGCAATGCAAGTGAAGCTGAGAGCAAGC -GCAAGCGC 294
DB 427 ACAAACAAGTTCGCGAGAGGCGTTGCAATGCAAGTGAAGCTGAGAGCAAGC -GCAAGCGC 486
QY 295 TCGGTTCTGAGCCCAACCGCA -GCTGAAGGCAATTGCGCGTATGTCATGCCCCGTAGAGAA 353
DB 487 TCGGTTCTGAGCCCAACCGCAAGGCTGAAAGGCAATTGCGCGTATGTCATGCCCCGTAGAGAA 546
QY 354 GTGTGCAAGTGGATTTAACTGTCATGAGATATGAGAGAGACCGGGGATTTGTACCG 413
DB 547 GTGTGCAAGTGGATTTAACTGTCATGAGATATGAGAGAGACCGGGGATTTGTACCG 606
QY 414 TAAACCAATGTCAGCTGGGGGTGTGTTCACTGCGTGGCGTGTGTCACATAGGCAACCTTGT 473
DB 607 TAAACCAATGTCAGCTGGGGGTGTGTTCACTGCGTGGCGTGTGTCACATAGGCAACCTTGT 666
QY 474 CCTGCGCCCGGCTCTCTTCAAGTTTAAAGTTAGAGATACCACTTTAAGCCAAAGAGCAC 533
DB 667 CCTGCGCCCGGCTCTCTTCAAGTTTAAAGTTAGAGATACCACTTTAAGCCAAAGAGCAC 726
QY 534 CAACCAAAATACCAAAATCTTCAACAGAAAGTGAACGTGGCTGGGCCAAGGGGAAATCGCTAG 593
DB 727 CAACCAAAATACCAAAATCTTCAACAGAAAGTGAACGTGGCTGGGCCAAGGGGAAATCGCTAG 786
QY 594 AGGTGCGCTGCGCTGTTGAAGATGCGCGCGTGAATCAAGTTGAGACTAAGATGGGGGTGACT 653
DB 787 AGGTGCGCTGCGCTGTTGAAGATGCGCGCGTGAATCAAGTTGAGACTAAGATGGGGGTGACT 846
QY 654 TGGGGCCCAACAATAGGACAGTGTCTTATGAGGAGTACTTGACAGATTAAGGCGCCAC 713
DB 847 TGGGGCCCAACAATAGGACAGTGTCTTATGAGGAGTACTTGACAGATTAAGGCGCCAC 906
QY 714 CTAGAGACTCGGCTCTTATGCTTGTATCTGCGAGTGAAGCTGTAGACAGTGAACCTTGT 773
DB 907 CTAGAGACTCGGCTCTTATGCTTGTATCTGCGAGTGAAGCTGTAGACAGTGAACCTTGT 966
QY 774 ACTTCAAGTGAATGTCAAGATGCGCATCTCATTCGAGATGAATGAGATGACACGATG 833
DB 967 ACTTCAAGTGAATGTCAAGATGCGCATCTCATTCGAGATGAATGAGATGACACGATG 1026
QY 834 GTGCGGAAGATTTTGTCAGTGAAGAACATTAACAAGAGACCACTACTGTGACCAACA 893
DB 1027 GTGCGGAAGATTTTGTCAGTGAAGAACATTAACAAGAGACCACTACTGTGACCAACA 1086
QY 894 CAGAAAAGATGAAAAGCGGCTCAATGCTGTGCTGGGCCMAACGTCAAAAGTTTGCT 953
DB 1087 CAGAAAAGATGAAAAGCGGCTCAATGCTGTGCTGGGCCMAACGTCAAAAGTTTGCT 1146
QY 954 GCCCAGCGGGGGGAAACCAATGCAACATGCGGTGAGTGAAGAAACGGGAGGAGTTTA 1013
DB 1147 GCCCAGCGGGGGGAAACCAATGCAACATGCGGTGAGTGAAGAAACGGGAGGAGTTTA 1206
QY 1014 AGCAGAGCAATGCAATGAGGCTTACAGAGTACGAAACAGCACTGAGAGCTCATTAATG 1073
DB 1207 AGCAGAGCAATGCAATGAGGCTTACAGAGTACGAAACAGCACTGAGAGCTCATTAATG 1266
QY 1074 AAAGTGTGTCCATCTGACAAAGGAAATTAATCCTGTGTAGTGAAGATGAATACGGGT 1133

DB 1267 AAAGTGTGTCCATCTGACAAAGGAAATTAATCCTGTGTGTGAGAGATGAATACGGGT 1326
QY 1134 CCATCAATCAACAGTACCACTGAGATGTTGTGAGCGATGCGCTCAACCGGCCATCTCC 1193
DB 1327 CCATCAATCAACAGTACCACTGAGATGTTGTGAGCGATGCGCTCAACCGGCCATCTCC 1386
QY 1194 AAGCGGACTGCGGGCAATGCTCTCAAGTGTGAGAGAGACCTAAGTTTGTCTCA 1253
DB 1387 AAGCGGACTGCGGGCAATGCTCTCAAGTGTGAGAGAGACCTAAGTTTGTCTCA 1446
QY 1254 AAGTTTACAGTATGCCCCAGCCCCCATCTCAGTGTATCAAGCCTGTGAAAAGACGCA 1313
DB 1447 AAGTTTACAGTATGCCCCAGCCCCCATCTCAGTGTATCAAGCCTGTGAAAAGACGCA 1506
QY 1314 GTTAAATACGGGCCGAGCGGGCTGCTTCAAGGTTCTCAAGCACTCGGGGATTAATA 1373
DB 1507 GTTAAATACGGGCCGAGCGGGCTGCTTCAAGGTTCTCAAGCACTCGGGGATTAATA 1566
QY 1374 GTTCCAAATGCAAGATGCTGCTGTCTTCAATGTGACCGAAGCGGATGCTGGGGAATATA 1433
DB 1567 GTTCCAAATGCAAGATGCTGCTGTCTTCAATGTGACCGAAGCGGATGCTGGGGAATATA 1626
QY 1434 TATGTAAAGTCTCAATTATATAGGAGGCAACCAAGTCTGCTCACTGTCTTC 1493
DB 1627 TATGTAAAGTCTCAATTATATAGGAGGCAACCAAGTCTGCTCACTGTCTTC 1686
QY 1494 CAAAACAGCAACGCTGTGAGAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGAA 1553
DB 1687 CAAAACAGCAACGCTGTGAGAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGAA 1746
QY 1554 TAGCCATTTACATGCAATAGGGGCTCTTAAATGCGCGTATGAGTGAACAGTATCTGT 1613
DB 1747 TAGCCATTTACATGCAATAGGGGCTCTTAAATGCGCGTATGAGTGAACAGTATCTGT 1806
QY 1614 GCGGAATGAAGAAACAGCAACAGAAAGCAGACTTGACAGCCAGCGGCTGTGCAAAAC 1673
DB 1807 GCGGAATGAAGAAACAGCAACAGAAAGCAGACTTGACAGCCAGCGGCTGTGCAAAAC 1866
QY 1674 TGAACCAAGTATCCCTGTCGAGACAGATTAAC---AGTTTGGCTGATGTCAGTTC 1729
DB 1867 TGAACCAAGTATCCCTGTCGAGACAGATTAAC---AGTTTGGCTGATGTCAGTTC 1926
QY 1730 TCCATGAATTCACAACCCCGCTGTGAGAGATTAACAACGCTCTCTTCAACGAGAAC 1789
DB 1927 TCCATGAATTCACAACCCCGCTGTGAGAGATTAACAACGCTCTCTTCAACGAGAAC 1986
QY 1790 ACCCCATGCTGGCAGGGGCTCTCCAGTATGAACCTTCCAGAGAACCCAAATGGAGTT 1849
DB 1987 ACCCCATGCTGGCAGGGGCTCTCCAGTATGAACCTTCCAGAGAACCCAAATGGAGTT 2046
QY 1850 CCAAGAGATAGCTGAACACTGGGCAAGCCCTGTGGGAAGGTTGCTTTGGGCAATGCTG 1909
DB 2047 CCAAGAGATAGCTGAACACTGGGCAAGCCCTGTGGGAAGGTTGCTTTGGGCAATGCTG 2106
QY 1910 ATGCGCGAAGCACTGGGAATTTGACAAAGCAAGCCCCAAGAGGCGGTCAACGTCGCGTG 1969
DB 2107 ATGCGCGAAGCACTGGGAATTTGACAAAGCAAGCCCCAAGAGGCGGTCAACGTCGCGTG 2166
QY 1970 AAGATGTTGAAGATGATGCTCAAGAGAAAGACTTTCATCTGTGTCAAGATGAG 2029
DB 2167 AAGATGTTGAAGATGATGCTCAAGAGAAAGACTTTCATCTGTGTCAAGATGAG 2226
QY 2030 ATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTCTTGAAGCTGCAACAG 2089
DB 2227 ATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTCTTGAAGCTGCAACAG 2286
QY 2090 GATGGGCTCTCTATGTCATATGTTGATGATGCTCTTAAAGGCAACCTCGAGAAATACCTC 2149
DB 2287 GATGGGCTCTCTATGTCATATGTTGATGATGCTCTTAAAGGCAACCTCGAGAAATACCTC 2346
QY 2150 CGAGCCCGAGGCGCAACCGGGATGAGTACTCCTATGACATTAACCGTGTCTGAGAG 2209

```

Db      2347 CGAGCCCGGAGGCGACCCGGGATGAGTACTCTATGACATTAACGTTGTTCCAGAGAG 2406
Qy      2210 CAGATGACCTTCAAGACCTTGTGTCTATGCACTTAACAGCTGGCCAGACGGAATGAGATAC 2269
Db      2407 CAGATGACCTTCAAGACCTTGTGTCTATGCACTTAACAGCTGGCCAGACGGAATGAGATAC 2466
Qy      2270 TTGGCTCCCAAAAATGATTTATTCAGATTTAGCAGCAGAAATGTTTGTATACAGA 2329
Db      2467 TTGGCTCCCAAAAATGATTTATTCAGATTTAGCAGCAGAAATGTTTGTATACAGA 2526
Qy      2330 AACATGATGATGATAATAGAGACTTTGATCTGCCAGAGATATCACAATATATAGTAT 2389
Db      2527 AACATGATGATGATAATAGAGACTTTGATCTGCCAGAGATATCACAATATATAGTAT 2586
Qy      2390 TACAAAAAGACCAACCAATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAGAGCCCTGTTT 2449
Db      2587 TACAAAAAGACCAACCAATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAGAGCCCTGTTT 2646
Qy      2450 GATGAGTATACACTCATCAGAGATGATGTCGGTCCGCGGGGTTTATGTTGGGAGATC 2509
Db      2647 GATGAGTATACACTCATCAGAGATGATGTCGGTCCGCGGGGTTTATGTTGGGAGATC 2706
Qy      2510 TTCACTTTAGGGGCTCGCCCTACCCAGAGATTCCTCGTGAAGAACTTTTAACTGCTG 2569
Db      2707 TTCACTTTAGGGGCTCGCCCTACCCAGAGATTCCTCGTGAAGAACTTTTAACTGCTG 2766
Qy      2570 AAGGAGAGACACAGATGATGATTAAGCCAGCCACTGCAACAGACTGTAATGATGATG 2629
Db      2767 AAGGAGAGACACAGATGATGATTAAGCCAGCCACTGCAACAGACTGTAATGATGATG 2826
Qy      2630 AAGGAGCTGTTGGATGAGAGGCTCCCTCCAGAGACCAACGTTCAAGCACTGTTGAAGAC 2689
Db      2827 AAGGAGCTGTTGGATGAGAGGCTCCCTCCAGAGACCAACGTTCAAGCACTGTTGAAGAC 2886
Qy      2690 TTGATGGAATTCCTCACTCTCAACAACATAGAGATTAATGATCTCAGCCCACTCTC 2749
Db      2887 TTGATGGAATTCCTCACTCTCAACAACATAGAGATTAATGATCTCAGCCCACTCTC 2946
Qy      2750 GAAACGATTAACCTAGTAACCTGACACAGAAAGTTCTTGTCTTCAAGAGATGATCT 2809
Db      2947 GAAACGATTAACCTAGTAACCTGACACAGAAAGTTCTTGTCTTCAAGAGATGATCT 3006
Qy      2810 GTTTTCTCCAGACCCCATGCTTACAGAACAGCTTCTCTCAATCAACATTAAC 2869
Db      3007 GTTTTCTCCAGACCCCATGCTTACAGAACAGCTTCTCTCAATCAACATTAAC 3066
Qy      2870 GGCAGTGTAAACATGATGATCTGTCTGCTGCTCCCAACAGAGACGACTGGAA 2929
Db      3067 GGCAGTGTAAACATGATGATCTGTCTGCTGCTCCCAACAGAGACGACTGGAA 3126
Qy      2930 CTTAGCTTACCTGAGAGAGAGACCATGCTCCCAAGCTTGTCTCTCACTTGTAT 2989
Db      3127 CTTAGCTTACCTGAGAGAGAGACCATGCTCCCAAGCTTGTCTCTCACTTGTAT 3186
Qy      2990 ATGATATGAGAGAGATTAATATGAGAAAGTAAATACATATGTTAAATTTATACAG 3049
Db      3187 ATGATATGAGAGAGATTAATATGAGAAAGTAAATACATATGTTAAATTTATACAG 3246
Qy      3050 TTGAAACCTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGAGAGTGAAGTGC 3106
Db      3247 TTGAAACCTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGAGAGTGAAGTGC 3303

```

```

RESULT 3
ADZ13092
ID ADZ13052 standard; cDNA; 5003 BP.
XX
AC ADZ13052;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated cDNA #167.
XX

```

```

KM Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ss.
OS Homo sapiens.
PN WO2005031001-A2.
XX
XX 07-APR-2005.
XX
XX 23-SEP-2004; 2004MO-US031617.
XX
XX 23-SEP-2003; 2003US-00669920.
XX
XX (CHIR ) CHIRON CORP.
PI Morris DW, Malandro MS;
XX
XX MPI; 2005-273395/28.
DR P-PSDB; ADZ13053.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
XX Disclosure; SEQ ID NO 572; 198pp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX The invention also relates to a peptide array comprising two or more
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX that binds to a polypeptide, an isolated antibody or its fragment which
XX binds to a polypeptide, which is prepared by immunizing a host animal
XX with a composition comprising the polypeptide or its antigen binding
XX fragment and collecting cells from the host expressing antibodies against
XX the antigen or its antigen binding fragment, a composition comprising the
XX antibody and a carrier, a method of screening for anticancer activity, a
XX method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX method of treating cancer and a method of inhibiting expression of a CA
XX nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX nucleic acids. The antibody is useful for detecting the presence or
XX absence of cancer cells in an individual which involves contacting cells
XX from the individual with the antibody and detecting a complex of a CA
XX protein from the cancer cells and the antibody, where the detection of
XX the complex correlates with the presence of cancer cells in the
XX individual. The composition is useful for inhibiting growth of cancer
XX cells in an individual or for delivering a therapeutic agent to cancer
XX cells in an individual. The invention is also useful for diagnosing
XX cancer, for treating cancer and for inhibiting expression of a CA gene in
XX a cell. This sequence represents human cancer-associated cDNA of the
XX invention.
SQ Sequence 5003 BP; 1330 A; 1189 C; 1260 G; 1224 T; 0 U; 0 Other;
XX
XX Query Match 97.4%; Score 3025.4; DB 14; Length 5003;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

```

Db	818	ACAACACAGGTCGGGAGAGACGTTGCAATTCAGAGTACCTGCACAGCACAGCGGCACCGCC	877
Qy	295	TCGGTTCCTGAGGCCACCGCA - GCTGAAGGCAATTGCAGTACATGCGCCGTAGAGAA	353
Db	878	TCGGTCTCGAGGCCACCGCAGCGTGAAGGCAATTGCCGTAAGTCAATGACCCGTAGAGAA	937
Qy	354	GTGTGCAGATGGGATTAACTTCCA CATTGAGATATGGAAGAGACCGGGATTGTATCCG	413
Db	938	GTGTGCAGATGGGATTAACTTCCA CATTGAGATATGGAAGAGACCGGGATTGTATCCG	997
Qy	414	TAAACAATGGTAGCGGGGTGTTCAATCTGCGCTGATGATCAATGGCAACTGT	473
Db	998	TAAACAATGGTAGCGGGGTGTTCAATCTGCGCTGATGATCAATGGCAACTGT	1057
Qy	474	CCCTGGCCGGCCCTCTTCAGTTTAACTTGAAGTAAACCAATTAGACCAGAAAGCCAC	533
Db	1058	CCCTGGCCGGCCCTCTTCAGTTTAACTTGAAGTAAACCAATTAGACCAGAAAGCCAC	1117
Qy	534	CAACCAAAATACCAAAATCTCTCAACCAAGAGTGTACGTGGCTGCGCCAGGGGAGTCGTTAG	593
Db	1118	CAACCAAAATACCAAAATCTCTCAACCAAGAGTGTACGTGGCTGCGCCAGGGGAGTCGTTAG	1177
Qy	594	AGGTGCGCTGCTGTTGAAAGATGCGCGCGGATCAGTTGGAACCTAAGAGATGGGTGCACT	653
Db	1178	AGGTGCGCTGCTGTTGAAAGATGCGCGCGGATCAGTTGGAACCTAAGAGATGGGTGCACT	1237
Qy	654	TGGGCCCCCAACATATAGGACAGTGTCTTATTTGGGGAGTACTTGCAGATAAAGGCGCCACAC	713
Db	1238	TGGGCCCCCAACATATAGGACAGTGTCTTATTTGGGGAGTACTTGCAGATAAAGGCGCCACAC	1297
Qy	714	CTAAGACTCCGGCCTCTATGCTTGTACTGCGCAGTAGAGACTGTAGACATGTGAACTTGGT	773
Db	1298	CTAAGACTCCGGCCTCTATGCTTGTACTGCGCAGTAGAGACTGTAGACATGTGAACTTGGT	1357
Qy	774	ACTTCATGCTGAATCTCAGATGTCATCTCATCCGAGATGAGAGATGACCGATG	833
Db	1358	ACTTCATGCTGAATCTCAGATGTCATCTCATCCGAGATGAGAGATGAGATGACCGATG	1417
Qy	834	GTGCGGAGATTTTGTCTCAGTGAAGAACATTAACAAAGAGACACCATCTGACCAACA	893
Db	1418	GTGCGGAGATTTTGTCTCAGTGAAGAACATTAACAAAGAGACACCATCTGACCAACA	1477
Qy	894	CAGAAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCCAACCTGTCAAGTTTGGCT	953
Db	1478	CAGAAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCCAACCTGTCAAGTTTGGCT	1537
Qy	954	GCCCAAGCCGGGGGAAACCCATGTCACCATGCGGTGGCTGTAAGAAACCGGAAGGAGTTTA	1013
Db	1538	GCCCAAGCCGGGGGAAACCCATGTCACCATGCGGTGGCTGTAAGAAACCGGAAGGAGTTTA	1597
Qy	1014	AGCAGAGATGCAATTTGAGAGGCTCAAGGTACGAAACACAGACTGAGAGCTCTTATATG	1073
Db	1598	AGCAGAGATGCAATTTGAGAGGCTCAAGGTACGAAACACAGACTGAGAGCTCTTATATG	1657
Qy	1074	AAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGGT	1133
Db	1658	AAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGGT	1717
Qy	1134	CCATCAATCAACATGACACTGTGATGTTGTGAGCGATCGCTCAACGGGCCCATCTCC	1193
Db	1718	CCATCAATCAACATGACACTGTGATGTTGTGAGCGATCGCTCAACGGGCCCATCTCC	1777
Qy	1194	AAGCCGAGCTGCGCGGAATGCTCCACAGGTGTGGAGAGAGCTAGAGTTTGTCTGCA	1253
Db	1778	AAGCCGAGCTGCGCGGAATGCTCCACAGGTGTGGAGAGAGCTAGAGTTTGTCTGCA	1837
Qy	1254	AGGTTTACAGTATGCGCCAGCCCAATCAGTGTATCAAGCACGTGNAAGAAACGCA	1313
Db	1838	AGGTTTACAGTATGCGCCAGCCCAATCAGTGTATCAAGCACGTGNAAGAAACGCA	1897
Qy	1314	GTAAATACGGGCGGACGGGCTGCTTACCTCAAGTTTCAAGCACTCGGGGATTAATA	1373

Db	1898	GTAAATACGGGCCCCGAGGGGCTGCCCTTACCTCAAGGTTCTTCAAGCACTCGGGATTAATA	1957
Qy	1374	GTTCCAATGCAAGAAAGTGTGGCTCTGTTCAATGTGACCGAGCGGAGTCTGGGAAATTA	1433
Db	1958	GTTCCAAATGCAGAAGTGTGGCTCTGTTCAATGTGACCGAGCGGAGTCTGGGAAATTA	2017
Qy	1434	TATGTAAAGTCTCCAAATTAATTAAGGGAAGCAACAGTCTGGCTGAGTCACTGTCTGC	1493
Db	2018	TATGTAAAGTCTCCAAATTAATTAAGGGAAGCAACAGTCTGGCTGAGTCACTGTCTGC	2077
Qy	1494	CAAAAACAGCAAGCCTGGAAGAGAAAAAGAGATTACAGCTTCCCACAGACTACCTGAGA	1553
Db	2078	CAAAACAGCAAGCCTGGAAGAGAAAAAGAGATTACAGCTTCCCACAGACTACCTGAGA	2137
Qy	1554	TAGCCATTACTGCATAGAGGATCTTTTAATTCGCTGTATGTGTGTAAAGTCACTCTGT	1613
Db	2138	TAGCCATTACTGCATAGAGGATCTTTTAATTCGCTGTATGTGTGTAAAGTCACTCTGT	2197
Qy	1614	GCCGAATGAAGAACACGACCAAGAAAGCCAGACTTCAAGAGCAACCGGCTGTGACAAGC	1673
Db	2198	GCCGAATGAAGAACACGACCAAGAAAGCCAGACTTCAAGAGCAACCGGCTGTGACAAGC	2255
Qy	1674	TGACCAAAAGTATCCCTCGCGGAGACAAGATAC---AGTTTGGGCTGAGTCCAGCTCC	1729
Db	2258	TGACCAAAAGTATCCCTCGCGGAGACAAGATACAAAGAAAGTTTGGGCTGAGTCCAGCTCC	2317
Qy	1730	TTCATGAATCCCAACACCCCGGTGTGAGATTAACAACAGCTCTCTTTCAACCGCAGAC	1788
Db	2318	TTCATGAATCCCAACACCCCGGTGTGAGATTAACAACAGCTCTCTTTCAACCGCAGAC	2377
Qy	1790	ACCCCAATCTGGCGAGGGGCTCTCGAGATGAACCTTCAGAGAAACCAAAATGGAGATT	1848
Db	2378	ACCCCAATCTGGCGAGGGGCTCTCGAGATGAACCTTCAGAGAAACCAAAATGGAGATT	2433
Qy	1850	CCAAGAGATTAAGCTGACACTGCGGCAAGCCCTCGGAGAAAGTTGCTTTGGCAAGTGTCT	1905
Db	2438	CCAAGAGATTAAGCTGACACTGCGGCAAGCCCTCGGAGAAAGTTGCTTTGGCAAGTGTCT	2497
Qy	1910	ATGCGGAGAACAGTGGGAATTGACAABAACAAGCCCAAGAGAGCGGTCAACGTGGCCGTG	1966
Db	2498	ATGCGGAGAACAGTGGGAATTGACAABAACAAGCCCAAGAGAGCGGTCAACGTGGCCGTG	2555
Qy	1970	AAGATGTTGAAGAAGATGGCCACAGAGAAAGCCTTTCGATCTGTGTCAAGAGATGAG	2025
Db	2558	AAGATGTTGAAGAAGATGGCCACAGAGAAAGCCTTTCGATCTGTGTCAAGAGATGAG	2611
Qy	2030	ATGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACAG	2085
Db	2618	ATGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACAG	2677
Qy	2090	GATGGGCTCTGTATGTGCATAGTTGATGTGCTCTAAAGGCAACTCCGAGAAATACCTC	2144
Db	2678	GATGGGCTCTGTATGTGCATAGTTGATGTGCTCTAAAGGCAACTCCGAGAAATACCTC	2733
Qy	2150	CGAGCCCGGAGCCACCGGGAGTAGAGTACTCTAATGACATTAACCGATGCTCTAGAGAG	2209
Db	2738	CGAGCCCGGAGCCACCGGGAGTAGAGTACTCTAATGACATTAACCGATGCTCTAGAGAG	2797
Qy	2210	CAGATGACCTTCAGAGCTTGGTGTATGCACTACCTACAGCTGGCCAGACGAGATGAGTAC	2265
Db	2798	CAGATGACCTTCAGAGCTTGGTGTATGCACTACCTACAGCTGGCCAGAGGCAATGAGTAC	2855
Qy	2270	TTGGCTTCCCAAAATGTAATTCATGAGAGTTTAGCAGCCAGAAATGTTTGGTAAACAGA	2322
Db	2858	TTGGCTTCCCAAAATGTAATTCATGAGAGTTTAGCAGCCAGAAATGTTTGGTAAACAGA	2911
Qy	2330	AACAATGTATGAAAAATAGCAGACTTTGGAATCGCAGAGATATCAACAATATAGACTAT	2381
Db	2918	AACAATGTATGAAAAATAGCAGACTTTGGAATCGCAGAGATATCAACAATATAGACTAT	2977
Qy	2390	TACAAAAAACCAACCATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTT	2441
Db	2978	TACAAAAAACCAACCATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTT	3033

QY	2450	GATTAAAGTATTCACCTGATCAGAGTGAATGTCTGTGCTCTGGGGGTGTTAATGTGGAGATC	2509
Db	3038	GATTAAAGTATTAACCTCATCAGAGTGAATGTGTGTCTCTGGGGGTGTTAATGTGGAGATTC	3097
QY	2510	TTCACTTTAGGGGGGTCTGCCCTTACCAGAGGATTTCCGTGAGAGAACTTTTAAAGCTGCTG	2569
-Db	3098	TTCACTTTAGGGGGGTCTGCCCTTACCAGAGGATTTCCGTGAGAGAACTTTTAAAGCTGCTG	3157
QY	2570	AAGGAAGACACAGAAATGGAATAGCCAGCCAACTGCAACAAAGAACTGTACATGATGATG	2629
Db	3158	AAGGAAGACACAGAAATGGAATAGCCAGCCAACTGCAACAAAGAACTGTACATGATGATG	3217
QY	2630	AGGGACTGTGGCAGTCAGCTGCTCCCTCCAGAGAACCAAGTTCAAGCAATGTGTGAAGAC	2689
Db	3218	AGGGACTGTGTGCAGTCAGCTGCTCCCTCCAGAGAACCAAGTTCAAGCAATGTGTGAAGAC	3277
QY	2690	TTGGATCGAAATTCCTCATCTCCCAACCAATGAGGAATCTTGGACCTTCAGCCAACTCTC	2749
Db	3278	TTGGATCGAAATTCCTCATCTCCCAACCAATGAGGAATCTTGGACCTTCAGCCAACTCTC	3337
QY	2750	GAACAGTATTCACCTAGTTACCTTGACACAAAGAACTTTGTCTTCCAGAGATGATCT	2809
Db	3338	GAACAGTATTCACCTAGTTACCTTGACACAAAGAACTTTGTCTTCCAGAGATGATCT	3397
-QY	2810	GTTTTTTTCTCCAGACCCCATGCTTACGAACCAATGCTTCTCCATGATCCACATTAAC	2869
Db	3398	GTTTTTTTCTCCAGACCCCATGCTTACGAACCAATGCTTCTCCATGATCCACATTAAC	3457
QY	2870	GGCAGGTGTTAAAACATGATGATGCTGTGTCTGTCTGCCCAACAGACACACTGGGAA	2929
Db	3458	GGCAGGTGTTAAAACATGATGATGCTGTGTCTGTCTGCCCAACAGACACACTGGGAA	3517
QY	2930	CTTACGTCACCTGAGCAGGAGAACCATGCTCTCCAGACTTGTGTCTTCCACTTGTATAT	2989
Db	3518	CTTACGTCACCTGAGCAGGAGAACCATGCTCTCTCCAGACTTGTGTCTTCCACTTGTATAT	3577
QY	2990	ATGATATCAGAGGAGTAAATTAATTGGAATAATGATATGATATGATATGATATTAATACAG	3049
Db	3578	ATGATATCAGAGGAGTAAATTAATTGGAATAATGATATGATATGATATGATATTAATACAG	3637
QY	3050	TTGAAAACTTGTAAATCTTCCCGCAGAGAGAGAAAGGTTTCTGAGCAGTGTGACTGC	3106
-Db	3638	TTGAAAACTTGTAAATCTTCCCGCAGAGAGAGAAAGGTTTCTGAGCAGTGTGACTGC	3694
RESULT 4			
ADL61208			
ID	ADL61208	standard; DNA; 4574 BP.	
XX	ADL61208;		
AC			
XX			
DT	03-JUN-2004	(first entry)	
XX			
DE		Human tyrosine kinase biomarker fibroblast growth factor receptor 2 DNA.	
XX			
KM		predictor sec; protein tyrosine kinase; cytosolic; antiangiogenic;	
KM		vasoactive; vulnerable; pharmacogenomic; drug sensitivity; breast cancer;	
KM		hypertrophic disease; angiogenesis; wound healing scar; human;	
XX		biomarker; ds; gene; fibroblast growth factor receptor 2.	
XX			
-OS	homo sapiens.		
XX			
PN	WO2004020583-A2.		
XX			
PD	11-MAR-2004.		
XX			
PF	26-AUG-2003; 2003WO-US026491.		
XX			
PR	27-AUG-2002; 2002US-0406385P.		
XX			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX			

Pt	Huang F, Han X, Reeves KA, Amlier L, Fairchild CR, Lee F;
PI	Shaw P;
XX	WI; 2004-239171/22.
DR	P-PSDB; ADL61330.
XX	New predictor sets with a plurality of polynucleotides and/or
PT	polypeptides whose expression pattern predicts cell response to a
PT	compound that modulates protein tyrosine kinase activity, useful in
XX	treating breast cancer.
PS	Claim 2; SEQ ID NO 132; 649pp; English.
XX	
CC	The invention relates to a novel predictor set comprising a plurality of
CC	polynucleotides and/or polypeptides whose expression pattern is
CC	predictive of the response of cells to treatment with a compound that
CC	modulates protein tyrosine kinase activity or members of the protein
CC	tyrosine kinase pathway. The molecules of the invention demonstrate
CC	cytostatic, antiangiogenic, vasotropic and vulnerary activities and may
CC	be useful in the field of pharmacogenomics, in particular for determining
CC	drug sensitivity and in treating breast cancer, hypervascular diseases,
CC	angiogenesis and scars in wound healing. The current sequence is that of
CC	a human protein tyrosine kinase biomarker DNA of the invention.
XX	
SEQ	Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;
Query Match	97.0%; Score 3013.2; DB 12; Length 4574;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 3097; Conservative	0; Mismatches 8; Indels 9; Gaps 7
OY	1 CCCGCGACAAAGTTTGATGAGGCAAG-CAGCCTGAAGTCTTTCTTCCTCGTTCC 59
Db	168 CTCGCGAACAAAGTTTGATGAGGCAGCAAGCCAGCTTAGTCTTCTTCCTCGTTCC 227
OY	60 CCAATCCGAGGGGAGGCCCGGGGGGTATG--GGGTCCTCCGCAAGCCTGGGGTAACC 116
Db	228 CCAATTCGA-GGCAGCCCCGGGGGGGTATGCCCGCGCTCTTCGCAAGCCTGGGGTAACC 286
OY	117 G-TGAGGCCGGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTTTCGATTGGA 175
Db	287 GCTGAGGCCGGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTTTCGATTGGA 346
OY	176 GTTGCTCCCGCAAACCCCGGGCTGTCGCTTTCTCATCCGACCCAAGCGGGGC-CGGG 234
Db	347 GTTGCTCCCGCAAACCCCGGGCTGTCGCTTTCTCATCCGACCCAAGCGGGGC-CGGG 406
OY	235 GACAAACACAGTGTGGGAGAGCGTTGGCATTCAGTGAATGACACAGAGC-GGACGCG 293
Db	407 GACAAACACAGTGTGGGAGAGCGTTGGCATTCAGTGAATGACACAGAGCGGACGCGC 466
OY	294 CTGCGTTCCTAGGCCACCGCA-GGTGAAGGATTCGCGTATGTCATGCGGTAGAGA 352
Db	467 CTCGTTCTTAGGCCCACCGCAGGTGAAGGATTCGCGTATGTCATGCGGTAGAGA 526
OY	353 AGTGTGACATGAGATTAAAGTCCACATGAGATATGGAAGAGACC GGGAATTGGTACC 412
Db	527 AGTGTGACATGAGATTAAAGTCCACATGAGATATGGAAGAGACC GGGAATTGGTACC 586
OY	413 GTAACCATGTGCAGTGGGGTCTTTCAATCTGCTGTCGTGAGTCAACATGGCAACTTG 472
Db	587 GTAACCATGTGCAGTGGGGTCTTTCAATCTGCTGTCGTGAGTCAACATGGCAACTTG 646
OY	473 TCCTGGGCGGGCCCTCTTCAAGTTTAGTTGAGATAACAATTAGAGCAGAAAGGCA 532
Db	647 TCCTGGGCGGGCCCTCTTCAAGTTTAGTTGAGATAACAATTAGAGCAGAAAGGCA 706
OY	533 CCAACCAAAATCAAAATCTTCAACAGAGAATGTAAGTGTGCGCCAGGGGAGTTCCTA 592
Db	707 CCAACCAAAATCAAAATCTTCAACAGAGAATGTAAGTGTGCGCCAGGGGAGTTCCTA 766
OY	593 GAGGTGCGCTGCTGTTGAAGAATGCCGCGTGAATCAAGTTGACCTTAAGATGGGTGAC 652
Db	767 GAGGTGCGCTGCTGTTGAAGAATGCCGCGTGAATCAAGTTGACCTTAAGATGGGTGAC 826

OY	653	TTGGGGCCCAACAAATAGACAGATGCTTATTTGGGGAGTACTTGCAGATTAAGGGCCGACA	712
Db	827	TTGGGGCCCAACAAATAGACAGATGCTTATTTGGGGAGTACTTGCAGATTAAGGGCCGACA	886
OY	713	CTTAGAGCTCCGGGCTCTATAGCTTGATCTGATCCGAGTGGAGCTGTAGACAGTGTAACTTGG	772
Db	887	CTTAGAGCTCCGGGCTCTATAGCTTGATCTGATCCGAGTGGAGCTGTAGACAGTGTAACTTGG	946
OY	773	TACTTCATGTGAAATGTCAACAGATGCATCTCATCGGAGATGATGAGATGACCCGAT	832
Db	947	TACTTCATGTGAAATGTCAACAGATGCATCTCATCGGAGATGATGAGATGACCCGAT	1006
OY	833	GGTGGGAGATTTTGTGTCAGTGAACAAGTAAACAAGAGAGACCATCTGACCAAC	892
Db	1007	GGTGGGAGATTTTGTGTCAGTGAACAAGTAAACAAGAGAGACCATCTGACCAAC	1066
OY	893	ACAGAAAAGATGGAAGAAAGCGGCTCATGCTGTGCTCGGCGCAACCTGTCAAGTTTCG	952
Db	1067	ACAGAAAAGATGGAAGAAAGCGGCTCATGCTGTGCTCGGCGCAACCTGTCAAGTTTCG	1126
OY	953	TGCCAGCCGGGGGGAACCAATGCGAACATGCGGTGGCTGAAAAACGGAAAGAGTTT	1012
Db	1127	TGCCAGCCGGGGGGAACCAATGCGAACATGCGGTGGCTGAAAAACGGAAAGAGTTT	1186
OY	1013	AAGCAGAGCATCGATTTGAGAGGCTACAAAGTAAAGAAACAGGACTGAGCCCTCATATG	1072
Db	1187	AAGCAGAGCATCGATTTGAGAGGCTACAAAGTAAAGAAACAGGACTGAGCCCTCATATG	1246
OY	1073	GAAATGTAGTCCATCTGACAAAGGAAATTATACCTGTGTATGTGAGAAATGAATACGG	1132
Db	1247	GAAATGTAGTCCATCTGACAAAGGAAATTATACCTGTGTATGTGAGAAATGAATACGG	1306
OY	1133	TCCATCAATCACACGTACCACTGAGATTTGAGACGATGCTCAACCGGCCATCTC	1192
Db	1307	TCCATCAATCACACGTACCACTGAGATTTGAGACGATGCTCAACCGGCCATCTC	1366
OY	1193	CAGCCGGACTCCGCGCAATGCTCTCCACAGTGTCCGAGAGAGACGTAGATTGTCTGC	1252
Db	1367	CAGCCGGACTCCGCGCAATGCTCTCCACAGTGTCCGAGAGAGACGTAGATTGTCTGC	1426
OY	1253	AAGGTTTACAGTATGCCAGGCCCAACATCCAGTGTATCAAGCACTGTGAAAGAACGGC	1312
Db	1427	AAGGTTTACAGTATGCCAGGCCCAACATCCAGTGTATCAAGCACTGTGAAAGAACGGC	1486
OY	1313	AGTAAATACGGGCGGACGGGCTGCTTACCTCAAGGTTCTCAGCACTCGGGGATTAAT	1372
Db	1487	AGTAAATACGGGCGGACGGGCTGCTTACCTCAAGGTTCTCAGCACTCGGGGATTAAT	1546
OY	1373	AGTTCCATGCGAAGATGTGCTCTGTTCATATGACCGAGGGGGAATGCTGGGGAATAT	1432
Db	1547	AGTTCCATGCGAAGATGTGCTCTGTTCATATGACCGAGGGGGAATGCTGGGGAATAT	1606
OY	1433	ATATGTAAGSTCCCAATTAATTAAGGACAGGCCAACAGTCTGCTCACTGTCTCG	1492
Db	1607	ATATGTAAGSTCCCAATTAATTAAGGACAGGCCAACAGTCTGCTCACTGTCTCG	1666
OY	1493	CCAAAACAGCAAGCGCTTGAAAGAGAAAAGAGATTAACGCTTCCCACTACCTGGAG	1552
Db	1667	CCAAAACAGCAAGCGCTTGAAAGAGAAAAGAGATTAACGCTTCCCACTACCTGGAG	1726
OY	1553	ATAGCCATTTACTGCTATAGGGCTCTTAAATCGCTGTATAGGTGTAAACGTACATCTG	1612
Db	1727	ATAGCCATTTACTGCTATAGGGCTCTTAAATCGCTGTATAGGTGTAAACGTACATCTG	1786
OY	1613	TGCGGAATGAAGAACAGCAACAAGAACCACTTACAGAGCCAGCCGGCTGTGCACAG	1672
Db	1787	TGCGGAATGAAGAACAGCAACAAGAACCACTTACAGAGCCAGCCGGCTGTGCACAG	1846
OY	1673	CTGACCAACGTATCCCTGTGGGAGACAGGTAAAGTTTGGCTAGCTCAGCTCTCC	1732
Db	1847	CTGACCAACGTATCCCTGTGGGAGACAGGTAAAGTTTGGCTAGCTCAGCTCTCC	1906

QY	1733	ATGAATCTCAACACCCCGCTGGTGAAGATTAACAACACGCTCTCTTTCGAACGGACAAC	1792
Db	1907	ATGAATCTCAACACCCCGCTGGTGAAGATTAACAACACGCTCTCTTTCGAACGGACAAC	1966
QY	1793	CCCATGCTGGCAGGGGGCTCCAGTAAATCTTCAGAGGACCCAAATATGGAGTTTCCA	1852
Db	1967	CCCATGCTGGCAGGGGGCTCCAGTAAATCTTCAGAGGACCCAAATATGGAGTTTCCA	2026
QY	1853	AGAGATTAAGCTGACACCTGGCCAAAGCCCCCTGGAGAAAGTTGCTTGGCCAAAGTGTCAATG	1912
Db	2027	AGAGATTAAGCTGACACCTGGCCAAAGCCCCCTGGAGAAAGTTGCTTGGCCAAAGTGTCAATG	2086
QY	1913	GCGGAAGCAGTGGGAATTTGACAAGAACAAGCCCAAGAGGCGGTTCACCGTGGCCGTGAAG	1972
Db	2087	GCGGAAGCAGTGGGAATTTGACAAGAACAAGCCCAAGAGGCGGTTCACCGTGGCCGTGAAG	2146
QY	1973	ATGTTGAAAGATGATGCGACAGAGAAAGACCTTTCTGATCTGATGTCACAGATGAGATG	2032
Db	2147	ATGTTGAAAGATGATGCGACAGAGAAAGACCTTTCTGATCTGATGTCACAGATGAGATG	2206
QY	2033	ATGAAGATGATGGGAAAACAAGAAATATCATAAATCTTGGAGCTGACACAGAT	2092
Db	2207	ATGAAGATGATGGGAAAACAAGAAATATCATAAATCTTGGAGCTGACACAGAT	2266
QY	2093	GGGCGCTCTATGTCATGTTGAAGTATGCTCTTAAAGCAACCTCCGAGAAATCCGCCA	2152
Db	2267	GGGCGCTCTATGTCATGTTGAAGTATGCTCTTAAAGCAACCTCCGAGAAATCCGCCA	2326
QY	2153	GGCCGGAAGCCACCCGGGATGGAGTACCTCCATGACATTTAACCGTGTCTGAGAGCAG	2212
Db	2327	GGCCGGAAGCCACCCGGGATGGAGTACCTCCATGACATTTAACCGTGTCTGAGAGCAG	2386
QY	2213	ATGACCTTCAAGGACCTTGCTGCATGACCTTACCAAGCTGGCCAGACGATGAGTACTTG	2272
Db	2387	ATGACCTTCAAGGACCTTGCTGCATGACCTTACCAAGCTGGCCAGACGATGAGTACTTG	2446
QY	2273	GCTTCCCAAAAATGTATTCATCGAGATTTAGACAGCAGAAATGTTTGGTATACAGAAAC	2332
Db	2447	GCTTCCCAAAAATGTATTCATCGAGATTTAGACAGCAGAAATGTTTGGTATACAGAAAC	2506
QY	2333	AATGTGATGAAAATATGACGACTTTGGAGCTTGCGCAGAGATATCAACAATATATGACTTAC	2392
Db	2507	AATGTGATGAAAATATGACGACTTTGGAGCTTGCGCAGAGATATCAACAATATATGACTTAC	2566
QY	2393	AAAAAGACCAACAATGGGCGGCTTCCAGTCAATGATGATGCTCCAGAAAGCCCTGTTGAT	2452
Db	2567	AAAAAGACCAACAATGGGCGGCTTCCAGTCAATGATGATGCTCCAGAAAGCCCTGTTGAT	2626
QY	2453	AGAGTATATCATCATCAAGTATATGTCGTGCTTCCGGGGGTATTAATGTGGGAATCTTC	2512
Db	2627	AGAGTATATCATCATCAAGTATATGTCGTGCTTCCGGGGGTATTAATGTGGGAATCTTC	2686
QY	2513	ACTTTAAGGGGGTCCGCCCTTCCAGAGGATTCGCCGTGAGGAACTTTTAACTCTGTAAG	2572
Db	2687	ACTTTAAGGGGGTCCGCCCTTCCAGAGGATTCGCCGTGAGGAACTTTTAACTCTGTAAG	2746
QY	2573	GAAGGACACAGATGATTAAGCCAGCCAACTGACCAACGATCTTACATGATGATGAGG	2632
Db	2747	GAAGGACACAGATGATTAAGCCAGCCAACTGACCAACGATCTTACATGATGATGAGG	2806
QY	2633	GACTGTTGGCATGACAGTGCCTCCACAGACCAACGTTCAAGCAAGTGTATGAAGACTTG	2692
Db	2807	GACTGTTGGCATGACAGTGCCTCCACAGACCAACGTTCAAGCAAGTGTATGAAGACTTG	2866
QY	2693	GATCGAATTCATCACTCTCAACAACATGAGAAATCTTGGACCTCAGCCAACTCTCGAA	2752
Db	2867	GATCGAATTCATCACTCTCAACAACATGAGAAATCTTGGACCTCAGCCAACTCTCGAA	2926
QY	2753	CAGTATTTCACTAGTTTACCTTGACAACAAGATGTTTGTCTTTCAGAGATGATTTGTT	2812
Db	2927	CAGTATTTCACTAGTTTACCTTGACAACAAGATGTTTGTCTTTCAGAGATGATTTGTT	2986
QY	2813	TTTTCTCCAGACCCCATGCTTACGAAACCATGCTTCTCAGTATCAACATTAACGGC	2872

Db 2987 TTTTCTCCAGACCCCATGCTTACGAAACATGCTTCTCTCATGATCCACATTAAGGCG 3046
 Qy 2873 AGTGTAAACATGAATGACTGTGTCTGCTGTCTGCCAAACAGAGACAGCATGGAACTT 2932
 Db 3047 AGTGTAAACATGAATGACTGTGTCTGCTGTCTGCCAAACAGAGACAGCATGGAACTT 3106
 Qy 2933 AGTCACTACAGAGAGAGAGACATGCTCTCCAGAGCTTGTGTCTCCACTTGTATATATG 2992
 Db 3107 AGCTACACTGAGAGAGAGACATGCTCTCCAGAGCTTGTGTCTCCACTTGTATATATG 3166
 Qy 2993 GATCAGAGAGATTAATTAATGAGAAAGATATACAGATATGTATTAAGATTATACAGTTG 3052
 Db 3167 GATCAGAGAGATTAATTAATGAGAAAGATATACAGATATGTATTAAGATTATACAGTTG 3226
 Qy 3053 AAAACTGTATATCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3106
 Db 3227 AAAACTGTATATCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3280
 RESULT 5
 ID ADQ80247 standard; cDNA; 4574 BP.
 AC ADQ80247;
 XX 21-OCT-2004 (first entry)
 DT 21-OCT-2004 (first entry)
 DE Fibroblast growth factor receptor 2 cDNA.
 XX
 KM bsi; gene; cytosolic; epidermal growth factor receptor modulator;
 KW identification; therapeutic response; cancer; EGFR; biomarker.
 OS Homo sapiens.
 XX
 PN NO2004063709-A2.
 XX 29-JUL-2004.
 PD 08-JAN-2004; 2004MO-US000368.
 PF 08-JAN-2003; 2003US-0438735P.
 PR 08-JAN-2003; 2003US-0438735P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Amlex LC, Januario T;
 DR WPI: 2004-544114/52.
 DR P-PSDB; ADQ80367.
 XX
 PT Identifying a mammal that will respond therapeutically to a method of
 PT treating cancer comprises comparing the level of a biomarker in a mammal
 PT before and after exposure to an epidermal growth factor receptor (EGFR)
 PT modulator.
 XX
 PS Disclosure; SEQ ID NO 19; 520bp; English.
 PS
 CC The invention relates to a method of identifying a mammal that will
 CC respond therapeutically to a method of treating cancer by administering
 CC an epidermal growth factor receptor (EGFR) modulator by comparing the
 CC level of a biomarker in a mammal before and after exposure to an EGFR
 CC modulator. The method comprises: (a) measuring, in the mammal, the level
 CC of at least one biomarker identified in the specification; (b) exposing
 CC the mammal to the EGFR modulator; and (c) measuring in the mammal the
 CC level of the biomarker, where a difference in the level in step (c)
 CC compared to step (a) indicates that the mammal will respond
 CC therapeutically to the method of treating cancer. The method and
 CC biomarkers are useful for identifying a mammal that will respond
 CC therapeutically to a method of treating cancer by administering an
 CC epidermal growth factor receptor (EGFR) modulator. This sequence
 CC corresponds to one of the biomarkers whose levels of gene expression is
 CC measured in the method of the invention.
 CC
 XX

SQ Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;
 Query Match 97.0%; Score 3013.2; DB 13; Length 4574;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;
 Qy 1 CCCGAGAGCAAGTTGGTGGAGCAACG-CAAGCTGAGCTCTTCTTCTCTGCTTCC 59
 Db 168 CTGCGAGAGAAAGTTGGTGGAGGAGCAAGCTGAGTCTTCTCTCTGCTTCC 227
 Qy 60 CCAATCCAGAGGACCGCGCGGCTCATG--GGCTCTCTCCGAGCTTGGGATACCG 116
 Db 228 CCAATCCGA-GGCAGCGCGCGGCTCATGCGCGCTCTCTCCGAGCTTGGGATACCG 286
 Qy 117 G-TGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGCAACAACCTCTCTGCTTGA 175
 Db 287 GCTGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGCAACAACCTCTCTGCTTGA 346
 Qy 176 GTTGCTCCCGCAACCCGCGCTGCTGCTTCTCCATCCGACCCAGCGCGGCG-CGGG 234
 Db 347 GTTGCTCCCGCAACCCGCGGCTGCTGCTTCTCCATCCGACCCAGCGCGGCGGCG 406
 Qy 235 GACCAACAGGTGCGGAGAGAGGCTTCCATTCAGTGACTGACAGACAGC-GCAGCGC 293
 Db 407 GACCAACAGGTGCGGAGAGAGGCTTCCATTCAGTGACTGACAGAGCGGCGAGCGC 466
 Qy 294 CTGCGTCTGAGCCCAACCGCA-GCTGAAGGCAATGCGGCTGATCCATGCCGTAGAGA 352
 Db 467 CTGCGTCTGAGCCCAACCGCAAGGCTGAAGGCAATGCGGCTGATCCATGCCGTAGAGA 526
 Qy 353 AGTGTGAGATGGATTAACGTCACATGAGATATGAAGAGAGACCGGGATTTGTATAC 412
 Db 527 AGTGTGAGATGGATTAACGTCACATGAGATATGAAGAGAGACCGGGATTTGTATAC 586
 Qy 413 GTAACATGATGACTGAGGAGTGTGCTTCACTGCTGCTGCTGCTACCATGCAACTTG 472
 Db 587 GTAACATGATGACTGAGGAGTGTGCTTCACTGCTGCTGCTGCTGCTACCATGCAACTTG 646
 Qy 473 TCCCTGGCCCGGCGCTTCACTTGAATGAGAGATCAACATTAAGCAAGAGAGCA 532
 Db 647 TCCCTGGCCCGGCGCTTCACTTGAATGAGAGATCAACATTAAGCAAGAGAGCA 706
 Qy 533 CCAACCAATACCAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 592
 Db 707 CCAACCAATACCAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 766
 Qy 593 GAGTGCCTGCTGCTTGAAGAGATGCGCGGTGATGATGATGATGATGATGATGATGATGAT 652
 Db 767 GAGTGCCTGCTGCTTGAAGAGATGCGCGGTGATGATGATGATGATGATGATGATGATGAT 826
 Qy 653 TTGGGCGCCCAATGAGACAGTCTTATTTGGGAGTACTTTCAGATTAAGGGCGCAC 712
 Db 827 TTGGGCGCCCAATGAGACAGTCTTATTTGGGAGTACTTTCAGATTAAGGGCGCAC 886
 Qy 713 CTTAGAGACTCGGCGCTTATGCTTACTGACAGTGAAGCTGTAGACAGTGAACCTTGG 772
 Db 887 CTTAGAGACTCGGCGCTTATGCTTACTGACAGTGAAGCTGTAGACAGTGAACCTTGG 946
 Qy 773 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
 Db 947 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
 Qy 833 GGTGCGAAGATTTTGTGATGAGAACAGTGAACAAGAGACACATCTGTGACCAAC 892
 Db 1007 GGTGCGAAGATTTTGTGATGAGAACAGTGAACAAGAGACACATCTGTGACCAAC 1066
 Qy 893 ACGAAGAAAGTGAAGAAAGGCGCTCAATGCTGCTGCGGCAACCTGTCAAGTTTGC 952
 Db 1067 ACGAAGAAAGTGAAGAAAGGCGCTCAATGCTGCTGCGGCAACCTGTCAAGTTTGC 1126
 Qy 953 TGCCAGCGCGGGGGAACCAATGCAACCATGCGGTGCTGTAAGAAAGGAGATTT 1012
 Db 1127 TGCCAGCGCGGGGGAACCAATGCAACCATGCGGTGCTGTAAGAAAGGAGATTT 1186

OY	1013	AAGCAGAGACATGCGATTGGAGGCTCAACAGTACGAAGAACAGCACTGACCTCATATG	1072
Db	1187	AAGCAGAGACATGCGATTGGAGGCTCAACAGTACGAAGAACCAAGCACTGACCTCATATG	1246
OY	1073	GAAAGTGTGTCCCATCTGACCAAGGAAATTATACCTGTGTATGTGAGAAATGAATACGGG	1132
Db	1247	GAAAGTGTGTCCCATCTGACCAAGGAAATTATACCTGTGTGTGTGGAAATGAATACGGG	1306
OY	1133	TCGATTCATATCAAGTATCCACTGTGAGATGTTGTGAGAGGATATGCTTCACCGGCCATCTCT	1192
Db	1307	TCGATTCATATCAAGTATCCACTGTGAGATGTTGTGAGAGGATATGCTTCACCGGCCATCTCT	1366
OY	1193	CAAGCCGGACCTGCGCGCAATATGCTTCACAGTGTGTGGAGAGACGTAGATTGTCTGC	1252
Db	1367	CAAGCCGGACCTGCGCGCAATATGCTTCACAGTGTGTGGAGAGACGTAGATTGTCTGC	1426
OY	1253	AAGGTTTACAGTATATGCCAGGCCCACTCCAGTGTATCAAGCACCTGTGAAAAAGAACGGC	1312
Db	1427	AAGGTTTACAGTATATGCCAGGCCCACTCCAGTGTATCAAGCACCTGTGAAAAAGAACGGC	1486
OY	1313	AGTAAATACGGGAGCCGACGGGCTGCGCTCACTCAAGGTTCTCAAGCACTCGGGGATTAAT	1372
Db	1487	AGTAAATACGGGAGCCGACGGGCTGCGCTCACTCAAGGTTCTCAAGCACTCGGGGATTAAT	1546
OY	1373	AGTTCCATATGACAGATGTCTGCTCTGTTCAATGTATCCAGGCGGATGCTGTGGGAAATAT	1432
Db	1547	AGTTCCATATGACAGATGTCTGCTCTGTTCAATGTATCCAGGCGGAGATGCTGTGGGAAATAT	1606
OY	1433	ATATGTAAAGTCTCCAAATTATATATGAGGAGGACCAACAGTGTGCTGGCTCACTGTCTGT	1492
Db	1607	ATATGTAAAGTCTCCAAATTATATATGAGGAGGACCAACAGTGTGCTGGCTCACTGTCTGT	1666
OY	1493	CCAAAACAGCAAGCGCTGTGAAGAGAAAAAGAGATTACAGCTTCCCAAGTACCTTGGAG	1552
Db	1667	CCAAAACAGCAAGCGCTGTGAAGAGAAAAAGAGATTACAGCTTCCCAAGTACCTTGGAG	1726
OY	1553	ATAGCGATTATCTGATATAGGGGTCTTCTTAATGCGCTGATAGTGTGTATACATATCTGT	1612
Db	1727	ATAGCGATTATCTGATATAGGGGTCTTCTTAATGCGCTGATAGTGTGTATACATATCTGT	1786
OY	1613	TGCCAATGGAAGAACAGACCAAGAACCAAGCACTTCAGCAGCCGCGCTGTGCAACAG	1672
Db	1787	TGCCAATGGAAGAACAGACCAAGAACCAAGCACTTCAGCAGCCGCGCTGTGCAACAG	1846
OY	1673	CTGACCAAACTGATCCCTCTGCGGAGACAGGTATACAGTTTGGCTGATCCAGCTCTCTCC	1732
Db	1847	CTGACCAAACTGATCCCTCTGCGGAGACAGGTATACAGTTTGGCTGATCCAGCTCTCTCC	1906
OY	1733	ATGAATCTCCAAACACCCCGCTGGTGAAGATTAACAAGCGCTCTCTTCAACCGGACAGCAC	1792
Db	1907	ATGAATCTCCAAACACCCCGCTGGTGAAGATTAACAAGCGCTCTCTTCAACCGGACAGCAC	1966
OY	1793	CCCATGTCTGGCAGGGGTCTCCGAGTATGAATCTTCAGAGAACCCAAAATGGGAGTTTCCA	1852
Db	1967	CCCATGTCTGGCAGGGGTCTCCGAGTATGAATCTTCAGAGAACCCAAAATGGGAGTTTCCA	2026
OY	1853	AGAGATTAAGCTACACTGTGGGACAAGCCCTGTGGAGAAAGTTGCTTGGGCAAGTGTCTATG	1912
Db	2027	AGAGATTAAGCTACACTGTGGGACAAGCCCTGTGGAGAAAGTTGCTTGGGCAAGTGTCTATG	2086
OY	1913	GGCGAAGCAGTGGGAATTTACAACAACAAGCCCAAGAGAGGCGGTACCCGTGCGCGTGAAG	1972
Db	2087	GGCGAAGCAGTGGGAATTTACAACAACAAGCCCAAGAGAGGCGGTACCCGTGCGCGTGAAG	2146
OY	1973	ATGTTGAAAGATGATATGCCACAGAGAAAGACCTTTCTGATCTGTGTCTCAGATGTGAGATG	2032
Db	2147	ATGTTGAAAGATGATATGCCACAGAGAAAGACCTTTCTGATCTGTGTCTCAGATGTGAGATG	2206
OY	2033	ATGAAGAATATTTGGGAAAAACAAGAAATATCATAAATCTTTGGAGCGCTGCACACAGAT	2092
Db	2207	ATGAAGAATATTTGGGAAAAACAAGAAATATCATAAATCTTTGGAGCGCTGCACACAGAT	2266

Qy	2093	GGGCTCTCTCATATGCAATAGTTGGATAGTGCCTCTAAAGAGGCAACCTCGAGAAATACCTCCGA	2152
Db	2267	GGGGCTCTCTCATATGCAATAGTTGGATAGTGCCTCTAAAGAGGCAACCTCGAGAAATACCTCCGA	2326
Qy	2153	GCCCGAGAGGCACCCCGGAGTGAAGTACTCCTATGACATTAACCGTGTCTCTGAGAGCAG	2212
Db	2327	GCCCGAGAGGCACCCCGGAGTGAAGTACTCCTATGACATTAACCGTGTCTCTGAGAGCAG	2386
Qy	2213	ATGACCTTCAAGACTTGGTGTCAATGACCTTACCAGTGGCCGAGCGAGATGAGTACTTG	2272
Db	2387	ATGACCTTCAAGACTTGGTGTCAATGACCTTACCAGTGGCCGAGAGCAGATGAGTACTTG	2446
Qy	2273	GCTTCCCAAAAAATGATATTCATCCGAGATTGACAGCCAGAAATGTTTGTATACAGAAAC	2332
Db	2447	GCTTCCCAAAAAATGATATTCATCCGAGATTGACAGCCAGAAATGTTTGTATACAGAAAC	2506
Qy	2333	AATGTGATGAAAAATAGACAGACTTGTGACTGCGCCAGAGATATCAACATATAGACTATAC	2392
Db	2507	AATGTGATGAAAAATAGACAGACTTGTGACTGCGCCAGAGATATCAACATATAGACTATAC	2566
Qy	2393	AAAAAGACCAACCAATGGGGCGGCTTCCAGTCAATGGATGGCTCCAGAAAGCCCTGTTGAT	2452
Db	2567	AAAAAGACCAACCAATGGGGCGGCTTCCAGTCAATGGATGGCTCCAGAAAGCCCTGTTGAT	2626
Qy	2453	AGACTATTAACCTCATCAGAGATGATGTGGGCTCTGGGGGTGTAAATGTGGAGATCTTC	2512
Db	2627	AGACTATTAACCTCATCAGAGATGATGTGGGCTCTGGGGGTGTAAATGTGGAGATCTTC	2686
Qy	2513	ACTTTAGGGGGCTCGCCCTACCCAGGGATTTCCCGTGGAGGAATTTTTAAGCTGCTGAAG	2572
Db	2687	ACTTTAGGGGGCTCGCCCTACCCAGGGATTTCCCGTGGAGGAATTTTTAAGCTGCTGAAG	2746
Qy	2573	GAAGGACACAGATGATGATAGCCAGCCACTGACCAACCAACCACTGTACATGATATGAG	2632
Db	2747	GAAGGACACAGATGATGATAGCCAGCCACTGACCAACCAACCACTGTACATGATATGAG	2806
Qy	2633	GACGTGGGACATGAGAGGCCCTCCACAGACCAACGTTCAAGCAGTTGTGTGAGAGACTTG	2692
Db	2807	GACGTGGGACATGAGAGGCCCTCCACAGACCAACGTTCAAGCAGTTGTGTGAGAGACTTG	2866
Qy	2693	GATGGAATTTCTCACTCTCAACAACCAATGAGGAATATGTGACCTCAAGCCAACCTCTCGAA	2752
Db	2867	GATGGAATTTCTCACTCTCAACAACCAATGAGGAATATGTGACCTCAAGCCAACCTCTCGAA	2926
Qy	2753	CAGTATTCACCTAGTACCTGACCAACAAGAGTTCTTGTCTTCAAGAGATGATTTCTGTT	2812
Db	2927	CAGTATTCACCTAGTACCTGACCAACAAGAGTTCTTGTCTTCAAGAGATGATTTCTGTT	2986
Qy	2813	TTTTCTCCAGACCCCAATGCCCTTAAGAACCAAGCCCTTCTCAATATCCACATATAAGGC	2872
Db	2987	TTTTCTCCAGACCCCAATGCCCTTAAGAACCAAGCCCTTCTCAATATCCACATATAAGGC	3046
Qy	2873	AGGTGTTAAACATGAAATGACTGTGTCTGTCCGTGCCCAACAGACACAGCACTGGGAACTT	2932
Db	3047	AGGTGTTAAACATGAAATGACTGTGTCTGTGCCCTGCCCAACAGACACAGCACTGGGAACTT	3106
Qy	2933	AGCTACACTGACGAGGAGACCATGCTCTCCAGAGCTTGTGTCTCCACTTGATATATG	2992
Db	3107	AGCTACACTGACGAGGAGACCATGCTCTCCAGAGCTTGTGTCTCCACTTGATATATG	3166
Qy	2993	GATCAGAGAGCAATTAATTTGGAAAAAGTAAACACACATATGTGTAAAGTTTATACAGTTG	3052
Db	3167	GATCAGAGAGCAATTAATTTGGAAAAAGTAAACACACATATGTGTAAAGTTTATACAGTTG	3226
Qy	3053	AAAACTGTATATCTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGCATGCG	3106
Db	3227	AAAACTGTATATCTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGCATGCG	3280
RESULT 6			
ACFP1631			
ID ACFP1631 standard; DNA; 4574 BP.			
XX			

AC ACP91631;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human SIRS/sepsis diagnostic marker DNA fragment 10491.
 XX
 KM Systemic inflammatory response syndrome; SIRS; antibacterial;
 XX immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
 OS Homo sapiens.
 PN MO2004087949-A2.
 PD 14-OCT-2004.
 XX
 PF 31-MAR-2004; 2004WO-EP003419.
 XX
 PR 02-APR-2003; 2003DE-01015031.
 PR 08-AUG-2003; 2003DE-01036511.
 PR 02-SEP-2003; 2003DE-01040395.
 XX
 PA (SIRS-) SIRS LAB GMBH.
 XX
 PI Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;
 DR WPI; 2004-748070/73.
 XX
 PT In vitro detection of systemic inflammatory response syndrome and related
 PT conditions, for e.g. monitoring progression, comprises detecting abnormal
 PT expression of disease-related genes.
 XX
 PS Disclosure; Page: 75pp; German.
 XX
 CC The invention relates to a novel method for in vitro detection of
 CC systemic inflammatory response syndrome (SIRS). The method comprises
 CC detecting abnormal expression of disease-related genes, or their
 CC associated peptides. The method of the invention demonstrates
 CC antibacterial, immunosuppressive and antiinflammatory applications and
 CC may be used for early differential diagnosis, monitoring progression,
 CC assessing risk, assessing the likely response to treatment and for post
 CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and
 CC sepsis-like conditions. The recombinant or synthetic nucleic acid
 CC sequences of the invention, or derived proteins or peptides, may be
 CC useful as calibrants in assays for the specified diseases, for evaluating
 CC activity or toxicity in screening for active agents and/or for
 CC preparation of agents for treatment or prevention of the specified
 CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic
 CC marker DNA fragment of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at fcp.wipo.int/pub/published
 CC pct_sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
 CC disclosed within the specification, however, these have not been taken
 CC into account during indexing due to inconsistencies in application and
 CC format
 XX
 SO Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;
 Query Match 97.0%; Score 3013.2; DB 13; Length 4574;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

QY 176 GTTGCTCCCGCAACCCCGGGCTCGTCGCTTTCTCCATCCGACCCGCGGGCC -CGGG 234
 DB 347 GTTGCTCCCGCAACCCCGGGCTCGTCGCTTTCTCCATCCGACCCGCGGGCCGCGGG 406
 QY 235 GACAAACACAGGTGCGGAGGAGCGTTGCCATTGAATGACTGACGACGACG -GCGGCC 293
 DB 407 GACAAACACAGGTGCGGAGGAGCGTTGCCATTGAATGACTGACGACGACGCGC 466
 QY 294 CTGGTTCCTGAACCCCAACCGCA -GCTGAAGGCAATGCGGCTAGTCCATGCCCGTAGAGA 352
 DB 467 CTGGTTCCTGAACCCCAACCGCAAGGCAATGCGGCTAGTCCATGCCCGTAGAGA 526
 QY 353 AGTGCAGATGAGATTAAAGTCACATGAGATATGAGAGAGACCGGGATGATGATCC 412
 DB 527 AGTGCAGATGAGATTAAAGTCACATGAGATATGAGAGAGACCGGGATGATGATCC 586
 QY 413 GTAACATGATGAGATTAAAGTCACATGAGATATGAGAGAGACCGGGATGATGATCC 472
 DB 587 GTAACATGATGAGATTAAAGTCACATGAGATATGAGAGAGACCGGGATGATGATCC 646
 QY 473 TCCCTGGCCCGGCGCTCTCTCAATTTAGTTAGAGATACCAATTAGAGCCAGAAAGCCA 532
 DB 647 TCCCTGGCCCGGCGCTCTCTCAATTTAGTTAGAGATACCAATTAGAGCCAGAAAGCCA 706
 QY 533 CCAACCAATACCAAAATCTCTCAACAGAGTACGTGGCTCGCCAGGGAGTCTCTA 592
 DB 707 CCAACCAATACCAAAATCTCTCAACAGAGTACGTGGCTCGCCAGGGAGTCTCTA 766
 QY 593 GAGGTGCGTCTGTTGAAAGATGCGCGGTATCATGTTGACATTAAGATGGGGTGCAC 652
 DB 767 GAGGTGCGTCTGTTGAAAGATGCGCGGTATCATGTTGACATTAAGATGGGGTGCAC 826
 QY 653 TTGGGGCCCAAAATGAGAGATGCTTATGGGGAGTACTGAGATTAAGGGGCGCACA 712
 DB 827 TTGGGGCCCAAAATGAGAGATGCTTATGGGGAGTACTGAGATTAAGGGGCGCACC 886
 QY 713 CTTAGAGATCCCGGCTCTATGCTTGTACTGACAGTACGATGAGATGAGTAACTTGG 772
 DB 887 CTTAGAGATCCCGGCTCTATGCTTGTACTGACAGTACGATGAGATGAGTAACTTGG 946
 QY 773 TACTTCATGAGTGAATGACAGATGCTCATCTGAGATGATGAGATGACACCGAT 832
 DB 947 TACTTCATGAGTGAATGACAGATGCTCATCTGAGATGATGAGATGACACCGAT 1006
 QY 833 GGTGCGGAATTTTGTCACTGAGAGACATTAACAACAAGACACCATCTGACCAAC 892
 DB 1007 GGTGCGGAATTTTGTCACTGAGAGACATTAACAACAAGACACCATCTGACCAAC 1066
 QY 893 ACGAAAAGATGAAAAAGCGCTCATGCTGTGCTGCGCAACATGTCAGATTTCG 952
 DB 1067 ACGAAAAGATGAAAAAGCGCTCATGCTGTGCTGCGCAACATGTCAGATTTCG 1126
 QY 953 TGCCACGCGGGGGAAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAAGAGATT 1012
 DB 1127 TGCCACGCGGGGGAAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAAGAGATT 1186
 QY 1013 AAGCAGAGATGATGATGAGAGCTACAGTACGAAACCAAGCATGAGACCTCATATG 1072
 DB 1187 AAGCAGAGATGATGATGAGAGCTACAGTACGAAACCAAGCATGAGACCTCATATG 1246
 QY 1073 GAAAGTGTGCTCATGCAAGGGAATTAATACCTGTGTAGTGAAGATGAATAGAGG 1132
 DB 1247 GAAAGTGTGCTCATGCAAGGGAATTAATACCTGTGTAGTGAAGATGAATAGAGG 1306
 QY 1133 TCCATCAATCAACATGACATGATGTTGTGAGAGATGCTCTCAACCGGCCATCTTC 1192
 DB 1307 TCCATCAATCAACATGACATGATGTTGTGAGAGATGCTCTCAACCGGCCATCTTC 1366
 QY 1193 CAAGCCGATGCTGCGGAATGCTCTCAAGTGTGAGAGAGACATGAGATTGTCTGC 1252
 DB 1367 CAAGCCGATGCTGCGGAATGCTCTCAAGTGTGAGAGAGACATGAGATTGTCTGC 1426
 QY 1253 AAGGTTTACATGATGCTGAGCCCAATCATGATGATCAAGACATGTAAGAAAGACGGC 1312

Db 1427 AAGTTTACAGTATCCAGCCCAATCAGTGCATGAGCACTGGAAAAGACGCG 1486
Qy 1313 AGTAAATAGGGGCGGAGCGGCTGCTCTCAAGGTTCTCAAGCACTCGGGATTAAT 1372
Db 1487 AGTAAATAGGGGCGGAGCGGCTGCTCTCAAGGTTCTCAAGCACTCGGGATTAAT 1546
Qy 1373 AGTCCAAATGCAAGAGTGTGCTGTCTCAATGTGACCGAGCGGATGCTGGGAATAT 1432
Db 1547 AGTCCAAATGCAAGAGTGTGCTGTCTCAATGTGACCGAGCGGATGCTGGGAATAT 1606
Qy 1433 ATATGTAAAGTCTCAATTAATTAAGGCAAGCCACAGTCTGCTGCTCACTGCTCG 1492
Db 1607 ATATGTAAAGTCTCAATTAATTAAGGCAAGCCACAGTCTGCTGCTCACTGCTCG 1666
Qy 1493 CCAAAAACAGCAGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGTCACTGAG 1552
Db 1667 CCAAAAACAGCAGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGTCACTGAG 1726
Qy 1553 ATAGCAATTTAATGCAATAGGGGTCTTCTTAATGCGCTGTATGAGTGAACATCATCTG 1612
Db 1727 ATAGCAATTTAATGCAATAGGGGTCTTCTTAATGCGCTGTATGAGTGAACATCATCTG 1786
Qy 1613 TGCCTGAATGAACAACAGACCAAGAACCAAGCTTCAAGCAAGCCAGCGGCTGTGCAAG 1672
Db 1787 TGCCTGAATGAACAACAGACCAAGAACCAAGCTTCAAGCAAGCCAGCGGCTGTGCAAG 1846
Qy 1673 CTGACCAAAAGTATCCCTGCGGAGACAGGTAAAGTTTCCGCTGATGCTCACTGCTCC 1732
Db 1847 CTGACCAAAAGTATCCCTGCGGAGACAGGTAAAGTTTCCGCTGATGCTCACTGCTCC 1906
Qy 1733 ATGAACTCCAACAACCCGCTGTGTAGAGATTAACAACAGCCTCTCTTCAACGCGACACCC 1792
Db 1907 ATGAACTCCAACAACCCGCTGTGTAGAGATTAACAACAGCCTCTCTTCAACGCGACACCC 1966
Qy 1793 CCCATGTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGACCCAAAATGGAGTTTCCA 1852
Db 1967 CCCATGTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGACCCAAAATGGAGTTTCCA 2026
Qy 1853 AGAGATTAAGCTGACACTGCGGCAAGCCCTGGAGAAAGTTTGTGGGCAAGTGTGATG 1912
Db 2027 AGAGATTAAGCTGACACTGCGGCAAGCCCTGGAGAAAGTTTGTGGGCAAGTGTGATG 2086
Qy 1913 GCGGAAGCACTGGGAATTGAACAAGACCCCAAGAGGCGGTCAACGCTGCGCGTGAAG 1972
Db 2087 GCGGAAGCACTGGGAATTGAACAAGACCCCAAGAGGCGGTCAACGCTGCGCGTGAAG 2146
Qy 1973 ATGTTGAAGAATGATGCAACAGAAAGACCTTCTGATCTGCTGCAAGATGAGATG 2032
Db 2147 ATGTTGAAGAATGATGCAACAGAAAGACCTTCTGATCTGCTGCAAGATGAGATG 2206
Qy 2033 ATGAAGATGATGGGAAACAAGAATATCATTAATCTTCTGAGGCTGCACACAGAT 2092
Db 2207 ATGAAGATGATGGGAAACAAGAATATCATTAATCTTCTGAGGCTGCACACAGAT 2266
Qy 2093 GGGGCTCTCATATGTCATAGTTAGTATGCTCTAAAGGCAACCTCCGAGAAATCTCCGA 2152
Db 2267 GGGGCTCTCATATGTCATAGTTAGTATGCTCTAAAGGCAACCTCCGAGAAATCTCCGA 2326
Qy 2153 GCCCGAGAGCCACCCGGAGTGAATCTCTTATGACATTAACCTGTGCTGAGAGACAG 2212
Db 2327 GCCCGAGAGCCACCCGGAGTGAATCTCTTATGACATTAACCTGTGCTGAGAGACAG 2386
Qy 2213 ATGACCTTCAAGACTTGTGTGATGCACTACACAGCTGCGCAGACGATGAGTACTTG 2272
Db 2387 ATGACCTTCAAGACTTGTGTGATGCACTACACAGCTGCGCAGACGATGAGTACTTG 2446
Qy 2273 GCTTCCCAAAAATATATTCATGAGATTAGACCCAGAAATGTTTTGTAAAGAAAC 2332
Db 2447 GCTTCCCAAAAATATATTCATGAGATTAGACCCAGAAATGTTTTGTAAAGAAAC 2506
Qy 2333 AATGTGATGAATAATGCACTTTGAGCTGCGCAGAGATATCAATATATGACTATTAAC 2392

Db 2507 AATGTGATGAATAATGCACTTTGAGCTGCGCAGAGATATCAATATATGACTATTAAC 2566
Qy 2393 AAAAAACCAACATAGGCGGCTTCCAGTCAAATGATGCTCCGAAGCCCTGTTGAT 2452
Db 2567 AAAAAACCAACATAGGCGGCTTCCAGTCAAATGATGCTCCGAAGCCCTGTTGAT 2626
Qy 2453 AAGATTAACATCAATCAAGTGAATGTCGTGCTTCCGAGGATGTAATGAGGAGATCTTC 2512
Db 2627 AAGATTAACATCAATCAAGTGAATGTCGTGCTTCCGAGGATGTAATGAGGAGATCTTC 2686
Qy 2513 ACTTTAGGGGCTGCGCTTACCAGAGATCCCGTGAAGAACTTTTAAGCTGTGAAG 2572
Db 2687 ACTTTAGGGGCTGCGCTTACCAGAGATCCCGTGAAGAACTTTTAAGCTGTGAAG 2746
Qy 2573 GAAAGACACAGATGATAGCCAGCCAACTGACCAACGAACTGTACATGATGATGAG 2632
Db 2747 GAAAGACACAGATGATAGCCAGCCAACTGACCAACGAACTGTACATGATGATGAG 2806
Qy 2633 GACTGTGGCAATGAGTGGCCCTCCAGAGACCAAGTTCAGACAGTGTGAGAAAGCTTG 2692
Db 2807 GACTGTGGCAATGAGTGGCCCTCCAGAGACCAAGTTCAGACAGTGTGAGAAAGCTTG 2866
Qy 2693 GATCGAATTTCTCACTCTCAACAACAAATGAGATTAATCTGACCTCAGCCAACTTCGAA 2752
Db 2867 GATCGAATTTCTCACTCTCAACAACAAATGAGATTAATCTGACCTCAGCCAACTTCGAA 2926
Qy 2753 CAGTATTTCACTAGTTTACCTTGAACACAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2812
Db 2927 CAGTATTTCACTAGTTTACCTTGAACACAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2986
Qy 2813 TTTTTCGCAAGCCCAATGCTTACGAACCAATGCTCTCAGTATCCAACATTAACGCG 2872
Db 2987 TTTTTCGCAAGCCCAATGCTTACGAACCAATGCTCTCAGTATCCAACATTAACGCG 3046
Qy 2873 AGTGTAAACATGATGACTGTGTGCTGCTGCTGCCAAACAGAACAGCACTGGAACT 2932
Db 3047 AGTGTAAACATGATGACTGTGTGCTGCTGCTGCCAAACAGAACAGCACTGGAACT 3106
Qy 2933 AGCTACATGAGAGGAGACCAATGCTTCCAGAGCTTGTGTCTTCCACTTGTATATG 2992
Db 3107 AGCTACATGAGAGGAGACCAATGCTTCCAGAGCTTGTGTCTTCCACTTGTATATG 3166
Qy 2993 GATCAGAGAGTAAATTAATTTGAAAAGTATGACATATGTGTAAGATTTATACAGTTG 3052
Db 3167 GATCAGAGAGTAAATTAATTTGAAAAGTATGACATATGTGTAAGATTTATACAGTTG 3226
Qy 3053 AAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCACTGACCTGC 3106
Db 3227 AAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCACTGACCTGC 3280

RESULT 7
AEA81172
ID AEA81172 standard; DNA; 4574 BP.
XX
AC AEA81172;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human fibroblast growth factor receptor-2 transcript variant 2 DNA.
XX
KW screening; obesity; nutritional disorder; anorectic; db; gene;
XX
KW fibroblast growth factor receptor-2; FGF receptor-2; transcript variant.
XX
OS Homo sapiens.
XX
PN US2005136465-A1.
XX
XX 23-JUN-2005.
XX
XX 22-DEC-2004; 2004US-00019829.
XX
XX 22-DEC-2003; 2003EP-00104902.
XX
XX

Db 1847 CTGACCAAACTATCCCTCCGCGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCTCC 1906
 QY 1733 ATGAACTCCAAACACCCCGCTGTGTAGAGATTAACAACGCTCTTTCACCGGACACCC 1792
 Db 1907 ATGAACTCCAAACACCCCGCTGTGTAGAGATTAACAACGCTCTTTCACCGGACACCC 1966
 QY 1793 CCCATCTGTGACAGGGGTCTCCAGATATGAATCTCCAGAGAACCCAAAATGGAGTTTCCA 1852
 Db 1967 CCCATCTGTGACAGGGGTCTCCAGATATGAATCTCCAGAGAACCCAAAATGGAGTTTCCA 2026
 QY 1853 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTTGGGCAAGTGTCAATG 1912
 Db 2027 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTTGGGCAAGTGTCAATG 2086
 QY 1913 GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGGCGGTCAACGTGCGTGAAG 1972
 Db 2087 GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGGCGGTCAACGTGCGTGAAG 2146
 QY 1973 ATGTTGAAAGATATGATGACACAGAGAAAGACCTTTCTGATTTGGTGTCAAGATGAGATG 2032
 Db 2147 ATGTTGAAAGATATGATGACACAGAGAAAGACCTTTCTGATTTGGTGTCAAGATGAGATG 2206
 QY 2033 ATGAAATGATTTGGGAAACACAGAAATATGATTAATCTTCTGGAGCTTGCACACAGAT 2092
 Db 2207 ATGAAATGATTTGGGAAACACAGAAATATGATTAATCTTCTGGAGCTTGCACACAGAT 2266
 QY 2093 GGGCTCTCTATGTCATAGTTGAGTATGCTCTTAAAGGCAACCTCCGAGATATCTTCCGA 2152
 Db 2267 GGGCTCTCTATGTCATAGTTGAGTATGCTCTTAAAGGCAACCTCCGAGATATCTTCCGA 2326
 QY 2153 GCCCGAGGACACCCCGGATGAGATCTCTATGACATTTAACGGTGTCTTGAGAGACAG 2212
 Db 2327 GCCCGAGGACACCCCGGATGAGATCTCTATGACATTTAACGGTGTCTTGAGAGACAG 2286
 QY 2213 ATGACCTTCAAGGACTTGTGTATGATGACCTACACAGTGGCCACAGACGATGAGTACTTG 2272
 Db 2387 ATGACCTTCAAGGACTTGTGTATGATGACCTACACAGTGGCCACAGACGATGAGTACTTG 2446
 QY 2273 GCTTCCCAAAATGTATTCATGAGATTTAGACGCCGAAGTGTGTTGTTAACAGAAAC 2332
 Db 2447 GCTTCCCAAAATGTATTCATGAGATTTAGACGCCGAAGTGTGTTGTTAACAGAAAC 2506
 QY 2333 AATGTGATGAATAATAGACACTTTGACCTGCCAGAGATTTCAACAATATAGACTATAC 2392
 Db 2507 AATGTGATGAATAATAGACACTTTGACCTGCCAGAGATTTCAACAATATAGACTATAC 2566
 QY 2393 AAAAAGACCAATGAGGCGGCTTCAATCAAGTATGAGTGCACAGAGCCCTGTTGAT 2452
 Db 2567 AAAAAGACCAATGAGGCGGCTTCAATCAAGTATGAGTGCACAGAGCCCTGTTGAT 2626
 QY 2453 AGAGTATACATCTACAGATGATGTGTCCTTCGAGGATGTTAATGTGAGAGATCTTC 2512
 Db 2627 AGAGTATACATCTACAGATGATGTGTCCTTCGAGGATGTTAATGTGAGAGATCTTC 2686
 QY 2513 ACTTTAGGGGCTGTGCTTACCCAGAGATTTCCGTGAGAGAACTTTTAAGCTGCTGAAG 2572
 Db 2687 ACTTTAGGGGCTGTGCTTACCCAGAGATTTCCGTGAGAGAACTTTTAAGCTGCTGAAG 2746
 QY 2573 GAAGGACACAGAAATGATAAGCCAGCAACTGACCAACGAACGTGATCATGATGATGAGG 2632
 Db 2747 GAAGGACACAGAAATGATAAGCCAGCAACTGACCAACGAACGTGATCATGATGATGAGG 2806
 QY 2633 GACTGTTGGACATGACGTGCTTCCAGAGACCAACGTTCAAGAGTTGGTGAAGAACTTG 2692
 Db 2807 GACTGTTGGACATGACGTGCTTCCAGAGACCAACGTTCAAGAGTTGGTGAAGAACTTG 2866
 QY 2693 GATCGAATTTCTCATCTTCAACAACCAATGAGAAATATCTTGACCTCACCAACCTCTCGAA 2752
 Db 2867 GATCGAATTTCTCATCTTCAACAACCAATGAGAAATATCTTGACCTCACCAACCTCTCGAA 2926
 QY 2753 CAGATATTCACCTACTTACCTGACACAAAGAGTCTTGTGTTTCAAGAGATGATTTGTT 2812
 Db 2927 CAGATATTCACCTACTTACCTGACACAAAGAGTCTTGTGTTTCAAGAGATGATTTGTT 2986

QY 2813 TTTTCTCCAGACCCCATGCTTACGAAACATGCTTCCCTAGATTCACACATAAAGGC 2872
 Db 2987 TTTTCTCCAGACCCCATGCTTACGAAACATGCTTCCCTAGATTCACACATAAAGGC 3046
 QY 2872 AGTGTAAACATGATGATGCTGTCTGTCTGTCTTCCCAACAGACAGCACTGGAACT 2932
 Db 3047 AGTGTAAACATGATGATGCTGTCTGTCTGTCTTCCCAACAGACAGCACTGGAACT 3106
 QY 2933 AGCTACACTGACAGGAGACCATGCTTCCAGACTTGTGTCTTCCCTTATATATG 2992
 Db 3107 AGCTACACTGACAGGAGACCATGCTTCCAGACTTGTGTCTTCCCTTATATATG 3166
 QY 2993 GATCAGAGATTAATTAATTGAAAAGTATGCAATATGTTAAAGATTTATACAGTTG 3052
 Db 3167 GATCAGAGATTAATTAATTGAAAAGTATGCAATATGTTAAAGATTTATACAGTTG 3226
 QY 3053 AAAACTTGTATCTTCCCAAGAGAGAAAGAGTTTCTGAGACAGTGAAGTGC 3106
 Db 3227 AAAACTTGTATCTTCCCAAGAGAGAAAGAGTTTCTGAGACAGTGAAGTGC 3280

RESULT 8
 AEF06407
 ID AEF06407 standard; cDNA; 4574 BP.
 AC AEF06407;
 AC
 DT 23-FEB-2006 (first entry)
 XX
 DE Human fibroblast growth factor receptor 2 cDNA SEQ ID NO 25.
 XX
 KW immunostimulant; cytostatic; antiallergic; antiinflammatory;
 KW antimicrobial; cardiovascular-gen.; selectable marker; diagnostic;
 KW prognosis; screening; therapeutic; mastocytosis; leukemia; tumor;
 KW hematological disease; cardiovascular disease; infection; inflammation;
 KW immune disorder; allergy; cancer; neoplasm;
 KW fibroblast growth factor receptor 2; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 593..3061
 FT CDS /tag= a
 FT /product= "Human fibroblast growth factor receptor 2"
 XX
 PN MO2005085851-A2.
 XX
 PD 15-SEP-2005.
 XX
 PF 03-MAR-2005; 2005MO-US007519.
 XX
 PR 03-MAR-2004; 2004US-0549865P.
 XX
 PA (ADRA/) ADRA C N.
 XX
 PI Adra CN;
 XX
 DR WPI; 2006-117706/12.
 DR P-PSDB; AEF06408.
 DR GENBANK; NM_022969.
 XX
 PT Assay for identifying compound that alters physiological property of
 PT granulocyte, by contacting granulocyte with candidate compound that
 PT interacts with granulocyte marker, determining and comparing
 PT physiological property to reference.
 XX
 PS Disclosure; SEQ ID NO 25; 149bp; English.
 XX
 CC The invention describes an assay (M1) for identifying compound that
 CC alters physiological property of a granulocyte, by contacting a
 CC granulocyte with a candidate compound that interacts with a granulocyte-
 CC selective marker, determining physiological property of a granulocyte

CC after contacting with a candidate compound, and comparing the
 CC physiological property to a reference property to determine whether the
 CC candidate compound alters the physiological property of a granulocyte.
 CC (M1) is useful for identifying a compound that alters one or more
 CC physiological property of a granulocyte. (M2) is useful for diagnosing a
 CC physiological disorder, or non-neutrophil granulocyte disorder or mast cell
 CC disorder, in a biological sample, where the biological sample is a blood
 CC sample and tissue sample. The non-neutrophil granulocyte disorder is a
 CC basophil or eosinophil disorder, where the basophil disorder is a
 CC basophil-associated tumor or cancer, and the eosinophil-associated tumor
 CC or cancer. The mast cell disorder is a mast cell-associated disease or
 CC cancer. (M5) is useful for treating a granulocyte-associated disease or
 CC mast cell-associated disease. The compound identified by (M1) is useful
 CC for treating a granulocyte or mast cell-associated disease, useful for
 CC diagnosing and treating mast cell disorders such as systemic
 CC mastocytosis, indolent mastocytosis, mast cell leukemia, cutaneous
 CC mastocytosis such as urticaria pigmentosa and telangiectasia macularis
 CC eruptive perstans. (M1) or (C1) is useful for drug discovery, disease
 CC diagnosis and/or prognosis, granulocyte type detection and/or selection
 CC and/or manipulation, and/or therapeutic application. (M1) is useful for
 CC screening compounds to identify those that interact with one or more
 CC cell type selective markers. (M1) is useful in identifying leukocytes and
 CC leukocyte-selective markers, and for diagnostic or prognostic purposes
 CC e.g. allergies, cancers, helminthic infestations and eosinophilic
 CC eosinophilic pneumonia, helminthic infestations and eosinophilic
 CC gastrointestinal disorders that includes eosinophilic esophagitis,
 CC eosinophilic gastritis, eosinophilic duodenitis, eosinophilic colitis,
 CC eosinophilic gastroenteritis, and eosinophilic ileitis. (C1) is useful
 CC for treating diseases such as cancer, allergy, inflammation, infections
 CC diseases, cardiovascular disease, other diseases associated with one or
 CC more leukocyte cell types. This sequence encodes human fibroblast growth
 CC factor receptor 2, a granulocyte and/or mast cell-selective marker.

SQ Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;

Query Match 97.0%; Score 3013.2; DB 15; Length 4574;

Best Local Similarity 99.5%; Pred. No. 0; Mismatches 8; Indels 9; Gaps 7;

Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

QY 1 CCCGCGACCAAGTTGGTGGAGGCAAG-C-CAAGCTGAGTCTTTCTCTCTGTTCC 59
 DB 168 CTGCGGAGCAAGTTGGTGGAGGCAAGGCAAGCTGAGTCTTTCTCTCTGTTCC 227
 QY 60 CCAATTCGAGGAGGAGCCCGGGCGTCAATG--GCGTCTCTCCGAGCTGGGGTTACGC 116
 DB 228 CCAATTCGAG-GGAGGAGGAGGAGTCAATGCGGCGTCTCTCCGAGCTGGGGTTACGC 286
 QY 117 G-TGAAGCCGAGGAGGAGTGGCGCGCGGAGAGACCAAGAGCACTTTCTGGGTTTGA 175
 DB 287 GCTGAAGCCGAGGAGGAGTGGCGCGCGGAGAGACCAAGAGCACTTTCTGGGTTTGA 346
 QY 176 GTTCTCTCCGAGCAAGCCCGGGCTGTCGTTTCTCAATCCGAGCCCAAGCGGGAGC-CGGG 234
 DB 347 GTTCTCTCCGAGCAAGCCCGGGCTGTCGTTTCTCAATCCGAGCCCAAGCGGGAGC-CGGG 406
 QY 235 GACAAACAAGGTCGCGAGAGAGCGTTGCAATTCAGTGAAGTCAAGAGCAGC-GAAGGCG 293
 DB 407 GACAAACAAGGTCGCGAGAGAGCGTTGCAATTCAGTGAAGTCAAGAGCAGC-GAAGGCG 466
 QY 294 CTGCGTCTTCAAGGAGGAGGAGCGTTGCAATTCAGTGAAGTCAAGAGCAGC-GAAGGAG 352
 DB 467 CTGCGTCTTCAAGGAGGAGGAGCGTTGCAATTCAGTGAAGTCAAGAGCAGC-GAAGGAG 526
 QY 353 AGTGTGAGATGAGATTAAGTCAATTCAGTGAAGTGAAGAGAGCCGGGAGTTGTTACC 412
 DB 527 AGTGTGAGATGAGATTAAGTCAATTCAGTGAAGTGAAGAGAGCCGGGAGTTGTTACC 586
 QY 413 GTAACCATGTCAGTGGGGTCTTTCATCTGCTGTCGTCGTCGTCACATGCAACTTTG 472
 DB 587 GTAACCATGTCAGTGGGGTCTTTCATCTGCTGTCGTCGTCGTCACATGCAACTTTG 646
 QY 473 TCCCTGCGCGGCGCTCTCTTCAAGTTAGTGAAGTATCAATTAAGAGCAAGAGAGCA 532

DB 647 TCCCTGCGCGGCGCTCTCTTCAAGTTAGTGAAGTATCAATTAAGAGCAAGAGCA 706
 QY 533 CCAACCAATTAACCAATCTCTCAACAGAGTGTAGTGGAGTGGCGGAGGAGTGGCTTA 592
 DB 707 CCAACCAATTAACCAATCTCTCAACAGAGTGTAGTGGAGTGGCGGAGGAGTGGCTTA 766
 QY 593 GAGGTGCGTGGCTGTTGAAGAGTGGCGGCTGATGATGTTGAAGTGAAGTGGGTTGAC 652
 DB 767 GAGGTGCGTGGCTGTTGAAGAGTGGCGGCTGATGATGTTGAAGTGAAGTGGGTTGAC 826
 QY 653 TTGGGGCCCAATVAGACAGTGTCTTAATTTGGGAGTACTTGGAGATTAAGGCGGCA 712
 DB 827 TTGGGGCCCAATVAGACAGTGTCTTAATTTGGGAGTACTTGGAGATTAAGGCGGCA 886
 QY 713 CCTAGAGATCCGGGCTCTATGCTTGTACTGCGAGTGAAGCTGTAGACAGTGAACCTTG 772
 DB 887 CCTAGAGATCCGGGCTCTATGCTTGTACTGCGAGTGAAGCTGTAGACAGTGAACCTTG 946
 QY 773 TACTTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
 DB 947 TACTTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
 QY 833 GGTGCGGAAGATTTTGTCAAGTGAAGACAGTACACACAGAGACACATCTGAGCCAC 892
 DB 1007 GGTGCGGAAGATTTTGTCAAGTGAAGACAGTACACACAGAGACACATCTGAGCCAC 1066
 QY 893 ACGAAAAGATGAAAAGGCGCTCCATGCTGTCGCGGCGCAACCTGTCAGATTTCG 952
 DB 1067 ACGAAAAGATGAAAAGGCGCTCCATGCTGTCGCGGCGCAACCTGTCAGATTTCG 1126
 QY 953 TGCCAGCGGGGGGAAACCAATGCAACCATGCGGTGCTGTAAGAAACGGAGAGATT 1012
 DB 1127 TGCCAGCGGGGGGAAACCAATGCAACCATGCGGTGCTGTAAGAAACGGAGAGATT 1186
 QY 1013 AAGCAGAGAGATGCAATGAGGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1072
 DB 1187 AAGCAGAGAGATGCAATGAGGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1246
 QY 1073 GAAAGTGTGTCCTCATCTGCAAGGAGAAATTAACCTGTGTAGTGAAGTGAAGTGA 1132
 DB 1247 GAAAGTGTGTCCTCATCTGCAAGGAGAAATTAACCTGTGTGTAGTGAAGTGAAGTGA 1306
 QY 1133 TCCATCAATCAACAGTACACCTGATGTTGAGAGGATGCGCTCAACCGGCCATCTC 1192
 DB 1307 TCCATCAATCAACAGTACACCTGATGTTGAGAGGATGCGCTCAACCGGCCATCTC 1366
 QY 1193 CAAGCCGAGCTGCGGCAATGCTTCAAGTGTGAGAGAGAGAGTGAAGTGTGTGTC 1252
 DB 1367 CAAGCCGAGCTGCGGCAATGCTTCAAGTGTGAGAGAGAGAGTGAAGTGTGTGTC 1426
 QY 1253 AAGGTTTACAGTATGCGGAGCCCAATTCAGTGAATGAAGACCGTGAAGAAAGAGAG 1312
 DB 1427 AAGGTTTACAGTATGCGGAGCCCAATTCAGTGAATGAAGACCGTGAAGAAAGAGAG 1486
 QY 1313 AGTAAATAGGAGGAGCGGAGCTGAGCTCACTCAAGGTTTCAAGCACTCGGGAGTAAAT 1372
 DB 1487 AGTAAATAGGAGGAGCGGAGCTGAGCTCACTCAAGGTTTCAAGCACTCGGGAGTAAAT 1546
 QY 1373 AGTTCATGACAGAGTGTGCTGTGTTCAATGTGACAGAGCGGAGTGTGGGAAATAT 1432
 DB 1547 AGTTCATGACAGAGTGTGCTGTGTTCAATGTGACAGAGCGGAGTGTGGGAAATAT 1606
 QY 1433 ATATGTAAAGTCTTCAATTTATATAGGAGAGGCAACAGTGTGCTGAGCTCACTGTCTG 1492
 DB 1607 ATATGTAAAGTCTTCAATTTATATAGGAGAGGCAACAGTGTGCTGAGCTCACTGTCTG 1666
 QY 1493 CAAAAAGAGAGGCGCTGGAAGAGAAAGAGTTACAGCTTCCCAAGACTACCTGAG 1552
 DB 1667 CAAAAAGAGAGGCGCTGGAAGAGAAAGAGTTACAGCTTCCCAAGACTACCTGAG 1726
 QY 1553 ATAGCCATTTACTGATAGGAGGCTTCTTATATGCTGTATGTGTGAACAGTATCTGT 1612
 DB 1727 ATAGCCATTTACTGATAGGAGGCTTCTTATATGCTGTATGTGTGAACAGTATCTGT 1786

QY 1613 TGCAGATGAGAAACA GACCAAGAAAGCACTTCAGCAGCCGCGCTGTGCAAG 1672
 DB 1787 TGCAGATGAGAAACA GACCAAGAAAGCACTTCAGCAGCCGCGCTGTGCAAG 1846
 QY 1673 CTGACCAAAAGTATCCCTCCGCGAAGAGTAAAGTTTCGCGTGAAGTCCAGCTCTCC 1732
 DB 1847 CTGACCAAAAGTATCCCTCCGCGAAGAGTAAAGTTTCGCGTGAAGTCCAGCTCTCC 1906
 QY 1733 ATGAATCCCAACACCCCGCTGTGAGGATTAACAACGCTCTCTTCAACGCGAGACACC 1792
 DB 1907 ATGAATCCCAACACCCCGCTGTGAGGATTAACAACGCTCTCTTCAACGCGAGACACC 1966
 QY 1793 CCCATCTGCGAGGGGCTCTCCGAGTATGAACCTTCAGAGGACCCAAATGGAGTTTCCA 2026
 DB 1967 CCCATCTGCGAGGGGCTCTCCGAGTATGAACCTTCAGAGGACCCAAATGGAGTTTCCA 2026
 QY 1853 AGAGATTAAGTGAACCTGGGCAAGCCCTGGGGAAGGTTGCTTTGGGCAAGTGTCTAG 1912
 DB 2027 AGAGATTAAGTGAACCTGGGCAAGCCCTGGGGAAGGTTGCTTTGGGCAAGTGTCTAG 2086
 QY 1913 GCGGAGAGAGTGGGAATTTGCAAAAGCAAGCCCAAGAGGCGGTCAACCTGGCCGTGAAG 1972
 DB 2087 GCGGAGAGAGTGGGAATTTGCAAAAGCAAGCCCAAGAGGCGGTCAACCTGGCCGTGAAG 2146
 QY 1973 ATGTTGAAGATGATGCGACAGAGAAAGACCTTTCTGATCTGCTGTCAGATGAGATG 2032
 DB 2147 ATGTTGAAGATGATGCGACAGAGAAAGACCTTTCTGATCTGCTGTCAGATGAGATG 2206
 QY 2033 ATGAAGATGATTTGGGAACAAGAAATATCATTAATCTTGTGAGGCTGACACAGGAT 2092
 DB 2207 ATGAAGATGATTTGGGAACAAGAAATATCATTAATCTTGTGAGGCTGACACAGGAT 2266
 QY 2093 GGGCTCTCTATGTCATATGATGATGCTCTTAAAGCAACCTCCGAGATATCTCCGA 2152
 DB 2267 GGGCTCTCTATGTCATATGATGATGCTCTTAAAGCAACCTCCGAGATATCTCCGA 2326
 QY 2153 GCCCGAGAGCCACCCGGGATGAGATCTCCTATGACATTAACCGTGTCTCTGAGAGCAG 2212
 DB 2327 GCCCGAGAGCCACCCGGGATGAGATCTCCTATGACATTAACCGTGTCTCTGAGAGCAG 2386
 QY 2213 ATGACCTTCAAGACCTTGTGTGATGACCTACCAAGTGGCCAGACGAGATGAGTACTTG 2272
 DB 2387 ATGACCTTCAAGACCTTGTGTGATGACCTACCAAGTGGCCAGACGAGATGAGTACTTG 2446
 QY 2273 GCTTCCCAAAATGATTCATCGAGATTTAGCAGCCGAAATGTTTGTGTAACAGAAAC 2332
 DB 2447 GCTTCCCAAAATGATTCATCGAGATTTAGCAGCCGAAATGTTTGTGTAACAGAAAC 2506
 QY 2333 AATGTGATGAATATGACGACTTTGACTGCGCCAGAGATATCAACATATAGATATTAAC 2392
 DB 2507 AATGTGATGAATATGACGACTTTGACTGCGCCAGAGATATCAACATATAGATATTAAC 2566
 QY 2393 AAAAAAGCCCAATGAGCGGCTCCAGTCAAGTGAAGTGTCCAGAAAGCCGTTGAT 2452
 DB 2567 AAAAAAGCCCAATGAGCGGCTCCAGTCAAGTGAAGTGTCCAGAAAGCCGTTGAT 2626
 QY 2453 AGAGTATACACTCATCAGAGATGATGTGATCTTCCGCGGAGTAAATGAGAGATCTTC 2512
 DB 2627 AGAGTATACACTCATCAGAGATGATGTGATCTTCCGCGGAGTAAATGAGAGATCTTC 2686
 QY 2513 ACTTAAAGGGGCTCGCCCTTACCCAGGGAATTCCTGTGAGGAATCTTTTAAAGTCTGAG 2572
 DB 2687 ACTTAAAGGGGCTCGCCCTTACCCAGGGAATTCCTGTGAGGAATCTTTTAAAGTCTGAG 2746
 QY 2573 GAAGAGACAGAAATGAGTAAAGCCAGCAACTGCAACGAAGCTGTACATGATGATGAGG 2632
 DB 2747 GAAGAGACAGAAATGAGTAAAGCCAGCAACTGCAACGAAGCTGTACATGATGATGAGG 2806
 QY 2633 GACTGTGTCATGACGTGCTCTCCAGAGACCAAGCTTCAAGAGTGTGTAAGAGACTTG 2692
 DB 2807 GACTGTGTCATGACGTGCTCTCCAGAGACCAAGCTTCAAGAGTGTGTAAGAGACTTG 2866

QY 2693 GATCGAATTTCTCACTCTCAACCAAGTATGAGTAATCTGAGCACTCAGCAACTCTCGAA 2752
 DB 2867 GATCGAATTTCTCACTCTCAACCAAGTATGAGTAATCTGAGCACTCAGCAACTCTCGAA 2926
 QY 2753 CAGTATTCACCTAGTAACTCCCTGACACAAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2812
 DB 2927 CAGTATTCACCTAGTAACTCCCTGACACAAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2986
 QY 2813 TTTTCTCCAGACCCCATGCTTACGACCAACGATGCTTCCAGATATCCACATAAAGGCG 2872
 DB 2987 TTTTCTCCAGACCCCATGCTTACGACCAACGATGCTTCCAGATATCCACATAAAGGCG 3046
 QY 2873 AGGTAAACAATGATGATGCTGTCTGCTCTCCCAACAGAGACAGCACTGGAACCT 2932
 DB 3047 AGGTAAACAATGATGATGCTGTCTGCTCTCCCAACAGAGACAGCACTGGAACCT 3106
 QY 2933 AGCTACACTGACAGGAGAGACCATGCTTCCAGAGCTGTGTTCTTCCATTGATATATG 2992
 DB 3107 AGCTACACTGACAGGAGAGACCATGCTTCCAGAGCTGTGTTCTTCCATTGATATATG 3166
 QY 2993 GATCAGAGAGTAAATTAATTTGAAAAGTAAATGACATATGTTAAAGATTATACAGTTG 3052
 DB 3167 GATCAGAGAGTAAATTAATTTGAAAAGTAAATGACATATGTTAAAGATTATACAGTTG 3226
 QY 3053 AAACCTTGAATCTTCCCGAGAGAGAGAAAGTTTCTGAGCACTGAGACTGC 3106
 DB 3227 AAACCTTGAATCTTCCCGAGAGAGAGAAAGTTTCTGAGCACTGAGACTGC 3280

RESULT 9
 ADZ13094
 ID ADZ13094 standard; cDNA; 4485 BP.
 XX
 AC ADZ13094;
 XX
 AC
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Human cancer-associated cDNA #188.
 XX
 KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
 KW cytoskeletal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 EN W02005031001-A2.
 XX
 PD 07-APR-2005.
 XX
 PF 23-SEP-2004; 2004MO-US031617.
 XX
 PR 23-SEP-2003; 2003US-00669920.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI, 2005-273395/28.
 DR P-PSDB; ADZ13095.
 XX
 PT Nucleic acid array useful for detecting cancer associated nucleic acid,
 CC comprises two or more nucleic acid probes.
 CC
 PS Disclosure; SEQ ID NO 614; 198bp; English.
 CC
 CC The invention relates to a nucleic acid array for detecting a cancer
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
 CC The invention also relates to a peptide array comprising two or more
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
 CC that binds to a polypeptide, an isolated antibody or its fragment which
 CC binds to a polypeptide, which is prepared by immunizing a host animal
 CC with a composition comprising the polypeptide or its antigen binding
 CC fragment and collecting cells from the host expressing antibodies against
 CC the antigen or its antigen binding fragment, a composition comprising the

QY 1850 CCAAGATGATGCTGACACTGGGCAAGCCCTGGGGAAGGTTGCTTTGGGCAAGTGTTC 1909
DB 2438 CCAAGATGATGCTGACACTGGGCAAGCCCTGGGGAAGGTTGCTTTGGGCAAGTGTTC 2497
QY 1910 ATGGCGGAAGGAGTGGGAATTGACAAAGCAAGCCCAAGGAGGCGGTGACCGTGGCGCTG 1969
DB 2498 ATGGCGGAAGGAGTGGGAATTGACAAAGCAAGCCCAAGGAGGCGGTGACCGTGGCGCTG 2557
QY 1970 AAGATGTTGAAAAGATGATGCGCACAGAAAGACCTTTCTGATCTGTGTTCAGATGAG 2029
DB 2558 AAGATGTTGAAAAGATGATGCGCACAGAAAGACCTTTCTGATCTGTGTTCAGATGAG 2617
QY 2030 ATGATGAAGTGAATTGGGAAAACAAGAAATATCATTAATTTCTTGGAGCTTGCAACAG 2089
DB 2618 ATGATGAAGTGAATTGGGAAAACAAGAAATATCATTAATTTCTTGGAGCTTGCAACAG 2677
QY 2090 GATGGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
DB 2678 GATGGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2737
QY 2150 CGAGCCCGAGAGGCGACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGAGAG 2209
DB 2738 CGAGCCCGAGAGGCGACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGAGAG 2797
QY 2210 CAGATGACCTTCAAGAGCTTGTGTCTATGACCTTACAGTGGCCAGACGAGATGAGTAC 2269
DB 2798 CAGATGACCTTCAAGAGCTTGTGTCTATGACCTTACAGTGGCCAGACGAGATGAGTAC 2857
QY 2270 TTGGCTTCCCAAAAATGATATTCATCGAGATTTAGACGCGCAAAATGTTTGTGTAACGAA 2329
DB 2858 TTGGCTTCCCAAAAATGATATTCATCGAGATTTAGACGCGCAAAATGTTTGTGTAACGAA 2917
QY 2330 AACATGTGATGAAAATAGCAGACTTTGACTGCGCAGAGATATCAACATATATGACTAT 2389
DB 2918 AACATGTGATGAAAATAGCAGACTTTGACTGCGCAGAGATATCAACATATATGACTAT 2977
QY 2390 TACAAAAAGCACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCGTGTT 2449
DB 2978 TACAAAAAGCACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCGTGTT 3037
QY 2450 GATAGATATACACTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2509
DB 3038 GATAGATATACACTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3097
QY 2510 TTGACTTTAGGGGGCTGCGCCTACCCAGGAGATTCCTCCGTGAGGAACTTTTAAAGCTG 2569
DB 3098 TTGACTTTAGGGGGCTGCGCCTACCCAGGAGATTCCTCCGTGAGGAACTTTTAAAGCTG 3157
QY 2570 AAGGAAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2629
DB 3158 AAGGAAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3217
QY 2630 AGGAGCTGTGGGAGTGGAGTGGCTCCAGAGACCAAGTTCAGAGAGTGTGTAAGAGAC 2689
DB 3218 AGGAGCTGTGGGAGTGGAGTGGCTCCAGAGACCAAGTTCAGAGAGTGTGTAAGAGAC 3277
QY 2690 TTGGATGAAATTTCTCACTCTCAACAACCAATGAGAAATATTGACTCAAGCAACTCTCTC 2749
DB 3278 TTGGATGAAATTTCTCACTCTCAACAACCAATGAGAAATATTGACTCAAGCAACTCTCTC 3337
QY 2750 GAAACGATTCACCTAATTAACCTGACACAAAGAAATGTTGTTTTCAGAGAGATGATCT 2809
DB 3338 GAAACGATTCACCTAATTAACCTGACACAAAGAAATGTTGTTTTCAGAGAGATGATCT 3397
QY 2810 GTTTTCTCCAGAGCCCATGCTTACAGAACCATGCTCTCTCACTAGTATCCACATTAAC 2869
DB 3398 GTTTTCTCCAGAGCCCATGCTTACAGAACCATGCTCTCTCACTAGTATCCACATTAAC 3457
QY 2870 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2929
DB 3458 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3517
QY 2930 CTTAGCTACACTGATGAGGAGGAGACCATGCTCTCCAGAGCTTTGTGTCTCCACTTGTATAT 2989

DB 3518 CTTAGCTACACTGAGACGAGGAGACCATGCTCTCCAGAGCTTTGTGTCTCCACTTGTATAT 3577
QY 2990 ATGATCAGAGAGATTAATTAATTTGAAAAGTATGATGATGATGATGATGATGATGATGAT 3048
DB 3578 ATGATCAGAGAGATTAATTAATTTGAAAAGTATGATGATGATGATGATGATGATGATGAT 3636
RESULT 10
ACF91630
ID ACF91630 standard; DNA; 4587 BP.
XX
AC ACF91630;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human SIRS/sepsis diagnostic marker DNA fragment 10490.
XX
KW Systemic inflammatory response syndrome; SIRS; antibacterial;
XX immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
XX
OS Homo sapiens.
XX
PN MO2004087949-A2.
XX
PD 14-OCT-2004.
XX
PF 31-MAR-2004; 2004MO-EP003419.
XX
PR 02-APR-2003; 2003DE-01015031.
XX 08-AUG-2003; 2003DE-01036511.
PR 02-SEP-2003; 2003DE-01040395.
XX
PA (SIRS-) SIRS LAB GMBH.
XX
PI Russwurm S, Reinhardt K, Saluz H, Straube E, Zipfel PF, Deigner H;
XX
DR WPI, 2004-748070/73.
XX
PT In vitro detection of systemic inflammatory response syndrome and related
XX conditions, for e.g. monitoring progression, comprises detecting abnormal
XX expression of disease-related genes.
XX
PS Disclosure; Page; 75pp; German.
XX
XX The invention relates to a novel method for in vitro detection of
XX systemic inflammatory response syndrome (SIRS). The method comprises
XX detecting abnormal expression of disease-related genes, or their
XX associated peptides. The method of the invention demonstrates
XX antibacterial, immunosuppressive and antiinflammatory applications and
XX may be used for early differential diagnosis, monitoring progression,
XX assessing risk, assessing the likely response to treatment and for post
XX mortem diagnosis of systemic inflammatory response syndrome, sepsis and
XX sepsis-like conditions. The recombinant or synthetic nucleic acid
XX sequences of the invention, or derived proteins or peptides, may be
XX useful as calibrants in assays for the specified diseases, for evaluating
XX activity or toxicity in screening for active agents and/or for
XX preparation of agents for treatment or prevention of the specified
XX diseases. The current sequence is that of a human SIRS/sepsis diagnostic
XX marker DNA fragment of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at fdp.wipo.int/pub/published
XX pct.sequences. Furthermore, a number of arbitrary SRO ID NO.s are
XX disclosed within the specification, however, these have not been taken
XX into account during indexing due to inconsistencies in application and
XX format
SQ Sequence 4587 BP; 1240 A; 1079 C; 1150 G; 1118 T; 0 U; 0 Other;
Query Match 93.5%; Score 2904.2; DB 13; Length 4587;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;

1 CCGGAGCAAGTTTGTGAGGACAG-CAAGCTGAGCTTCTCTCTGCTCC 59
168 CTGGGAGCAAGTTTGTGAGGACAGCAAGCTGAGCTTCTCTCTCTGCTCC 227
Qy 60 CCAATTCGAGGAGCGCCGCGGCGTCAATG--GCGCTCTCGGAGCCTGGGGTAAGC 116
228 CCAATTCGAGGAGCGCCGCGGCGTCAATGCGCGCTCTCGGAGCCTGGGGTAAGC 287
Qy 117 GTGAGGCGGAGGAGCTTGGCGCGGAGAGACCCAGAGCACTCTTCTGCGTTTGAAG 176
288 GTGAGGCGGAGGAGCTTGGCGCGGAGAGACCCAGAGCACTCTTCTGCGTTTGAAG 347
Qy 177 TTGCTCCCGGAGCCCGGCGTGTGCTTCTTCATCCGAGCCAGCGGAGG-CGGG 235
348 TTGCTCCCGGAGCCCGGCGTGTGCTTCTTCATCCGAGCCAGCGGAGGCGGG 407
Db 236 ACAACAGAGTCCGCGAGAGCGTTGCAATTCAGAGTGCAGCAGCAGC-AGAGCGCC 294
408 ACAACAGAGTCCGCGAGAGCGTTGCAATTCAGAGTGCAGCAGCAGCAGCGCGC 467
Qy 295 TCGGTTCTGAGCCACCGCA-EGTGAAGCATTCGCGTATGTCATGCGCGTGAAGAA 353
468 TCGGTTCTGAGCCACCGCAAGCGCTGAAGGCAATTCGCGTATGTCATGCGCGTGAAGAA 527
Db 354 GTGTCAGATGGGATTAACTCCACATGAGATPAGAGAGAGACCGGGGATTGTACCG 413
528 GTGTCAGATGGGATTAACTCCACATGAGATPAGAGAGAGACCGGGGATTGTACCG 587
Qy 414 TAAACATGTCAGCTGGGGTCTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
588 TAAACATGTCAGCTGGGGTCTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
Db 474 CCTGCGCCGCGCTCTCTTCACTTGAAGTGAAGATCAACATTTAGAGCCAGAGAGCCAC 533
648 CCTGCGCCGCGCTCTCTTCACTTGAAGTGAAGATCAACATTTAGAGCCAGAGAGCCAC 707
Qy 534 CAACCAATACCAATCTCTCAACAGAGTACGTCGCGCGCGAGGGGAGTGGCTAG 593
708 CAACCAATACCAATCTCTCAACAGAGTACGTCGCGCGCGAGGGGAGTGGCTAG 767
Db 594 AGGTGCGCTGCTGTTGAAGATGCGCGCTGATCAGTTGAGCTTAAGATGGGTGCT 653
768 AGGTGCGCTGCTGTTGAAGATGCGCGCTGATCAGTTGAGCTTAAGATGGGTGCT 827
Qy 654 TGGGCGCCCAACATAGAGCAGTGTCTTATGGGAGTCTTGCAAGTAAAGGCGCCACGC 887
828 TGGGCGCCCAACATAGAGCAGTGTCTTATGGGAGTCTTGCAAGTAAAGGCGCCACGC 887
Db 714 CTAGAGCTCGGCTCTATGCTTGTATCTGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 773
888 CTAGAGCTCGGCTCTATGCTTGTATCTGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 947
Qy 774 ACTTCATGAGTGAATGTCAGATGTCAGATCTCATCCGAGATGATGAGATGACCGGATG 833
948 ACTTCATGAGTGAATGTCAGATGTCAGATCTCATCCGAGATGATGAGATGACCGGATG 1007
Db 834 GTGCGGAAGATTTTGTCAGTGAAGACAGTAAACAAGAGAGCACTTCTGAGCAACA 893
1008 GTGCGGAAGATTTTGTCAGTGAAGACAGTAAACAAGAGAGCACTTCTGAGCAACA 1067
Qy 894 CAGAAAAGATGGAAGAGCGCTTCATGCTGCTGCGGCAACATGTCAGAGTTTGCT 1127
1068 CAGAAAAGATGGAAGAGCGCTTCATGCTGCTGCGGCAACATGTCAGAGTTTGCT 1127
Db 954 GCCGAGCGGGGAGAACCAATGCAACATGCGGTGCTGAAAAAGGAGAGGATTTA 1013
1128 GCCGAGCGGGGAGAACCAATGCAACATGCGGTGCTGAAAAAGGAGAGGATTTA 1187
Qy 1014 AGCAGAGCATCGCATTTGAGAGGCTTACAGGTACAGAAACAGCAGCTGAGGCTCATTTAGG 1073
1188 AGCAGAGCATCGCATTTGAGAGGCTTACAGGTACAGAAACAGCAGCTGAGGCTCATTTAGG 1247
Db 1074 AAAGTGTGCTCCATTCGACAGAGGAATTTACTCTGTGTAGTGAAGATGAATAGCGGT 1133

1248 AAAGTGTGCTCCATTCGACAGAGGAATTTACTGTGTGTGAGGAATGAATAGCGGT 1307
Qy 1134 CCATCAATCAACATGTCACCTGAGATGTTGTGAGAGATGCGCTCACCGGCCCATCTCC 1193
1308 CCATCAATCAACATGTCACCTGAGATGTTGTGAGAGATGCGCTCACCGGCCCATCTCC 1367
Qy 1194 AAGCGGAGTCCGCGCAATGCTTCAAGTGTGAGAGAGCTGAGATTTGTCTGCA 1253
1368 AAGCGGAGTCCGCGCAATGCTTCAAGTGTGAGAGAGCTGAGATTTGTCTGCA 1427
Db 1254 AGGTTTACATGATGTCACCGCCCAATGCAATGATGATGATGATGATGATGATGATGATG 1313
1428 AGGTTTACATGATGTCACCGCCCAATGCAATGATGATGATGATGATGATGATGATGATG 1487
Qy 1314 GTAAATACGGGCGGAGCGGCTGCTTCAAGTGTTCAGAGCACTGGGGATTAATA 1373
1488 GTAAATACGGGCGGAGCGGCTGCTTCAAGTGTTCAGAGCGCGGGGTTTAA 1547
Db 1374 GTTCAATGAGAGAGTGGCTGTG-----TCAATGATGACGAGCGGATGCTGGG 1427
1548 CCAAGGACAAAGATTTAGAGTTCTTATATTCGAAATTAATTTTGAAGAGCTGGG 1607
Qy 1428 AATATATATGTAAGTCTCCATTAATATAGGCGAGCCCAACAGTGTGCTGCTCACTG 1487
1608 AATATATGTCCTTGGCGGGTAAATTTATATGAGATATCTTCACTGATGTTGACAG 1667
Db 1488 TCTGCGAAMACAGCAGCGCTGGAAGAGAAAGAGATTAAGCTTCCCGACATACC 1547
1668 TCTGCG-----AGGCGCTGGAAGAGAAAGAGATTAAGCTTCCCGACATACC 1718
Qy 1548 TGAAGATGAGCATTTATCTGATAGGGGTCTTCTTAATGCGCTGATAGTGAACATGCA 1607
1719 TGAAGATGAGCATTTATCTGATAGGGGTCTTCTTAATGCGCTGATAGTGAACATGCA 1778
Db 1608 TCTGTCGCGAATGGAAGAACAGACCAAGAGCCAGACTTCAGACGCGGCTGTGC 1838
1779 TCTGTCGCGAATGGAAGAACAGACCAAGAGCCAGACTTCAGACGCGGCTGTGC 1838
Qy 1668 ACAAGCTGACCAAGCTATCCCTGCGAGACAGGTAACAGTTTGGCTGAGTCCAGCT 1727
1839 ACAAGCTGACCAAGCTATCCCTGCGAGACAGGTAACAGTTTGGCTGAGTCCAGCT 1898
Db 1728 CTTCAAGTACCTCAACACCGCGTGTGAGATTAACAAGCGCTCTTCAACGCGCAG 1787
1899 CTTCAAGTACCTCAACACCGCGTGTGAGATTAACAAGCGCTCTTCAACGCGCAG 1958
Qy 1788 ACAACCCCATGCTGAGAGGGGTCTCCAGATATGAATTCACAGAGACCCAAATGGAGT 1847
1959 ACAACCCCATGCTGAGAGGGGTCTCCAGATATGAATTCACAGAGACCCAAATGGAGT 2018
Db 1848 TTCCAAGATATGCTGACACTGGGCAAGCCCTGGAGAGAGTTCTTGGGCAAGTGG 2078
2019 TTCCAAGATATGCTGACACTGGGCAAGCCCTGGAGAGAGTTCTTGGGCAAGTGG 2078
Qy 1908 TCAATGCGGAAGAGAGGGAATGACAAAGACAGCCCAAGAGGGGTCAACGTTGGCCG 1967
2079 TCAATGCGGAAGAGAGGGAATGACAAAGACAGCCCAAGAGGGGTCAACGTTGGCCG 2138
Db 1968 TGAAGATGTTGAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTCTGAGATGG 2027
2139 TGAAGATGTTGAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTCTGAGATGG 2198
Qy 2028 AGATGAGTGAAGATGATGGAAGAACAGAAATTCATTAATCTTCTTGAAGCTGACAC 2087
2199 AGATGAGTGAAGATGATGGAAGAACAGAAATTCATTAATCTTCTTGAAGCTGACAC 2258
Db 2088 AGATGAGCTCTCTATGTCATGTTGATGATGATGATGATGATGATGATGATGATGATG 2147
2259 AGATGAGCTCTCTATGTCATGTTGATGATGATGATGATGATGATGATGATGATGATG 2218
Qy 2148 TCCGAGCCCGAGAGCCACCGGAGTGAAGTACTCTATGACATTAACCGTGTCTGAGG 2207


```
QY 2628 TGAGGAGCTGTTGGCATGAGTGCCCTCCAGAGACCAAGTTCAAGAGCTGTAGAG 2687
    |||
DB 2799 TGAGGAGCTGTTGGCATGAGTGCCCTCCAGAGACCAAGTTCAAGAGCTGTAGAG 2858
QY 2688 ACTTGGATGGAATTTCTCACTCTTCACAAACCAATGAGAAATCTTGAACCTCAGCAACCTC 2747
    |||
DB 2859 ACTTGGATGGAATTTCTCACTCTTCACAAACCAATGAGAAATCTTGAACCTCAGCAACCTC 2918
QY 2748 TCGAAGCATTTTCACTCACTTACCTTCAGACAAAGATTCTTGTCTTGAGAGATGAT 2807
    |||
DB 2919 TCGAAGCATTTTCACTCACTTACCTTCAGACAAAGATTCTTGTCTTGAGAGATGAT 2978
QY 2808 CTGTTTTTCTCCAGACCCCAAGCCTTACGACCAATGCTCTTCTCAATTCACACATTA 2867
    |||
DB 2979 CTGTTTTTCTCCAGACCCCAATGCTCTTACGACCAATGCTCTTCTCAATTCACACATTA 3038
QY 2868 ACGGCGATGTTAAACATGATGACTGTGTCTGCTCCCAAGACAGACGACTGGG 2927
    |||
DB 3039 ACGGCGATGTTAAACATGATGACTGTGTCTGCTCCCAAGACAGACGACTGGG 3098
QY 2928 AACCTAGCTACACTGAGAGGAGACCAATGCTCCAGAGCTTGTCTCCACTTGTAT 2987
    |||
DB 3099 AACCTAGCTACACTGAGAGGAGACCAATGCTCCAGAGCTTGTCTCCACTTGTAT 3158
QY 2988 ATATGATCAGAGAGATTAATTAATTGAAAAATGATCAGATATGTTGTAAGATTATAC 3047
    |||
DB 3159 ATATGATCAGAGAGATTAATTAATTGAAAAATGATCAGATATGTTGTAAGATTATAC 3218
QY 3048 AGTTGAAAACTTGTATCTTCCCAAGAGAGAAAGTTCTTGAGACAGTGGACTGC 3106
    |||
DB 3219 AGTTGAAAACTTGTATCTTCCCAAGAGAGAAAGTTCTTGAGACAGTGGACTGC 3277

RESULT 12
ID ABE49323 standard, cDNA; 4587 BP.
XX
AC ABE49323;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human FCER-2 polynucleotide SEQ ID NO 242.
XX
XX immunosuppressive; cytostatic; nootropic; neuroprotective; antiarthritic;
XX antiinflammatory; antihemetic; vitruclide; pharmaceutical; therapeutic;
XX cell signaling; cell proliferation; angiogenesis; neovascularization;
XX neurodegenerative disease; neuroprotective; neurological disease;
XX inflammation; hyperproliferation; cancer; parasitic infection;
XX antiparasitic; viral infection; vitruclide; infection;
XX angiogenesis disorder; antiangiogenic; cardiovascular disease; tumor;
XX neoplasm; immune disorder; cell surface receptor; ds.
XX
OS Homo sapiens.
XX
PN WO2005113596-A2.
XX
PD 01-DEC-2005.
XX
PF 13-MAY-2005; 2005MO-US017051.
XX
PR 14-MAY-2004; 2004US-0571289P.
PR 18-JUN-2004; 2004US-0580990P.
PR 30-MAR-2005; 2005US-0666825P.
XX
PA (RECE-) RECEPTOR BIOLOGIX INC.
XX
PI Jin P, Shepard MH;
XX
DR WPI; 2005-812226/82.
XX
DR P-Psdb; ABE49350.
XX
PT New polypeptides, specifically isoforms of cell surface receptors, such
```

```
PT as EphA, VEGF, MET, RON, CSF, etc. useful treating cancer, or
PT inflammatory, infectious, angiogenesis-related conditions, or immune
PT disorders.
XX
XX Example 1; SEQ ID NO 242; 647bp; English.
PS
CC The invention describes an isolated polypeptide, comprising at least one
CC domain of an EphA or EphB receptor, where the polypeptide comprises an
CC ephrin ligand binding domain and the polypeptide lacks one or more amino
CC acids corresponding to the transmembrane domain of the EphA or EphB
CC receptor where the membrane localization of the polypeptide is reduced or
CC abolished compared to the EphA or EphB receptor. The polypeptides,
CC compositions, molecules and methods are useful for treating cancers,
CC inflammatory diseases, infectious diseases angiogenesis-related
CC conditions (conditions involving angiogenesis), cell proliferation-
CC related conditions, conditions involving hyperproliferation of cells,
CC immune disorders and neurodegenerative diseases. The disease or condition
CC is selected from rheumatoid arthritis, multiple sclerosis, posterior
CC intraocular inflammation, uveitic disorders, ocular surface inflammatory
CC disorders, neovascular disease, proliferative vitreoretinopathy,
CC atherosclerosis, rheumatoid arthritis, hemangioma, diabetes mellitus,
CC inflammatory bowel disease, psoriasis, Alzheimer's disease, lupus,
CC vascular stenosis, restenosis, inflammatory joint disease,
CC atherosclerosis, urinary obstructive syndromes, and asthma. The disease
CC or condition is selected from carcinoma, lymphoma, blastoma, sarcoma,
CC leukemia, lymphoid malignancies, squamous cell cancer, small-cell lung
CC cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous
CC carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer,
CC gastric cancer, stomach cancer, gastrointestinal cancer, pancreatic
CC cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer,
CC bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer,
CC colorectal cancer, endometrial or uterine carcinoma, salivary gland
CC carcinoma, kidney/renal cancer, prostate cancer, vulval cancer, thyroid
CC cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, and head and
CC neck cancer. The disease or condition includes infection by a virus or a
CC parasite. The virus is selected from Myxoma virus, Vaccinia virus,
CC Tanpopo virus, Epstein-Barr virus, Herpes simplex virus, Cytomegalovirus,
CC Herpesvirus saimiri, Hepatitis B virus, African swine fever virus,
CC Parvovirus, Human Immune deficiency virus (HIV), Hepatitis C virus,
CC Influenza virus, Respiratory syncytial virus, Measles virus, Vesicular
CC stomatitis virus, Dengue virus and Ebola virus. The combination is useful
CC for treating angiogenic-related disorder, a tumor and/or an immune
CC disorder. This sequence represents a cell surface receptor isoform
CC polynucleotide.
XX
SQ Sequence 4587 BP; 1240 A; 1079 C; 1150 G; 1118 T; 0 U; 0 Other;
XX
XX Query Match 93.5%; Score 2904.2; DB 14; Length 4587;
XX Best Local Similarity 97.3%; Pred. No. 0;
XX Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;
QY 1 CCCGCGAGCAAAAGTTGTTGAGAGGCAAG-CAAGCTTAGTCTTCTTCTGCTGCTCC 59
    |||
DB 168 CTCGGGAGCAAAAGTTGTTGTTGAGAGCAAGCGCAAGCTGAGTCTTCTTCTGCTGCTCC 227
    |||
QY 60 CCAATTCGAGGGGCAAGCCCGCGGGGCTCATG---CGGCTCTCCGAGCTGAGGAGTACGC 116
    |||
DB 228 CCAATTCGAGGGGCAAGCCCGCGGGGCTCATG---CGGCTCTCCGAGCTGAGGAGTACGC 287
    |||
QY 117 GTGAAGCCCGGAGAGGCTTGCGCGCGGAGAGACCAAGAGACCACTTTGCGTTTGGAG 176
    |||
DB 288 GTGAAGCCCGGAGAGGCTTGCGCGCGGAGAGACCAAGAGACCACTTTGCGTTTGGAG 347
    |||
QY 177 TTGCTCCCGCAACCCCGGGGCTTGCTGCTTCTTCATCCGACCAAGCGGGAGC-CGGGG 235
    |||
DB 348 TTGCTCCCGCAACCCCGGGGCTTGCTGCTTCTTCATCCGACCAAGCGGGAGC-CGGGG 407
    |||
QY 236 ACAACACAGGTGCGGAGAGAGGCTTGCTTCATTAAGTGAATGACAGACAGC-GCAGCGGC 294
    |||
DB 408 ACAACACAGGTGCGGAGAGAGGCTTGCTTCATTAAGTGAATGACAGACAGC-GCAGCGGC 467
    |||
QY 295 TGGGTTCCGAGCCGCAAGCGCA-GCTGAAGGCAATGCGGTAGTCAATGCCCTAGAGGAA 353
    |||
```

```
Db 468 TCGGTTCTCTAGACCCACCGAGGCTGAAGCAATTGCCGGTAGTTCATGCCCCGTAGAGAA 527
Qy 354 GTGTGCAATGGGATTTAACTTCAATGAGAGATATGAAAGAGACCCGGGATTTGGTACG 413
Db 528 GTGTGCAATGGGATTTAACTTCAATGAGAGATATGAAAGAGACCCGGGATTTGGTACG 587
Qy 414 TAAACATAGTTCAGTGGGGGTGTTTCAATCTGCTGGTCTGGTGTACCACTGGCACTTGT 473
Db 588 TAAACATAGTTCAGTGGGGGTGTTTCAATCTGCTGGTCTGGTGTACCACTGGCACTTGT 647
Qy 474 CCTGAGCCCGGACCTCTCTTCACTTGTAGTGAAGATACCACTTGAAGCCAGAGAGCCAC 533
Db 648 CCTGAGCCCGGACCTCTCTTCACTTGTAGTGAAGATACCACTTGAAGCCAGAGAGCCAC 707
Qy 534 CAACCAAAATACCAATCTCTCAACCAAGATGTACGTGGCTGGCCAGGGGAGTGGCTAG 593
Db 708 CAACCAAAATACCAATCTCTCAACCAAGATGTACGTGGCTGGCCAGGGGAGTGGCTAG 767
Qy 594 AGGTGCGCTGCTCTTGAAGAATGCCGCCGTGATCAGTGTGACTTAAAGATGGGGTGA 653
Db 768 AGGTGCGCTGCTCTTGAAGAATGCCGCCGTGATCAGTGTGACTTAAAGATGGGGTGA 827
Qy 654 TGGGGCCCAACATAGGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCGACAC 713
Db 828 TGGGGCCCAACATAGGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCGACAC 887
Qy 714 CTAGAGCTCCGACCTTATGCTTGTACTGCTGCACTGAGAGCTGTAGACAGTGAATCTTGT 773
Db 888 CTAGAGCTCCGACCTTATGCTTGTACTGCTGCACTGAGAGCTGTAGACAGTGAATCTTGT 947
Qy 774 ACTTCATGATGTAATGTCAAGATGCAATGCCATCTCATCCGAGATGAGAGATGACCCATG 833
Db 948 ACTTCATGATGTAATGTCAAGATGCAATGCCATCTCATCCGAGATGAGAGATGACCCATG 1007
Qy 834 GTGCGGAAGATTTTGTCACTGAGAGACAGTAAACAAGAAGAGACCACTACTGAGCAACA 893
Db 1008 GTGCGGAAGATTTTGTCACTGAGAGACAGTAAACAAGAAGAGACCACTACTGAGCAACA 1067
Qy 894 CAGAAAAGATGAAAAGCGGCTCAATGCTGTGCTGCGGCAACACTGTCAAGTTTGCT 953
Db 1068 CAGAAAAGATGAAAAGCGGCTCAATGCTGTGCTGCGGCAACACTGTCAAGTTTGCT 1127
Qy 954 GCCCAGCCGGGGGAAACCAATGCAACCAATGCGGTGCTGAAAACCGGAGAGATTTA 1013
Db 1128 GCCCAGCCGGGGGAAACCAATGCAACCAATGCGGTGCTGAAAACCGGAGAGATTTA 1187
Qy 1014 AGCAGAGCATCGCATTTGAGAGGCTACAAAGTACGAAAACAGCACTGAGCTCTATTATG 1073
Db 1188 AGCAGAGCATCGCATTTGAGAGGCTACAAAGTACGAAAACAGCACTGAGCTCTATTATG 1247
Qy 1074 AAAGTGTGCTCCATCTGACAAAGGAAATTAACCTGTGTAGTGAAGATGAATACGGGT 1133
Db 1248 AAAGTGTGCTCCATCTGACAAAGGAAATTAACCTGTGTAGTGAAGATGAATACGGGT 1307
Qy 1134 CCATCATCAACAGCTACCACTGTGATTTGTGAGGCAATGCCCTTCAACCGGCTCTCTCC 1193
Db 1308 CCATCATCAACAGCTACCACTGTGATTTGTGAGGCAATGCCCTTCAACCGGCTCTCTCC 1367
Qy 1194 AAGCCGAGCTGCGGCAAAATGCTCTCAACAGTGTGCGAGAGAGAGTGAAGTTTGTCTGCA 1253
Db 1368 AAGCCGAGCTGCGGCAAAATGCTCTCAACAGTGTGCGAGAGAGAGTGAAGTTTGTCTGCA 1427
Qy 1254 AGGTTTACAGTATGCCAGGCCCAACATCCAGTGTATCAAGCAGTGTGAAAAGACGGCA 1313
Db 1428 AGGTTTACAGTATGCCAGGCCCAACATCCAGTGTATCAAGCAGTGTGAAAAGACGGCA 1487
Qy 1314 GTAATAATGCGGCGCGAGCGGCTGCTTCAAGTTCATCAAGCTTCGCGGATTAATA 1373
Db 1488 GTAATAATGCGGCGCGAGCGGCTGCTTCAAGTTCATCAAGCTTCGCGGATTAATA 1547
Qy 1374 GTTCCAAATGCAAGATGCTGCTGT-----TCAATGTGACGAGCGGATGCTGGGG 1427
Db 1548 CCAACGACAAAGATTTGAGGTTCTTATATTCCGAGATTAATTTTGAAGACCTGGGG 1607
Qy 1428 AATATATATGTAAGGTCTCCAAATTAATAGGGGAGGCCAACAGTCTGCTGCTCACTG 1487
Db 1608 AATATATGTTCTTGGCGGGATTTCTATTTGGGATATCTTTCATCTGCAATGTTGACAG 1667
Qy 1488 TCTGCGCAAAACAGCAAGCCCTGGAAGAGAAAAGAGATTAAGCTTCCCGACATACC 1547
Db 1668 TTTCTGCC-----AGGCGCTGGAAGAGAAAAGAGATTAAGCTTCCCGACATACC 1718
Qy 1548 TGAAGATAGCATTTTACTGCAATAGGGGTCTTCTTAATGCGCTGTATGTTGTATCACTCA 1607
Db 1719 TGAAGATAGCATTTTACTGCAATAGGGGTCTTCTTAATGCGCTGTATGTTGTATCACTCA 1778
Qy 1608 TCCGTGCGGATGGAAGAACAGGACCAAGAGCCAGACTTCAGAGCCAGCGGCTGTGC 1667
Db 1779 TCCGTGCGGATGGAAGAACAGGACCAAGAGCCAGACTTCAGAGCCAGCGGCTGTGC 1838
Qy 1668 ACAAGCTGACCAAAACGTATCCCTCGCGAGACAGGTAAAGTTTCCGCTGAGTCCAGCT 1727
Db 1839 ACAAGCTGACCAAAACGTATCCCTCGCGAGACAGGTAAAGTTTCCGCTGAGTCCAGCT 1898
Qy 1728 CTTCCATGAATCTCCAAACCCCGCTGAGAGATTAACAACGCTCTTCAACGGCAG 1787
Db 1899 CTTCCATGAATCTCCAAACCCCGCTGAGAGATTAACAACGCTCTTCAACGGCAG 1958
Qy 1788 ACACCCCCACTGCTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGAACCCAAATGGAGT 1847
Db 1959 ACACCCCCACTGCTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGAACCCAAATGGAGT 2018
Qy 1848 TTCCAAGAGATTAAGCTGACACTGGGCAAGCCCTGAGAGAGGTTTGTGGCAATGG 1907
Db 2019 TTCCAAGAGATTAAGCTGACACTGGGCAAGCCCTGAGAGAGGTTTGTGGCAATGG 2078
Qy 1908 TCATGCGGAAGACGTGGAAATTTGACAAAGACAAAGCCCAAGAGGCGGTCAACGTGGCCG 1967
Db 2079 TCATGCGGAAGACGTGGAAATTTGACAAAGACAAAGCCCAAGAGGCGGTCAACGTGGCCG 2138
Qy 1968 TGAAGATGTTGAAAGATGATGCCACAGAGAAAGCTTTCTGATCTGGTGCAGAGATGG 2027
Db 2139 TGAAGATGTTGAAAGATGATGCCACAGAGAAAGCTTTCTGATCTGGTGCAGAGATGG 2198
Qy 2028 AGATGATGAGATGATTTGGGAAAACAACAAGATATCATTAATCTTCTTGGAGCTGCAAC 2087
Db 2199 AGATGATGAGATGATTTGGGAAAACAACAAGATATCATTAATCTTCTTGGAGCTGCAAC 2258
Qy 2088 AGATGAGGCTCTCTATGTCAATGTTGATGCTTAAAGGCAACCTCCAGAAATACC 2147
Db 2259 AGATGAGGCTCTCTATGTCAATGTTGATGCTTAAAGGCAACCTCCAGAAATACC 2318
Qy 2148 TCCGAGCCCGGAGGCCACCCGGGATGAGATCTCTATGACATTAACCGTGTCTGAGG 2267
Db 2319 TCCGAGCCCGGAGGCCACCCGGGATGAGATCTCTATGACATTAACCGTGTCTGAGG 2378
Qy 2208 AGCAGATGACCTTCAAGAGACTTGGGTGATGACACTACAGCTGAGCCAGACGAGTGAAT 2267
Db 2379 AGCAGATGACCTTCAAGAGACTTGGGTGATGACACTACAGCTGAGCCAGACGAGTGAAT 2438
Qy 2268 ACTTGGCTTCCAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACG 2327
Db 2439 ACTTGGCTTCCAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACG 2498
Qy 2328 AAAACAATGTATGAAAAATGACAGACTTTGAGCTGCGCAAGATATCAACATTAAGT 2387
Db 2499 AAAACAATGTATGAAAAATGACAGACTTTGAGCTGCGCAAGATATCAACATTAAGT 2558
Qy 2388 ATTACAAAAGACCAACCAATGCGGCGCTTCAAGTGAATGAGTGTCTCCAGAGCCCTGT 2447
Db 2559 ATTACAAAAGACCAACCAATGCGGCGCTTCAAGTGAATGAGTGTCTCCAGAGCCCTGT 2618
Qy 2448 TTGATAGATATACACTCATCAAGATGATGTGTGCTTTCGCGGTGTTAATGTGGAGA 2507
Db 2619 TTGATAGATATACACTCATCAAGATGATGTGTGCTTTCGCGGTGTTAATGTGGAGA 2678
```


QY 2508 TCTTCACTTTAGGGGGCTGCGCCCTACCAAGGATTCGCGTGAAGAACTTTTAAAGCTGC 2567
| | | | |
Db 2679 TCTTCACTTTAGGGGGCTGCGCCCTACCAAGGATTCGCGTGAAGAACTTTTAAAGCTGC 2738
| | | | |
QY 2568 TGAAGAAAGACACAGAAATGATTAAGCCCAACCTGACCAACCAAGCTGTAATGATGA 2627
| | | | |
Db 2739 TGAAGAAAGACACAGAAATGATTAAGCCCAACCTGACCAACCAAGCTGTAATGATGA 2798
| | | | |
QY 2628 TGAAGAACTTTGGCAATGACATGCGCCCTCCAGAGACCAAGCTTCAAGCACTTTGAAG 2687
| | | | |
Db 2799 TGAAGAACTTTGGCAATGACATGCGCCCTCCAGAGACCAAGCTTCAAGCACTTTGAAG 2858
| | | | |
QY 2688 ACTTGATGGAATTTCTCACTCTTCAACAACAATGAGAAATCTTGAACCTTCAAGCACTTC 2747
| | | | |
Db 2859 ACTTGATGGAATTTCTCACTCTTCAACAACAATGAGAAATCTTGAACCTTCAAGCACTTC 2918
| | | | |
QY 2748 TGAAGAAAGTTCACCTAGTAACTCCGACCAAGAAAGTCTTGTCTTGAAGAGATGAT 2807
| | | | |
Db 2919 TGAAGAAAGTTCACCTAGTAACTCCGACCAAGAAAGTCTTGTCTTGAAGAGATGAT 2978
| | | | |
QY 2808 CTGTTTCTTCTCCAGACCCCATGCTTACCAACCATGCTTCTTCACTTCAACATTA 2867
| | | | |
Db 2979 CTGTTTCTTCTCCAGACCCCATGCTTACCAACCATGCTTCTTCACTTCAACATTA 3038
| | | | |
QY 2868 ACGGCAAGTGTAAACATGATGATCTGTCTGCTGCTGCTCCCAACAGACAGCACTGG 2927
| | | | |
Db 3039 ACGGCAAGTGTAAACATGATGATCTGTCTGCTGCTGCTCCCAACAGACAGCACTGG 3098
| | | | |
QY 2928 AACCTAGCTACACTGAGGAGGAGACCAATGCTCCAGAGCTTGTCTCCACTTGTAT 2987
| | | | |
Db 3099 AACCTAGCTACACTGAGGAGGAGACCAATGCTCCAGAGCTTGTGTCTCCACTTGTAT 3158
| | | | |
QY 2988 ATATGATCAGAGAGATTAATTAATGAAAGTATCAGATATGATTAAGATTTATAC 3047
| | | | |
Db 3159 ATATGATCAGAGAGATTAATTAATGAAAGTATCAGATATGATTAAGATTTATAC 3218
| | | | |
QY 3048 AGTTGAAACTTGTATCTTCCCAAGAGAGAAAGGTTTCTGAGAGCTGACTGC 3106
| | | | |
Db 3219 AGTTGAAACTTGTATCTTCCCAAGAGAGAAAGGTTTCTGAGAGCTGACTGC 3277
| | | | |
RESULT 13
ADZ13056
ID ADZ13056 standard; cDNA; 4609 BP.
XX
AC ADZ13056;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated cDNA #169.
XX
KM Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX
KM cytostatic; gene; ss.
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR MPI; 2005-273395/28.
XX
XX P-PSDB; ADZ13057.
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
comprises two or more nucleic acid probes.

XX
PS Disclosure: SEQ ID NO 576; 198bp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated cDNA of the
CC invention.
XX
SQ Sequence 4609 BP; 1231 A; 1085 C; 1165 G; 1128 T; 0 U; 0 Other;
Query Match 93.1%; Score 2890.2; DB 14; Length 4609;
Best Local Similarity 97.2%; Pred.No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;
QY 1 CCCGAGAGCAAGTTGTGTGAGGCAAGC-CAAGCTGATCTTCTTCTCTGCTTCC 59
| | | | |
Db 187 CTCGGAGCAAGTTGTGTGAGGCAAGC-CAAGCTGATCTTCTTCTCTGCTTCC 246
| | | | |
QY 60 CCAATTCGAGGAGAGCCCGCGGCGTCAATG--GCGCTCTCCGAGCGTGGGTACCC 116
| | | | |
Db 247 CCAATTCGAGGAGAGCCCGCGGCGTCAATGCGCGGCTCTCCGAGCGTGGGTACCC 306
| | | | |
QY 117 GTGAAGCCCGGAGGAGGTTGGCGCGCGGCAAGCCCAAGGACCACTTCTGCGTTGAG 176
| | | | |
Db 307 GTGAAGCCCGGAGGAGGTTGGCGCGCGGCAAGCCCAAGGACCACTTCTGCGTTGAG 366
| | | | |
QY 177 TTGCTCCCGCAACCCCGGCGTCTGCTGCTTCTCAATCCCAACCGCGGCGC-CGGG 235
| | | | |
Db 367 TTGCTCCCGCAACCCCGGCGTCTGCTGCTTCTCAATCCCAACCGCGGCGC-CGGG 426
| | | | |
QY 236 ACAACACAGGTGCGGAGAGAGGTTGCCATTTCAAGTATGACAGACGACG-ACAGCGCC 294
| | | | |
Db 427 ACAACACAGGTGCGGAGAGAGGTTGCCATTTCAAGTATGACAGACGACG-ACAGCGCC 486
| | | | |
QY 295 TCGGTTCTGAGCGCCACGCA-GCTGAAGCAATTTGCGGTATGCTATGCGGTAGAGAA 353
| | | | |
Db 487 TCGGTTCTGAGCGCCACGCGGAGGTGAAGCAATTTGCGGTATGCTATGCGGTAGAGAA 546
| | | | |
QY 354 GTGTGAGATGAGATTAAGTCCACATGAGATATGAAAGAGACCGGGAATTTGTAACG 413
| | | | |
Db 547 GTGTGAGATGAGATTAAGTCCACATGAGATATGAAAGAGACCGGGAATTTGTAACG 606
| | | | |
QY 414 TAAACATGCTCAGCTGGGCTGTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
| | | | |
Db 607 TAAACATGCTCAGCTGGGCTGTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
| | | | |
QY 474 CCCTGACCGGCGCTCTTCAAGTTTGAAGATACCAATTTAGAGCCAGAAAGCCAC 533
| | | | |
Db 667 CCCTGACCGGCGCTCTTCAAGTTTGAAGATACCAATTTAGAGCCAGAAAGCCAC 726
| | | | |
QY 534 CAACCAATTAACCAATCTCTCAACCAAGATGATGCTGCGGACGAGGAGTCTGAG 593
| | | | |
Db 727 CAACCAATTAACCAATCTCTCAACCAAGATGATGCTGCGGACGAGGAGTCTGAG 786
| | | | |

QY 594 AGGTGGCTGCTGCTTTGTAAGATGCGCCCTGATCACTTGGAGTAAAGATGGGGTGCAC 653
DB AGGTGGCTGCTGCTTTGTAAGATGCGCCCTGATCACTTGGAGTAAAGATGGGGTGCAC 846
QY 654 TGGGGCCCAACATAGAGAGTGTATTGGGGAGTACTTGAGATTAAGGGGCCACAC 713
DB TGGGGCCCAACATAGAGAGTGTATTGGGGAGTACTTGAGATTAAGGGGCCACAC 906
QY 714 CTAGAGATCTCCGGCTCTTATGCTTTGTACTGCGAGTAGAGCTGTAGACAGTGAATCTTGGT 773
DB CTAGAGATCTCCGGCTCTTATGCTTTGTACTGCGAGTAGAGCTGTAGACAGTGAATCTTGGT 966
QY 774 ACTTCATGCTGATGTCAAGATGCTCTATCCGAGATGATGAGATGACACCGATG 833
DB ACTTCATGCTGATGTCAAGATGCTCTATCCGAGATGATGAGATGACACCGATG 1026
QY 834 GTGCGGAAGATTTTGTGATGAGAGAGTAAACAAGAGAGCACCATACTGAGCAACA 893
DB GTGCGGAAGATTTTGTGATGAGAGAGTAAACAAGAGAGCACCATACTGAGCAACA 1086
QY 894 CAGAAAAGATGAGAAAAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT 953
DB CAGAAAAGATGAGAAAAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT 1087
QY 954 GCCCAGCCGGGGGGAACCCCAATGCAACCAATGCGGTGGCTGAAAACGGAGAGAGTTTA 1013
DB GCCCAGCCGGGGGGAACCCCAATGCAACCAATGCGGTGGCTGAAAACGGAGAGAGTTTA 1147
QY 1014 AGCAGAGCATTCGATTTGAGGGCTACAAAGGACGAAACAGCACTGAGGCTCATTAATG 1073
DB AGCAGAGCATTCGATTTGAGGGCTACAAAGGACGAAACAGCACTGAGGCTCATTAATG 1207
QY 1074 AAAGTGTGCTCCATCTGACAGAGGAATTAATCTGTGTAGTGAAGATGAATCGGGT 1133
DB AAAGTGTGCTCCATCTGACAGAGGAATTAATCTGTGTGTGTGAGAAATGAATACGGGT 1267
QY 1134 CCATCAATCAACGATCAACCTGGAATTTGTGAGGCAATGCTTCAACCGGCTTCTTCC 1193
DB CCATCAATCAACGATCAACCTGGAATTTGTGAGGCAATGCTTCAACCGGCTTCTTCC 1327
QY 1194 AAGCCGAGCTGCGGGCAATAGCCCTCAAGTGTGAGGAGAGAGTGAAGTTTGTCTGCA 1253
DB AAGCCGAGCTGCGGGCAATAGCCCTCAAGTGTGAGGAGAGAGTGAAGTTTGTCTGCA 1387
QY 1254 AGGTTTACATGATGCTCCAGCCCAATCCAGTGTGATCAAGCACTGAGAAAAGACGCA 1313
DB AGGTTTACATGATGCTCCAGCCCAATCCAGTGTGATCAAGCACTGAGAAAAGACGCA 1447
QY 1314 GTAATATCGGGCCCGAGCGGCTGCTTAATCTCAAGTTTCTCAAGCACTCGGGATTAATA 1373
DB GTAATATCGGGCCCGAGCGGCTGCTTAATCTCAAGTTTCTCAAGCGCGGTGTTAACA 1507
QY 1374 GTTCCATGAGAGTGTGCTGCTGT-----TCAATGTGACCGAGGCGGATGCTGGGG 1427
DB GTTCCATGAGAGTGTGCTGCTGT-----TCAATGTGACCGAGGCGGATGCTGGGG 1567
QY 1428 AATATATATGTAAAGTCTCCATTAATATATAGGGCAGGCAACCAAGTGTGCTGAGCTCA 1487
DB AATATATATGTAAAGTCTCCATTAATATATAGGGCAGGCAACCAAGTGTGCTGAGCTCA 1627
QY 1488 TCCCTGCAAAAAGAGAGCGCTGAGAGAGAGAGAGAGATTAAGCTTCCCAAGTACC 1547
DB TCCCTGCAAAAAGAGAGCGCTGAGAGAGAGAGAGAGATTAAGCTTCCCAAGTACC 1687
QY 1548 TGGAGATAGGCAATTAATGCAATAGGGCTTTTAATGCTGTATGTGTGTATCAAGTCA 1607
DB TGGAGATAGGCAATTAATGCAATAGGGCTTTTAATGCTGTATGTGTGTATCAAGTCA 1738
QY 1608 TCCCTGCGGAGATGAGAGACGACCAAGAGCGAGATTCAGAGCGCGGCTGTGC 1667
DB TCCCTGCGGAGATGAGAGACGACCAAGAGCGAGATTCAGAGCGCGGCTGTGC 1798
QY 1798 TCCCTGCGGAGATGAGAGACGACCAAGAGCGAGATTCAGAGCGCGGCTGTGC 1857

QY 1668 ACAAGCTGACCAAAACGATATCCCTGCGGAGACAGGTAAAC----AGTTTCGCTGATGCC 1723
DB ACAAGCTGACCAAAACGATATCCCTGCGGAGACAGGTAAACAGAAAGTTTCGCTGATGCC 1858
QY 1724 AGCTCTCCATGAACTTCAACACCCCGCTGTGTGAAGATTAACAACAGCTCTCTTCAACG 1783
DB AGCTCTCCATGAACTTCAACACCCCGCTGTGTGAAGATTAACAACAGCTCTCTTCAACG 1918
QY 1784 GCAGACACCCCAATGCTGGCAGGGGTCTCCAGTATGAATTCACAGAGGACCCAAATAG 1843
DB GCAGACACCCCAATGCTGGCAGGGGTCTCCAGTATGAATTCACAGAGGACCCAAATAG 1978
QY 1844 GAGTTTCAAGAGATTAAGCTGACACTGCGGCAACCCCTGGAGAGAGTTGCTTTGGCA 1903
DB GAGTTTCAAGAGATTAAGCTGACACTGCGGCAACCCCTGGAGAGAGTTGCTTTGGCA 2038
QY 2038 GAGTTTCAAGAGATTAAGCTGACACTGCGGCAACCCCTGGAGAGAGTTGCTTTGGCA 2097
DB GAGTTTCAAGAGATTAAGCTGACACTGCGGCAACCCCTGGAGAGAGTTGCTTTGGCA 1904
QY 1904 GTGTGATGCGGAGACAGTGGGAATTTGACAAAGACAGCCCAAGAGAGGCTGACCTGTG 1963
DB GTGTGATGCGGAGACAGTGGGAATTTGACAAAGACAGCCCAAGAGAGGCTGACCTGTG 2098
QY 1964 GCGGTGAAGTGTGAAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGACAG 2023
DB GCGGTGAAGTGTGAAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGACAG 2158
QY 2158 GCCGTGAAGTGTGAAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGACAG 2217
DB GCCGTGAAGTGTGAAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGACAG 2024
QY 2024 ATGAGATGATGAAGATGATGAGGAAACAAAGAAATATCAATAATCTTTGAGGCTGC 2083
DB ATGAGATGATGAAGATGATGAGGAAACAAAGAAATATCAATAATCTTTGAGGCTGC 2218
QY 2084 ACAAGAGATGAGGCTCTGTATGTATATGATGATGATGCTTTAAGGCAACTTCCAGAA 2143
DB ACAAGAGATGAGGCTCTGTATGTATATGATGATGATGCTTTAAGGCAACTTCCAGAA 2278
QY 2278 ACAAGAGATGAGGCTCTGTATGTATATGATGATGATGCTTTAAGGCAACTTCCAGAA 2337
DB ACAAGAGATGAGGCTCTGTATGTATATGATGATGATGCTTTAAGGCAACTTCCAGAA 2144
QY 2144 TACCTCCAGCCCGGAGGCAACCCGGAGATGAGTATCTCCATGATCAATTAACGGTTCCT 2203
DB TACCTCCAGCCCGGAGGCAACCCGGAGATGAGTATCTCCATGATCAATTAACGGTTCCT 2338
QY 2338 TACCTCCAGCCCGGAGGCAACCCGGAGATGAGTATCTCCATGATCAATTAACGGTTCCT 2397
DB TACCTCCAGCCCGGAGGCAACCCGGAGATGAGTATCTCCATGATCAATTAACGGTTCCT 2204
QY 2204 GAGAGAGATGATGATCAAGAGACTGTGTCAATGCACTTACAGGCTGCGCAGAGGATG 2263
DB GAGAGAGATGATGATCAAGAGACTGTGTCAATGCACTTACAGGCTGCGCAGAGGATG 2398
QY 2398 GAGAGAGATGATGATCAAGAGACTGTGTCAATGCACTTACAGGCTGCGCAGAGGATG 2457
DB GAGAGAGATGATGATCAAGAGACTGTGTCAATGCACTTACAGGCTGCGCAGAGGATG 2264
QY 2264 GAGTACTGTGCTTCCCAAAATGATTAATGATGATGATGATGATGATGATGATGATG 2323
DB GAGTACTGTGCTTCCCAAAATGATTAATGATGATGATGATGATGATGATGATGATG 2458
QY 2458 GAGTACTGTGCTTCCCAAAATGATTAATGATGATGATGATGATGATGATGATGATG 2517
DB GAGTACTGTGCTTCCCAAAATGATTAATGATGATGATGATGATGATGATGATGATG 2324
QY 2324 ACHGAAAACAAATGATGAAATTAAGCAAGCTTGTGACTGCGCAGAGATTAACAATA 2383
DB ACHGAAAACAAATGATGAAATTAAGCAAGCTTGTGACTGCGCAGAGATTAACAATA 2518
QY 2518 ACHGAAAACAAATGATGAAATTAAGCAAGCTTGTGACTGCGCAGAGATTAACAATA 2577
DB ACHGAAAACAAATGATGAAATTAAGCAAGCTTGTGACTGCGCAGAGATTAACAATA 2384
QY 2384 GACTATTAACAAAAGACCAACATAGGGCGGCTTCAAGTGAATGCTTCCAGAAAGCC 2443
DB GACTATTAACAAAAGACCAACATAGGGCGGCTTCAAGTGAATGCTTCCAGAAAGCC 2578
QY 2578 GACTATTAACAAAAGACCAACATAGGGCGGCTTCAAGTGAATGCTTCCAGAAAGCC 2637
DB GACTATTAACAAAAGACCAACATAGGGCGGCTTCAAGTGAATGCTTCCAGAAAGCC 2444
QY 2444 CTGTGTGATGATGATCACTCATCAAGATGATGATGATGATGATGATGATGATGATG 2503
DB CTGTGTGATGATGATCACTCATCAAGATGATGATGATGATGATGATGATGATGATG 2638
QY 2638 CTGTGTGATGATGATCACTCATCAAGATGATGATGATGATGATGATGATGATGATG 2697
DB CTGTGTGATGATGATCACTCATCAAGATGATGATGATGATGATGATGATGATGATG 2504
QY 2504 GAGATCTTCACTTTAGGGGCTGCGCTTACCCAGAGATTTCCCGTGAAGAACTTTTAAG 2563
DB GAGATCTTCACTTTAGGGGCTGCGCTTACCCAGAGATTTCCCGTGAAGAACTTTTAAG 2698
QY 2698 GAGATCTTCACTTTAGGGGCTGCGCTTACCCAGAGATTTCCCGTGAAGAACTTTTAAG 2757
DB GAGATCTTCACTTTAGGGGCTGCGCTTACCCAGAGATTTCCCGTGAAGAACTTTTAAG 2564
QY 2564 CTGCTGAAGAGAGACAGAGATGATTAAGCCAGGCACTGACCAAGAGAGTGTACATG 2623
DB CTGCTGAAGAGAGACAGAGATGATTAAGCCAGGCACTGACCAAGAGAGTGTACATG 2758
QY 2758 CTGCTGAAGAGAGACAGAGATGATTAAGCCAGGCACTGACCAAGAGAGTGTACATG 2817
DB CTGCTGAAGAGAGACAGAGATGATTAAGCCAGGCACTGACCAAGAGAGTGTACATG 2624
QY 2624 ATGATGAGGAGCTGTGTGCAATGCAATGCTTCCCAAGAGCAAGTTCAAGAGTTGTA 2683
DB ATGATGAGGAGCTGTGTGCAATGCAATGCTTCCCAAGAGCAAGTTCAAGAGTTGTA 2818
QY 2818 ATGATGAGGAGCTGTGTGCAATGCAATGCTTCCCAAGAGCAAGTTCAAGAGTTGTA 2877
DB ATGATGAGGAGCTGTGTGCAATGCAATGCTTCCCAAGAGCAAGTTCAAGAGTTGTA 2684
QY 2684 GAAGACTTGAATGATTTCTCACTTCAACAAGAGAGAGAAATCTTGAAGCTTCAAGCA 2743
DB GAAGACTTGAATGATTTCTCACTTCAACAAGAGAGAGAAATCTTGAAGCTTCAAGCA 2878
QY 2878 GAAGACTTGAATGATTTCTCACTTCAACAAGAGAGAGAAATCTTGAAGCTTCAAGCA 2937
DB GAAGACTTGAATGATTTCTCACTTCAACAAGAGAGAGAAATCTTGAAGCTTCAAGCA 2744
QY 2744 CTTCTGGAACAGTATTAATCACTTAATCCCTGACCAAGAGAGTTCTTGTCTTCAAGAGAT 2803

```
Db      ||| 2938 CCTCTCGAAGAGTATTCACCTAGTTACCTGACACAAAGAGTTCTTGTCTTCAAGAGAT 2997
Qy      ||| 2804 GATTCGTTTTTCTCAGACCCCATGCTTACGAAACATGCTTCTCAGTATCCACAC 2863
Db      ||| 2998 GATTCGTTTTTCTCAGACCCCATGCTTACGAAACATGCTTCTCAGTATCCACAC 3057
Qy      ||| 2864 ATAAACGCGAGTGTAAACATGAAATGACTGTGTCTGCTGTCCCAACAGACAGCAC 2923
Db      ||| 3058 ATAAACGCGAGTGTAAACATGAAATGACTGTGTCTGCTGTCCCAACAGACAGCAC 3117
Qy      ||| 2924 TGGGAACCTTAGTACACTGAGCAGGAGACATGCTTCCCAAGCTTTGTCTCCACT 2983
Db      ||| 3118 TGGGAACCTTAGTACACTGAGCAGGAGACATGCTTCCCAAGCTTTGTCTCCACT 3177
Qy      ||| 2984 GTATATATGATGATGAGAGATTAATATGAAAGTAAATGATATGATGTAAGATT 3043
Db      ||| 3178 GTATATATGATGATGAGAGATTAATATGAAAGTAAATGATATGATGTAAGATT 3237
Qy      ||| 3044 ATACAGTTGAAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAC 3103
Db      ||| 3238 ATACAGTTGAAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAC 3297
Qy      ||| 3104 TGC 3106
Db      ||| 3298 TGC 3300
```

RESULT 14

AD213044 standard; cDNA; 5000 BP.

AD213044;

16-JUN-2005 (first entry)

Human cancer-associated cDNA #163.

Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

cytostatic; gene; ss.

Homo sapiens.

WO2005031001-A2.

07-APR-2005.

23-SEP-2004; 2004WO-US031617.

23-SEP-2003; 2003US-00669920.

(CHIR) CHIRON CORP.

Morris DW, Malandro MS;

WPI; 2005-273395/28.

P-PSDB; AD213045.

Nucleic acid array useful for detecting cancer associated nucleic acid,

comprises two or more nucleic acid probes.

Disclosure; SEQ ID NO 564; 198bp; English.

The invention relates to a nucleic acid array for detecting a cancer

associated (CA) nucleic acid, comprising two or more nucleic acid probes.

The invention also relates to a peptide array comprising two or more

isolated polypeptides encoded by a CA nucleic acid sequence, a compound

that binds to a polypeptide, an isolated antibody or its fragment which

binds to a polypeptide, which is prepared by immunizing a host animal

with a composition comprising the polypeptide or its antigen binding

fragment and collecting cells from the host expressing antibodies against

the antigen or its antigen binding fragment, a composition comprising the

antibody and a carrier, a method of screening for anticancer activity, a

method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents human cancer-associated cDNA of the invention.

Sequence 5000 BP; 1323 A; 1184 C; 1260 G; 1233 T; 0 U; 0 Other;

Query Match 93.1%; Score 2890.2; DB 14; Length 5000;

Best Local Similarity 97.2%; Pred. No. 0;

Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;

Qy 1 CCCGAGCAAGTTGTTGAGGAGCAAG-CAAGCTGATCTTCTTCTCTGTTCC 59

Db 578 CTGGAGCAAGTTGTTGTTGAGGAGCAAGCTGATCTTCTCTCTGTTCC 637

Qy 60 CCAATCCGAGGAGCCCGCGGGGTCATG--GGCTCTCCGAGCGTGGGTAAGCC 116

Db 638 CCAATCCGAGGAGCCCGCGGGGTCATG--GGCTCTCCGAGCGTGGGTAAGCC 697

Qy 117 GTGAAGCCCGGAGGCTTGGCCCGGAGAGCAAGCAAGCACTTCTGCTTGGAG 176

Db 698 GTGAAGCCCGGAGGCTTGGCCCGGAGAGCAAGCAAGCACTTCTGCTTGGAG 757

Qy 177 TTGCTCCCGCAACCCCGGCTGTGCTTCTTCCATCCGACCGCGGGGC-CGGG 235

Db 758 TTGCTCCCGCAACCCCGGCTGTGCTTCTTCCATCCGACCGCGGGGC-CGGG 817

Qy 236 ACACACAGTGGCGGAGAGAGGTTGCCATGAGATGTCAGACGACG-GCAGCGCC 294

Db 818 ACACACAGTGGCGGAGAGGTTGCCATGAGATGTCAGACGACG-GCAGCGCC 877

Qy 295 TCGGTTCTGAGCCCAACGCA-GCTGAAGGCAATGCGCTGATGCTGCGTGAAGAA 353

Db 878 TCGGTTCTGAGCCCAACGCGGCTGAAGGCAATGCGCTGATGCTGCGTGAAGAA 937

Qy 354 GTGTGAGATGGAGTTAACGTCACATGAGATATGAAAGAGACCGGGATTGGACG 413

Db 938 GTGTGAGATGGAGTTAACGTCACATGAGATATGAAAGAGACCGGGATTGGACG 997

Qy 414 TAAACATGTCAGCTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473

Db 998 TAAACATGTCAGCTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057

Qy 474 CCTGACCGGCGCTCTCAGTTTGAAGATGCAATGAGATGAGGAGGAGGAGGAGGAG 533

Db 1058 CCTGACCGGCGCTCTCAGTTTGAAGATGCAATGAGATGAGGAGGAGGAGGAGGAG 1117

Qy 534 CAACCAATACCAATCTCTCAACGAGAGTGAAGTGTGCTGCTGCGCCAGGGAGTGGCTAG 593

Db 1118 CAACCAATACCAATCTCTCAACGAGAGTGAAGTGTGCTGCTGCGCCAGGGAGTGGCTAG 1177

Qy 594 AGGTGCGCTGCTCTGTTGAAGATGCGCGGTATGCTGAGTGAAGATGAGGAGGAGGAG 653

Db 1178 AGGTGCGCTGCTCTGTTGAAGATGCGCGGTATGCTGAGTGAAGATGAGGAGGAGGAG 1237

Qy 654 TGGGCGCCCAACATAGAGAGTCTTATTGGGAGTACTTGGAGATTAAGAGGCGCCACAC 713

Db 1238 TGGGCGCCCAACATAGAGAGTCTTATTGGGAGTACTTGGAGATTAAGAGGCGCCACAC 1297

Qy 714 CTAGAGACTCCGGCTCTTATGCTTGTACTGCACTGAGAGCTGAGACAGTGAACCTTGGT 773

Db 1298 CTAGAGACTCCGGCTCTTATGCTTGTACTGCACTGAGAGCTGAGACAGTGAACCTTGGT 1357

QY 774 ACTTCATGTAAGTATGCAAGATCCATCTCATCCGAGATGATGAGATGACCCGATG 833
DB 1358 ACTTCATGTAAGTATGCAAGATCCATCTCATCCGAGATGATGAGATGACCCGATG 1417
QY 834 GTGCGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGACACATCTACTGACCAACA 893
DB 1418 GTGCGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGACACATCTACTGACCAACA 1477
QY 894 CAGAAAAGATGAAAAGCGCTCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCT 953
DB 1478 CAGAAAAGATGAAAAGCGCTCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCT 1537
QY 954 GCCCGAGCGGGGGGAAACCAATGCGCAACCATGCGGTGCTGAAAAGGGGAGGTTTA 1013
DB 1538 GCCCGAGCGGGGGGAAACCAATGCGCAACCATGCGGTGCTGAAAAGGGGAGGTTTA 1597
QY 1014 AGCAGAGCATCGATTTGAGAGGCTACAGAGTACGAAAACAGCACTGAGCTCTATATG 1073
DB 1598 AGCAGAGCATCGATTTGAGAGGCTACAGAGTACGAAAACAGCACTGAGCTCTATATG 1657
QY 1074 AAGGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTAGTGAAGATGATACGGGT 1133
DB 1658 AAGGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTGTGAAGATGATACGGGT 1717
QY 1134 CCATCATCACAAGTACCACTGATGTTGTGAGGCGATGCGCTCAACGGGCCATCTCTCC 1193
DB 1718 CCATCATCACAAGTACCACTGATGTTGTGAGGCGATGCGCTCAACGGGCCATCTCTCC 1777
QY 1194 AAGCGGAGCTGCGCGGCAAAATGCTCCACAGTGTGCGAGAGAGGTAGTTTGTCTGCA 1253
DB 1778 AAGCGGAGCTGCGCGGCAAAATGCTCCACAGTGTGCGAGAGAGGTAGTTTGTCTGCA 1837
QY 1254 AGGTTTACAGTATGCGCCAGCCCAATCCAGTGTATCAGACACGTGAAAAGAACGGCA 1313
DB 1838 AGGTTTACAGTATGCGCCAGCCCAATCCAGTGTATCAGACACGTGAAAAGAACGGCA 1897
QY 1314 GTAAATACGGGCGCGAGCGGCTGCTTACTCAAGTTCTCAAGCACTCGGGGATTAATA 1373
DB 1898 GTAAATACGGGCGCGAGCGGCTGCTTACTCAAGTTCTCAAGCACTCGGGGATTAATA 1957
QY 1374 GTTCATATGACAGTGTGCTGCTGT-----TCAATGTAGCGAGCGGATGCTGGGG 1427
DB 1958 CCACGAGCAAAAGATTTAGAGTTCTCTATATTCGAGATGTAACTTTGAGAGACCTGGGG 2017
QY 1428 AATAATATATGATGAGTCTCCAAATTAATATAGGCAAGGCCAACAGTCTGCTCACTG 1487
DB 2018 AATAATATGATGAGTCTCCAAATTAATATAGGCAATCTTTCACTGCTCATGTTGACAG 2077
QY 1488 TCCTGCGCAAAACAGACGCGCTGAGAGAGAAAAGAGATTAACAGTTTCCCAAGACTAC 1547
DB 2078 TCCTGCGCAAAACAGACGCGCTGAGAGAGAAAAGAGATTAACAGTTTCCCAAGACTAC 2128
QY 1548 TGGAGATGAGCAATTAATGCAATAGGGGCTCTTAATGCGCTGTATGTTGGTAAACAGTCA 1607
DB 2129 TGGAGATGAGCAATTAATGCAATAGGGGCTCTCTTAATGCGCTGTATGTTGGTAAACAGTCA 2188
QY 1608 TCCTGCGCAATGAGAGAACAGCAAGAACAGCACTTCAAGACCGCGGCTGTGC 1667
DB 2189 TCCTGCGCAATGAGAGAACAGCAAGAACAGCACTTCAAGACCGCGGCTGTGC 2248
QY 1668 ACAAGCTGACAAACGTATCCCGCTGCGAGAGCAGGTAAACAGAAAGTTTCGCTGAGTCC 2308
DB 2249 ACAAGCTGACAAACGTATCCCGCTGCGAGAGCAGGTAAACAGAAAGTTTCGCTGAGTCC 2368
QY 1724 AGCTCTCATGAAATCCACAACCGCGGTGAGATAAACAACGCGCTCTTCAACG 1783
DB 2309 AGCTCTCATGAAATCCACAACCGCGGTGAGATAAACAACGCGCTCTTCAACG 2368
QY 1784 GCAGACACCCCATGCTGCGAGGGGCTCTCCAGTATGAATCTTCCAGAGACCCAAATGG 1843
DB 2369 GCAGACACCCCATGCTGCGAGGGGCTCTCCAGTATGAATCTTCCAGAGACCCAAATGG 2428
QY 1844 GAGTTTCAAGAGATTAAGCTGACCTGGGCAAGCCCTGCGAGAAAGTTGCTTGGGCA 1903

DB 2429 GAGTTTCAAGAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTGGGCA 2488
QY 1904 GTGCTCATGCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGGGGCTCACCTG 1963
DB 2489 GTGCTCATGCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGGGGCTCACCTG 2548
QY 1964 GCGGTGAAGATGTTGAAGATGAGCCACAGAGAAAGACCTTCTGATCTGTGTCCAGAG 2023
DB 2549 GCGGTGAAGATGTTGAAGATGAGCCACAGAGAAAGACCTTCTGATCTGTGTCCAGAG 2608
QY 2024 ATGAGATGATGAAAGATGATTTGGGAAACAAGAAATATCAATAATCTTTGAGGCTGC 2083
DB 2609 ATGAGATGATGAAAGATGATTTGGGAAACAAGAAATATCAATAATCTTTGAGGCTGC 2668
QY 2084 ACAAGATGCGGCTCTCTATGTCTATGTTGAGTATGCTCTTAAAGCAACCTCCGAGAA 2143
DB 2669 ACAAGATGCGGCTCTCTATGTCTATGTTGAGTATGCTCTTAAAGCAACCTCCGAGAA 2728
QY 2144 TACCTCGAGCCCGGAGGGCCACCGGGATGAGTACTATGACATTAACCGTGTCT 2203
DB 2729 TACCTCGAGCCCGGAGGGCCACCGGGATGAGTACTCTATGACATTAACCGTGTCT 2788
QY 2204 GAGAGCAGATGACCTTCAAGACTTGTGTCTATGCACTTACAGCTGCGCAGACGATG 2263
DB 2789 GAGAGCAGATGACCTTCAAGACTTGTGTCTATGCACTTACAGCTGCGCAGAGCATG 2848
QY 2264 GAGTACTGTGCTCCCAAAATGATTAATCATGAGATTTAGACGCGAGAAATGTTTGTA 2323
DB 2849 GAGTACTGTGCTCCCAAAATGATTAATCATGAGATTTAGACGCGAGAAATGTTTGTA 2908
QY 2324 ACAGAAAACATGATGATGAAATATGACAGCTTTGGAATGCGCAGAGATTAACAATATA 2383
DB 2909 ACAGAAAACATGATGATGAAATATGACAGCTTTGGAATGCGCAGAGATTAACAATATA 2968
QY 2384 GACTATTAACAAAAGACCAACAAATGGGCGCTTCAAGTCAAGTGTGCTCCAGAAACC 2443
DB 2969 GACTATTAACAAAAGACCAACAAATGGGCGCTTCAAGTCAAGTGTGCTCCAGAAACC 3028
QY 2444 CTGTTGATGATGATTAACACTCATCAGAGTATGTCTGTCTTCCGGGCTTTAATGTGG 2503
DB 3029 CTGTTGATGATGATTAACACTCATCAGAGTATGTCTGTCTTCCGGGCTTTAATGTGG 3088
QY 2504 GAGATCTTCACTTTAAGGGGCTGCGCTCAACCGGATTCGCGGAGAACTTTTAAG 2563
DB 3089 GAGATCTTCACTTTAAGGGGCTGCGCTCAACCGGATTCGCGGAGAACTTTTAAG 3148
QY 2564 CTGCTGAAGAGGACACAGATGATTAAGCCAGCCAACTGCAACAGACTGTACATG 2623
DB 3149 CTGCTGAAGAGGACACAGATGATTAAGCCAGCCAACTGCAACAGACTGTACATG 3208
QY 2624 ATGATGAGGAGCTGTGGATGACAGTGCCTCTCCAGAGCAACGTTCAAGCACTGGTA 2683
DB 3209 ATGATGAGGAGCTGTGGATGACAGTGCCTCTCCAGAGCAACGTTCAAGCACTGGTA 3268
QY 2684 GAAGACTTGAATGAAATTTCTCACTTCAACAAATGAGAAATCTTGAACCTAGCCAA 2743
DB 3269 GAAGACTTGAATGAAATTTCTCACTTCAACAAATGAGAAATCTTGAACCTAGCCAA 3328
QY 2744 CCTCTGAAAGATTAACCTAGTTACCTGACACAGAAAGTTTGTCTTCAAGAGAT 2803
DB 3329 CCTCTGAAAGATTAACCTAGTTACCTGACACAGAAAGTTTGTCTTCAAGAGAT 3368
QY 2804 GATTCTGTTTTTCTCAGAACCCCATGCTTACAGACCATGCTTCTCAGATACAC 2863
DB 3389 GATTCTGTTTTTCTCAGAACCCCATGCTTACAGACCATGCTTCTCAGATACAC 3448
QY 2864 ATTAACGCACTGTTAAACATGAATGATGTCTGCTGCTCCCAAGACAGACGAC 2923
DB 3449 ATTAACGCACTGTTAAACATGAATGATGTCTGCTGCTCCCAAGACAGACGAC 3508
QY 2924 TGGAGCTAGCTCACTGAGCAGGAGACCATGCTCCGAGAGCTTGTGTCTCACTT 2983

Db 3509 TGGGAACCTAGCTACGACGAGGACCATGCTCCAGAGCTTGTTCCTCCACTT 3568
 QY 2984 GTATATATGATCAGAGGATTAATTAATTGAAAAGTAATCAGCATATGTGTAAGATT 3043
 Db 3569 GATATATATGATCAGAGGATTAATTAATTGAAAAGTAATCAGCATATGTGTAAGATT 3628
 QY 3044 ATACAGTTGAAAACCTGTAATCTTCCCGAGAGGAGAAAGAGTTTCTGACAGAGGAC 3103
 Db 3629 ATACAGTTGAAAACCTGTAATCTTCCCGAGAGGAGAAAGAGTTTCTGACAGAGGAC 3688
 QY 3104 TGC 3106
 Db 3689 TGC 3691
 RESULT 15
 AD213114
 ID AD213114 standard; cDNA; 4990 BP.
 AC AD213114;
 DT 16-JUN-2005 (first entry)
 XX
 DE Human cancer-associated cDNA #198.
 KW diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
 KW cytosolic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO2005031001-A2.
 PD 07-APR-2005.
 PF 23-SBP-2004; 2004WO-US031617.
 PR 23-SBP-2003; 2003US-00669920.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Morris DM, Malandro MS;
 DR WPI, 2005-273395/28.
 DR P-PSDB; AD213115.
 PT Nucleic acid array useful for detecting cancer associated nucleic acid,
 PT comprises two or more nucleic acid probes.
 XX
 PS Disclosure; SEQ ID NO 634; 198bp; English.
 XX
 CC The invention relates to a nucleic acid array for detecting a cancer
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
 CC The invention also relates to a peptide array comprising two or more
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
 CC that binds to a polypeptide, an isolated antibody or its fragment which
 CC binds to a polypeptide, which is prepared by immunizing a host animal
 CC with a composition comprising the polypeptide or its antigen binding
 CC fragment and collecting cells from the host expressing antibodies against
 CC the antigen or its antigen binding fragment, a composition comprising the
 CC antibody and a carrier, a method of screening for anticancer activity, a
 CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
 CC method of treating cancer and a method of inhibiting expression of a CA
 CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
 CC nucleic acids. The antibody is useful for detecting the presence or
 CC absence of cancer cells in an individual which involves contacting cells
 CC from the individual with the antibody and detecting a complex of a CA
 CC protein from the cancer cells and the antibody, where the detection of
 CC the complex correlates with the presence of cancer cells in the
 CC individual. The composition is useful for inhibiting growth of cancer
 CC cells in an individual or for delivering a therapeutic agent to cancer
 CC cells in an individual. The invention is also useful for diagnosing
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in
 CC a cell. This sequence represents human cancer-associated cDNA of the

CC invention.
 XX
 SQ Sequence 4990 BP; 1317 A; 1183 C; 1258 G; 1232 T; 0 U; 0 Other;
 Query Match 92.8%; Score 2882.2; DB 14; Length 4990;
 Best Local Similarity 97.1%; Pred. No. 0;
 Matches 3028; Conservative 0; Mismatches 63; Indels 28; Gaps 8;
 QY 1 CCCGAGAGCAAAAGTTTGGTGAAGGCAAG-CAGAGCTAGATCTTCTTCCCTGGTCC 59
 Db 578 CTGCGAGAGCAAAAGTTTGGTGAAGGCAAGCCCAAGCCTAGTCTTCTTCCCTGGTCC 637
 QY 60 CCAAAATCGAGAGGAGCCGCGCGGCGGTCAATG--GCGCTCTCCGAGCCTGGGTACGC 116
 Db 638 CCAAAATCGAGAGGAGCCGCGCGGCGGTCAATGCGGCGCTCTCTCCGAGCCTGGGTACGC 697
 QY 117 GTGAAGCCCGAGAGGCTTGGCGCGGCGGAGAGCCCAAGAGACCACTCTTCTGGTTGAG 176
 Db 698 GTGAAGCCCGAGAGGCTTGGCGCGGCGGAGAGCCCAAGAGACCACTCTTCTGGTTGAG 757
 QY 177 TTGCTCCCGCAACCCCGGCTGTCGCTTTCTCCATCCGACCCAGCGGGGGC-CGGGG 235
 Db 758 TTGCTCCCGCAACCCCGGCTGTCGCTTTCTCCATCCGACCCAGCGGGGGC-CGGGG 817
 QY 236 ACAACACAGGTGCGGAGAGAGGCTTGCATTCAGAGTCACTGACGAGCAGC-CGAGCGCC 294
 Db 818 ACAACACAGGTGCGGAGAGAGGCTTGCATTCAGAGTCACTGACGAGCAGC-CGAGCGCC 877
 QY 295 TCGGTTCTGAGCCGACCGCA-GCTGAAGGCAATTCGCGTACTGATGCGCGTGAAGAA 353
 Db 878 TCGGTTCTGAGCCGACCGCAAGGTCGAGGCAATTCGCGTACTGATGCGCGTGAAGAA 937
 QY 354 GTGTGCAATGGGATTAAGTCCACATGAGAGTAATGAGAGAGAGCCGGGATTTGATCCG 413
 Db 938 GTGTGCAATGGGATTAAGTCCACATGAGAGTAATGAGAGAGAGCCGGGATTTGATCCG 997
 QY 414 TAACCATGATCAGCTGAGGTCGTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
 Db 998 TAACCATGATCAGCTGAGGTCGTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
 QY 474 CCTGGCCCGGCGCTCTCTCACTTGAAGTGAATACCAATTAAGCCAGAAAGCCAC 533
 Db 1058 CCTGGCCCGGCGCTCTCTCACTTGAAGTGAATACCAATTAAGCCAGAAAGCCAC 1117
 QY 534 CAACCAATTAACCAATCTCTCAACCAAGAGTGAAGTGGCTCCGCGGAGGAGTGGCTAG 593
 Db 1118 CAACCAATTAACCAATCTCTCAACCAAGAGTGAAGTGGCTCCGCGGAGGAGTGGCTAG 1177
 QY 594 AGGTGCGTGCCTGTTGAAGAATGCGCGGTGATCAGTTGAGTGAAGTGGGTTGACT 653
 Db 1178 AGGTGCGTGCCTGTTGAAGAATGCGCGGTGATCAGTTGAGTGAAGTGGGTTGACT 1237
 QY 654 TGGGGCCCAACATAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGCGCCACAC 713
 Db 1238 TGGGGCCCAACATAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGCGCCACAC 1297
 QY 714 CTAGAGACTCCGGCTCTTATGCTTGTGATCCAGTAGAGCTGTAGACATGAACTTGGT 773
 Db 1298 CTAGAGACTCCGGCTCTTATGCTTGTGATCCAGTAGAGCTGTAGACATGAACTTGGT 1357
 QY 774 ACTTCAATGATGATGACAGATGCGATCTCAATCCGAGATGATGAGTGAACCGATG 833
 Db 1358 ACTTCAATGATGATGACAGATGCGATCTCAATCCGAGATGATGAGTGAACCGATG 1417
 QY 834 GTGCGAGAGATTTTGTCACTGAGAAACAGTAACACAGAGAGACCAATCTGAGACCA 893
 Db 1418 GTGCGAGAGATTTTGTCACTGAGAAACAGTAACACAGAGAGACCAATCTGAGACCA 1477
 QY 894 CAGAAAGATGAGAAAGCGGCTTCATGCTGTGCTCCGCGCAACCTGCAAGTTTCGT 953
 Db 1478 CAGAAAGATGAGAAAGCGGCTTCATGCTGTGCTCCGCGCAACCTGCAAGTTTCGT 1537
 QY 954 GCCCAGCCGAGGAGAAACCAATGCCAATGCATGCGGTGAGAAAAAGGAGAGTTTA 1013

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:37:58 ; Search time 541 Seconds
(without alignments)
10742.447 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106
Sequence: 1 cccgcgagcaaatgttgcgtg.....ttcttgagcagtgactgc 3106

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 140366 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/FP_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/RB_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/RB_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2806.2	90.3	3080	US-09-954-556-25	Sequence 25, Appl
2	2781.8	89.6	4268	US-09-954-556-3	Sequence 3, Appl
3	2728.6	87.8	2923	US-09-954-556-20	Sequence 20, Appl
4	2723.4	87.7	2826	US-09-954-556-21	Sequence 21, Appl
5	2722	87.6	2868	US-09-954-556-19	Sequence 19, Appl
6	2722	87.6	2941	US-09-954-556-18	Sequence 18, Appl
7	2714.2	87.4	3416	US-08-451-822A-15	Sequence 15, Appl
8	2714.2	87.4	3416	US-08-323-430-15	Sequence 15, Appl
9	2327.4	74.9	3244	US-09-954-556-24	Sequence 24, Appl
10	2320	74.7	2650	US-09-954-556-28	Sequence 28, Appl
11	2320	74.7	2676	US-08-471-570-7	Sequence 7, Appl
12	2201	70.9	3306	US-09-954-556-10	Sequence 10, Appl
13	2072.2	66.7	3025	US-09-954-556-23	Sequence 23, Appl
14	1946	62.7	1954	US-08-471-570-5	Sequence 5, Appl
15	1890.4	60.9	2079	US-09-949-016-3171	Sequence 3171, Ap
16	1890.4	60.9	2079	US-09-949-016-3172	Sequence 3172, Ap
17	1890.4	60.9	2079	US-09-949-016-3173	Sequence 3173, Ap
18	1890.4	60.9	2079	US-09-949-016-3174	Sequence 3174, Ap
19	1890.4	60.9	2079	US-09-949-016-3175	Sequence 3175, Ap
20	1890.4	60.9	2079	US-09-949-016-3176	Sequence 3176, Ap
21	1890.4	60.9	2079	US-09-949-016-3177	Sequence 3177, Ap
22	1890.4	60.9	2079	US-09-949-016-3178	Sequence 3178, Ap
23	1890.4	60.9	2079	US-09-949-016-3179	Sequence 3179, Ap

24	1890.4	60.9	2079	US-09-949-016-3180	Sequence 3180, Ap
25	1823.2	58.7	2310	US-08-471-570-9	Sequence 9, Appl
26	1449.2	46.7	1603	US-08-471-570-3	Sequence 3, Appl
27	1345	43.3	1475	US-09-954-556-27	Sequence 27, Appl
28	1339.8	43.1	2681	US-08-070-165F-9	Sequence 9, Appl
29	1339.8	43.1	2681	US-08-885-418-9	Sequence 9, Appl
30	1269.4	40.9	2675	US-08-070-165F-5	Sequence 5, Appl
31	1269.4	40.9	2675	US-08-885-418-5	Sequence 5, Appl
32	1090	35.1	2469	US-07-997-133-2	Sequence 2, Appl
33	1090	35.1	2469	US-08-459-296-1	Sequence 1, Appl
34	1090	35.1	2469	US-07-997-133-2	Sequence 2, Appl
35	1088.4	35.0	2662	US-08-451-822A-14	Sequence 14, Appl
36	1088.4	35.0	2662	US-08-323-430-14	Sequence 14, Appl
37	1067	34.4	2733	US-08-371-001-14	Sequence 14, Appl
38	1063.6	34.2	2733	PCT-US96-00331-14	Sequence 14, Appl
39	1063.6	34.2	1079	US-08-471-570-13	Sequence 13, Appl
40	1053.6	33.9	3503	US-07-631-717A-1	Sequence 1, Appl
41	1053.6	33.9	3503	US-08-166-717D-1	Sequence 1, Appl
42	1042	33.5	2360	US-09-023-655-1288	Sequence 1288, Ap
43	982.2	31.6	1541	US-09-954-556-26	Sequence 26, Appl
44	921.8	29.7	3944	US-09-949-016-1876	Sequence 1876, Ap
45	921.8	29.7	3944	US-09-949-016-1877	Sequence 1877, Ap

ALIGNMENTS

RESULT 1
US-09-954-556-25
Sequence 25, Application US/09954556
Patent No. 6900053
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freiler
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
FILE REFERENCE: RTS-0250
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 25
LENGTH: 3080
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (612)...(3080)
US-09-954-556-25

Query Match	90.3%	Score 2806.2	DB 3	Length 3080
Best Local Similarity	99.4%	Pred. No. 0		
Matches 2879	Conservative	0	Mismatches	8
			Indels	8
			Gaps	6
QY	1	CCCCGAGCAAAATTGTTGAGGCAACG-CAAGCTGAGTCTTCTCTCGTTCC	59	
DB	186	CTGCGACGAAAGTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCGTTCC	245	
QY	60	CCAAATCCGAGGAGCCCGGCGGCTCATG--GGCTCTCTCGAGCTTGCGTACGC	116	
DB	246	CCAAATCCGAGGAGCCCGGCGGCTCATGCGGCTCTCTCGAGCTTGCGTACGC	305	
QY	117	G-TGAGCCCGGAGGCTTGCGCGCGGCAAGACCAAGGACCACTTCTGCGTTGGA	175	
DB	306	GCTGAAGCCCGGAGGCTTGCGCGCGGCAAGACCAAGGACCACTTCTGCGTTGGA	365	
QY	176	GTTGCTCCCGCAACCCCGGCTGCTGCTTCTCCATCCGACCCAGCGGCGGC-CGGG	234	
DB	366	GTTGCTCCCGCAACCCCGGCTGCTGCTTCTCCATCCGACCCAGCGGCGGCGGC	425	
QY	235	GACACACAGTTCGCGAGAGCGTTTCCATTCACTGACGAGCAGCAGC-GCAGCGC	293	
DB	426	GACACACAGTTCGCGAGAGCGTTTCCATTCACTGACGAGCAGCAGCAGCGCAGCGC	485	

QY	294	CTCGGTTCTGAAGCCACACCGA-gtGAAAGGCATTGGCGCGTAAgTCAATGCCCCGTAAAGGA	352
Db	486	CTCGGTTCTGAAGCCACACCGAGCGTAAAGGCATTGGCGCGTAAgTCAATGCCCCGTAAAGGA	545
QY	353	AGTGGCAGATGGGATTTAAAGTTCACATGAGATATGAAAGAGGACCGGGGATTTGGTAAC	412
Db	546	AGTGGCAGATGGGATTTAAAGTTCACATGAGATATGAAAGAGGACCGGGGATTTGGTAAC	605
QY	413	GTAAACATAGTCAGCTGGGGTCGTTTCATCTGCTGGTCGTGATCACCATGGCAACTTG	472
Db	606	GTAAACATAGTCAGCTGGGGTCGTTTCATCTGCTGGTCGTGATCACCATGGCAACTTG	665
QY	473	TCCCTGGCCCCGCGCTCTTCAAGTTTAAGTAAATACACATTAAGGCCAAGAAAGCCA	532
Db	666	TCCCTGGCCCCGCGCTCTTCAAGTTTAAGTAAATACACATTAAGGCCAAGAAAGCCA	725
QY	533	CCAAACCAATTAACCAATCTCTCAACACGAAGGTAAAGGCTGGCCAGGGGAGTGGCTA	592
Db	726	CCAAACCAATTAACCAATCTCTCAACACGAAGGTAAAGGCTGGCCAGGGGAGTGGCTA	785
QY	593	GAGGTGCGCTGCTGCTGTTGAAAGATGCGCGCGTGAATCAAGTTGAACTAAAGATGGGGTGCAC	652
Db	786	GAGGTGCGCTGCTGCTGTTGAAAGATGCGCGCGTGAATCAAGTTGAACTAAAGATGGGGTGCAC	845
QY	653	TTGGGGCCCAACATAGGACAGTGTCTTAATGGGAGATCTTGACAGATTAAGGGGCGCAC	712
Db	846	TTGGGGCCCAACATAGGACAGTGTCTTAATGGGAGATCTTGACAGATTAAGGGGCGCAC	905
QY	713	CCTAAGACTCCGGCTCTGATAGCTTGTATCTGCAGATAGGACGTGAAGACATGAAACTTGG	772
Db	906	CCTAAGACTCCGGCTCTGATAGCTTGTATCTGCAGATAGGACGTGAAGACATGAAACTTGG	965
QY	773	TACTTCATGTTGAATGTCCAGATGCGACTCTCATCCGAGATGATAGAGATGACACCGAT	832
Db	966	TACTTCATGTTGAATGTCCAGATGCGACTCTCATCCGAGATGATAGAGATGACACCGAT	1025
QY	833	GGTGGGGAAGATTTTGTCACTGATGAGAACATGTAACAACAAGAGACCACTACTGACCAAC	892
Db	1026	GGTGGGGAAGATTTTGTCACTGATGAGAACATGTAACAACAAGAGACCACTACTGACCAAC	1085
QY	893	ACAGAAAAAGATGGAAGAACGGCTCCATCTGTGCGTGGGCGCAACATGTCTAAATTTGCG	952
Db	1086	ACAGAAAAAGATGGAAGAACGGCTCCATCTGTGCGTGGGCGCAACATGTCTAAATTTGCG	1145
QY	953	TGCCAGCGCGGGGGAGAACCAATGCGCAACATGCGGTGGTGAAGAAACGGGAAAGAGATTT	1012
Db	1146	TGCCAGCGCGGGGGAGAACCAATGCGCAACATGCGGTGGTGAAGAAACGGGAAAGAGATTT	1205
QY	1013	AAGCAGAGACATGCACTTGGAGGCTTACAAGGTACGAACAGACACTGAGGCTCTCATTAATG	1072
Db	1206	AAGCAGAGACATGCACTTGGAGGCTTACAAGGTACGAACAGACACTGAGGCTCTCATTAATG	1265
QY	1073	GAAAGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTAAGTGAAGAAATGATPACGGG	1132
Db	1266	GAAAGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTAAGTGAAGAAATGATPACGGG	1325
QY	1133	TTCATCAATCAACAGTACCAACTGTGATGTTGAGAGCATGCGCTCAACGCGCCATCCTC	1192
Db	1326	TTCATCAATCAACAGTACCAACTGTGATGTTGAGAGCATGCGCTCAACGCGCCATCCTC	1385
QY	1193	CAAGCCGACCTCCGCAAAATGCTTCCACAGTGTGTCGAGAGAGACGTAAAGATTTGTCTGC	1252
Db	1386	CAAGCCGACCTCCGCAAAATGCTTCCACAGTGTGTCGAGAGAGACGTAAAGATTTGTCTGC	1445
QY	1253	AAGGTTTAAAGTAAATGACCGGCCCAATCCAGTGTGAATCAAGACATGTGAAAGAAACGCG	1312
Db	1446	AAGGTTTAAAGTAAATGACCGGCCCAATCCAGTGTGAATCAAGACATGTGAAAGAAACGCG	1505
QY	1313	AGTAAATTAAGGGGCGGAGGGGCTGACCTTCACTCAAGGTTCTCAAGCACTCGGGGATAAT	1372
Db	1506	AGTAAATTAAGGGGCGGAGGGGCTGACCTTCACTCAAGGTTCTCAAGCACTCGGGGATAAT	1555
QY	1373	AGTTCCAAATGACGAAGTGTGCTCTGTTCATATGTACCGAAGCGGATGCTGGGGATAAT	1432

Db	1566	AGTTCGAAATGCGAAGAGCTGGCTCTCTGTAATGTGACCGAGGGGAGATGCTGGGGAAATAT	1625
OY	1433	ATATGTAAGGCTCCATATTATATATGAGGCGAGGCCAACAGTCTGGCTCACTGCTCTG	1492
Db	1626	ATATGTAAAGTCTTCATATTATATAGGGCAGGCCAACAGTCTGGCTCACTGCTCTG	1685
OY	1493	CCAAAACAGCAGCGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGCTACCTGAG	1552
Db	1686	CCAAAACAGCAGCGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGCTACCTGAG	1745
OY	1553	ATAGCCATTATCTGCATATAGGGGTCTTCTTAATGCGCTGTATAGGAGTTACAGTACCTG	1612
Db	1746	ATAGCCATTATCTGCATATAGGGGTCTTCTTAATGCGCTGTATAGGAGTTACAGTACCTG	1805
OY	1613	TGCGGAATGAAAGACATGACCCAGAACCCAGACTTCAGACGCCAGCGGCTGTGCAAG	1672
Db	1806	TGCGGAATGAAAGACATGACCCAGAACCCAGACTTCAGACGCCAGCGGCTGTGCAAG	1865
OY	1673	CTGACCAAACTGATCCCGCTGCGGAGCAGGTTACAGTTTCGGTGAAGTCAAGCTCTCC	1732
Db	1866	CTGACCAAACTGATCCCGCTGCGGAGCAGGTTACAGTTTCGGTGAAGTCAAGCTCTCC	1925
OY	1733	ATGAAATCTCCACACCCCGCTGTGTAGGATTAACAAGCGCTCTTCAAGGGCAGACCC	1792
Db	1926	ATGAAATCTCCACACCCCGCTGTGTAGGATTAACAAGCGCTCTTCAAGGGCAGACCC	1985
OY	1793	CCCAATGCTGGCAGGGGCTCCGAGTATGAACCTTCAGAGGACCCCAAAATGGAGTTTCCA	1852
Db	1986	CCCAATGCTGGCAGGGGCTCCGAGTATGAACCTTCAGAGGACCCCAAAATGGAGTTTCCA	2045
OY	1853	AGAGATAGCTGACACTGGGCAAGCCCTGAGGAGAGGTTGCTTTGGGCAAGTGTCAATG	1912
Db	2046	AGAGATAGCTGACACTGGGCAAGCCCTGAGGAGAGGTTGCTTTGGGCAAGTGTCAATG	2105
OY	1913	GCGGAGCAGTGGGAAATTGACAAAGACAAAGGCGGTCAACCTGTGGCCGTAAAG	1972
Db	2106	GCGGAGCAGTGGGAAATTGACAAAGACAAAGGCGGTCAACCTGTGTGGCGGTAAAG	2165
OY	1973	ATGTTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGAGTGCAGAGATGGAATG	2032
Db	2166	ATGTTGAAAGATGATGCCACAGAGAAAGACCTTCTGATCTGAGTGCAGAGATGGAATG	2225
OY	2033	ATGAAGATGATTTGGGAAACAACAAGATATCAATAATCTTCTTGGAGCCTGACACAGAT	2092
Db	2226	ATGAAGATGATTTGGGAAACAACAAGATATCAATAATCTTCTTGGAGCCTGACACAGAT	2285
OY	2093	GGGCTCTCTATGTCAATGTTAGTATGCTCTCTTAAAGCACTTCCGAGATTACTCTCGA	2152
Db	2286	GGGCTCTCTATGTCAATGTTAGTATGCTCTCTTAAAGCACTTCCGAGATTACTCTCGA	2345
OY	2153	GCCCGSAGGCAACCCGGGATGGAAGTACCTCATGAACATTAACCGTGTTCTTGAAGAGAG	2212
Db	2346	GCCCGSAGGCAACCCGGGATGGAAGTACCTCATGAACATTAACCGTGTTCTTGAAGAGAG	2405
OY	2213	ATGACCTTCAAGAGACTTGTGTCAATGCACTTACAGAGCTGGCCAGACGATGGAATCTTG	2272
Db	2406	ATGACCTTCAAGAGACTTGTGTCAATGCACTTACAGAGCTGGCCAGACGATGGAATCTTG	2465
OY	2273	GCTTCCAAAAATGTATTATTCAGAGATTTAGCAGCCAGAAATGTTTGGTAAACGAAAAC	2332
Db	2466	GCTTCCAAAAATGTATTATTCAGAGATTTAGCAGCCAGAAATGTTTGGTAAACGAAAAC	2525
OY	2333	AATGTGAAGAAAATGCGAGACCTTGGATTCGCGCAGAGATATCAACAATATGACTAATAC	2392
Db	2526	AATGTGAAGAAAATGCGAGACCTTGGATTCGCGCAGAGATATCAACAATATGACTAATAC	2585
OY	2393	AAAAAGATCAACCAATGAGCGGCTTCAGTCAAGTGAAGGCTTCAGAAAGCCCTGTTGAT	2452
Db	2586	AAAAAGATCAACCAATGAGCGGCTTCAGTCAAGTGAAGGCTTCAGAAAGCCCTGTTGAT	2645
OY	2453	AGAGATATCACTCATCAGATGATGTCTGTGCTTCCGGGATGTTAATGTGGAGATCTTC	2512

Db	2646	AGAGTATACACTCATCAGAGTGATGTCTGGTCTCTCGGGGTGTTAAATGTGGGAATCTTC	2705
Oy	2513	ACCTTAGGGGGCTCGCCCTCAACCCAGGAGATCCCGTGAGGAACTTTTAACTGCTGAAG	2572
Db	2706	ACTTTAGGGGGCTGGCCTTACCAGGATTCCTCGTAGGAACTTTTAACTGCTGAAG	2765
Oy	2573	GAAGACACAGAAATGATATAGCCAGCCAACTGCACACGAACTGTACATGATGATGAGG	2632
Db	2766	GAAGACACAGAAATGATATAGCCAGCCAACTGCACACGAACTGTACATGATGATGAGG	2825
Oy	2633	GACTGTTGGATGCAGTGCCTCTCCAGAGACCAAGTTCAAGCAAGTTGGTAGAAGACTTG	2692
Db	2826	GACTGTTGGCATTGCAGTGCCTCTCCAGAGACCAAGTTCAAGCAAGTTGGTAGAAGACTTG	2885
Oy	2693	GATCGAATTCCTCACTCTCAACAACCAATGAGAAATCTTGAACCTCAGCCAACTCTCGAA	2752
Db	2886	GATCGAATTCCTCACTCTCAACAACCAATGAGAAATCTTGAACCTCAGCCAACTCTCGAA	2945
Oy	2753	CAGTATTCACCTAGTATACCTCGACACAAAGAACTTGTCTTCAAGAGATGATCTGT	2812
Db	2946	CAGTATTCACCTAGTATACCTCGACACAAAGAACTTGTCTTCAAGAGATGATCTGT	3005
Oy	2813	TTTTTCTCAAGACCCCATGCTTTAGAACCAATGCTTCTCTCAGTATCCACAATAAACGGC	2872
Db	3006	TTTTTCTCAAGACCCCATGCTTTAGAACCAATGCTTCTCTCAGTATCCACAATAAACGGC	3065
Oy	2873	AGTGTAAACATGA 2887	
Db	3066	AGTGTAAACATGA 3080	

```

RESULT 2
US-09-954-556-3
; Sequence 3, Application US/09954556
; Patent No. 690053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274) ... (2739)
US-09-954-556-3

```

Query Match	89.6%	Score 2781.8;	DB 3;	Length 4268;
Best Local Similarity	97.3%	Pred. No. 0;		
Matches 2887; Conservative	0;	Mismatches 62;	Indels 18;	Gaps 5;

Qy	149	CCCAAGACCACTCTTCTGCGTTGGAGATTGCTCCCGCAACCCCGGCTGTGTGCTTTC	208
Db	1	CCAAAGACCACTCTTCTGCGTTTGAATTGCTCCCAACAACCCCGGCTGTGTGCTTTC	60
Qy	209	TCCATCCCGACCCACAGCGGGGCG--CGGGGACAAACAAGTTCGCGAGAGCGTTGTGCATTTC	267
Db	61	TCATATCCGACCCCAAGCGGGGCGGGGACAAACAAGTTCGCGAGAGCGTTGTGCATTTC	120
Qy	268	AAGTACATGCAGCAGCAGC--GCAGCGCTCGGTTCTGTAGGCCACCGCA--GCTGAAGCA	325
Db	121	AAGTACATGCAGCAGCAGCGGCGCGCTCGGTTCTGTAGGCCACCGCAGGCTGAAGCA	180
Qy	326	TTGCGCGTAGTTCATGCCCGTAGAGGAAAGTGTGCAGATGGGATTTAACTCCACATGAGGA	385
Db	181	TTGCGCGTAGTTCATGCCCGTAGAGGAAAGTGTGCAGATGGGATTTAACTCCACATGAGGA	240

OY	386	TATGAAAGAGGACCGGGGATTGGTACCGTAAACATGGTCAGCTGGGGTCGTTTCATCTGC	445
Db	241	TATGAAAGAGGACCGGGGATTGGTACCGTAAACATGGTCACTGGGGTCGTTTCATCTGC	300
OY	446	CTGGTCGGTGCACCATGACCACTTTGCTCCCTGGCCGGGCTCTCTCACTTATGTTAG	505
Db	301	CTGGTCGGTGCACCATGACCACTTTGCTCCCTGGCCGGGCTCTCTCACTTATGTTAG	360
OY	506	GATACCACTTAGAGCCAGAAAGCCACCAACCAATATCCAAATCTTCAACAGAAAGTG	565
Db	361	GATACCACTTAGAGCCAGAAAGCCACCAACCAATATCTTCAACAGAAAGTG	420
OY	566	TACGTGGCTGGCCAGGGGAGTGCCTAGAGGTGGCTGCTGTGAAAGATGCCCGTG	625
Db	421	TACGTGGCTGGCCAGGGGAGTGCCTAGAGGTGGCTGCTGTGAAAGATGCCCGTG	480
OY	626	ATCAGTTGGACTAAGATGGGGTGCATTTGGGGCCCAACAATAGACAGTGTCTATTGGG	685
Db	481	ATCAGTTGGACTAAGATGGGGTGCATTTGGGGCCCAACAATAGACAGTGTCTATTGGG	540
OY	686	GAGTACTTGCAGATTAAGGGGCGCCACACTTAGAGACTTCGGGCTCTATGCTTGTACTGCC	745
Db	541	GAGTACTTGCAGATTAAGGGGCGCCACACTTAGAGACTTCGGGCTCTATGCTTGTACTGCC	600
OY	746	AGTAGAGCTGTAGA CAGTGAACCTTGGTACTTCATGCTGAATGTCA CAGATGCCATCTCA	805
Db	601	AGTAGAGCTGTAGA CAGTGAACCTTGGTACTTCATGCTGAATGTCA CAGATGCCATCTCA	660
OY	806	TTCGGAGATGATGAGATGACCCGATGGTGGGAAATTTTGTCACTGAGAAACAGTAC	865

601 AGTAGGACTGTAGACAGTGAACCTTGGTACTTCATGCTGAATGTCACACAGATGCCATCTCA 660

806 TCCGAGATGATGAGGATGACACCGATGGTCCGGAAGATTTTGTCACTGAGAACAGTAAAC 865

661 TCCGAGATGATGAGATGACACCGATGGTCCGAAGATTTTGTCAGTGAAACGTAAC 720

866 AACACGAGCACCCTACTGGAACCAACAGAAAAAGATGGAAGCGGCTCCATGCTGTG 925

721 AACAGAGACCACTACTGGACCAACAGAAAGATGGAAGCGGCTCCATGCTGTG 780

925 CATTGCGGACACACTGTTCACAGTTTTCGTCACCCAGCCGGGGGGAACCCCAATGCCAACATG 985

[illegible][illegible]

986 CGGTGCGTGAACCAACCGGAGAGAGCTTAAAGCAGGAGCATCGCATTGGAGGCTACCAACGTA 1043

841 CGGTGGCTGAAAAACGGGAAGAGCTTAAACAGAGCATCGATTGAGGCTACAGGTA 900

1046 CGAATCAGCATCTGAGCCTCATTTATGTGAAGTGTGTCCTCCATCTGACAAAGGAAATTAT 1105

901 CGAACGACACTGGAGCTCATTTATGGAAGTGTGTCCTCATCTGACAAGGAAATTAT 960

1106 ACCGTGTAAGTGAGATGATACGGGTCATCATCACACGTAACCACTGATGTTGTG 1165

961 ACCGTGTGTGGAGATGAATACGGTTCATCAATCACACGTACCACTGTGATGTGTG 1020

1166 GAGCGATCGCCTCACCGGCCCATCTCTCCAGCCGGA CTGCCGCAATGCTTCCACAGTG 1225

1021 GAGCGATCGCCTCACCGGCCCATCTCCAAAGCCGGA CTGCCGCGCAATGCTTCCACAGTG 1080

1226 GTCCGACGAGACGTAGAATTGTCTGCAAGCTTACAGTGATGCCACGACCCCACTTCAG 1285

[illegible][illegible]

1286 TGGATCAGCAGCGTGGAGGAGGAGCAGTAAATATCCGGCCCGCCAGCGAGTATCCCTATCCCTC 1374

1141 TGGATCAGCAGCTGGAAAAGAACCGCAGTAAATACGGGGCCGACGGGCTGCCCCACCTC 1200

1346 AAGTTCTCAGCACTCGGGATAATATCTCCATGCAGAGTCTGGCTCTG----- 1400

1201 AAGTTCACAGCCGCGGTGTTACACACGACAAGAGATTGAGTTCCTAATTT 1260

1401 -TCAATGACCGAGCGGATGCTGGGAATATATATGTAGGCTCCAAATTATATAGG 1459

1261 CGGATGTAACTTTTGAGGACGCTGGGGAATATACGTCTTGGCGGTAATCTATTGGG 1320

1460 CAGGCCAACCACTCTGCCTGGCTCACTGTCTCTGCCAAAAACAGCAAGCGCTTGAAGAGAA 1519

OY	121	AGCCCGGAGGCTTGGCGCGCGGCGAAGACCAAGACCACTCTTCTGCGTTTGGAGTTGC	180
Db	121	AGCCCGGAGGCTTGGCGCGCGCGAAGACCAAGACCACTCTTCTGCGTTTGGAGTTGC	180
OY	181	TTCCCGCAACCCCGGGGCTGGTGGCTTTCCATCTCCATCCGACCCGCGGGGCGCGGGAGCAAC	240
Db	181	TTCCCGCAACCCCGGGGCTGGTGGCTTTCCATCTCCATCCGACCCGCGGGGCGCGGGAGCAAC	240
OY	241	ACAGGTGCGGAGGAGCGTTGCGCATCTCAATGATCTGACGACGACGCGAGCGCTCGGTT	300
Db	241	ACAGGTGCGGAGGAGCGTTGCGCATCTCAATGATCTGACGACGACGCGAGCGCTCGGTT	300
OY	301	CCTGAACCCACCGGACGTGAAGGCACTTGGCGGTAGTCCATATCCCGTGAAGGAATGTGTCA	360
Db	301	CCTGAACCCACCGGACGTGAAGGCACTTGGCGGTAGTCCATATCCCGTGAAGGAATGTGTCA	360
OY	361	GATGGGATTAAGTTCACATGAGAGATATGAGAAAGGACCGGGGATTTGGTACCGTAAACAT	420
Db	361	GATGGGATTAAGTTCACATGAGAGATATGAGAAAGGACCGGGGATTTGGTACCGTAAACAT	420
OY	421	GATGAGCTGGGGTGGTTCACTCGCTGGTGGTGTCACTATGCAACTTGTCCCTGGC	480
Db	421	GATGAGCTGGGGTGGTTCACTCGCTGGTGGTGTCACTATGCAACTTGTCCCTGGC	480
OY	481	CGGCGCTCTCTTCAAGTTTATGTTAGGAAATCACTTAAAGCCAGAAAGCCACCAACCA	540
Db	481	CGGCGCTCTCTTCAAGTTTATGTTAGGAAATCACTTAAAGCCAGAAAGCCACCAACCA	540
OY	541	ATACCAATCTCTCAACCAAGAGTGAATGATGGCTGGCAGGGGAGTGGCTAAGAGTGGC	600
Db	541	ATACCAATCTCTCAACCAAGAGTGAATGATGGCTGGCAGGGGAGTGGCTAAGAGTGGC	600
OY	601	CTGCGCTGTTGAAAGATGCGCGCGGTGATCAGTTGACATAAGATGGGTGCACTTTGGGCG	660
Db	601	CTGCGCTGTTGAAAGATGCGCGCGGTGATCAGTTGACATAAGATGGGTGCACTTTGGGCG	660
OY	661	CAACAAATGAGCAAGTGTCTTATTTGGGAGATCTTGACATTAAGGGCGCCACCTTAAGA	720
Db	661	CAACAAATGAGCAAGTGTCTTATTTGGGAGATCTTGACATTAAGGGCGCCACCTTAAGA	720
OY	721	CTCGGCGCTTATGCTTTTACTGCGCAGTGAAGCTGTAAACAGTAAACTTGGTACTTCAT	780
Db	721	CTCGGCGCTTATGCTTTTACTGCGCAGTGAAGCTGTAAACAGTAAACTTGGTACTTCAT	780
OY	781	GATGAATGTCAAGATGTCATCTCAATCCGAGATATAGGATGACCCGATGTTGTGCGA	840
Db	781	GATGAATGTCAAGATGTCATCTCAATCCGAGATATAGGATGACCCGATGTTGTGCGA	840
OY	841	AGATTTTGTCAGTGAGAAACAGTAAACAAAGAGACCATATCTGAGCCAAACAGAAAA	900
Db	841	AGATTTTGTCAGTGAGAAACAGTAAACAAAGAGACCATATCTGAGCCAAACAGAAAA	900
OY	901	GATGAAAAAGGGGCTCAATGCTGTGCTGGCGCAACATGTCAAGTTTCTGCTGCCAGC	960
Db	901	GATGAAAAAGGGGCTCAATGCTGTGCTGGCGCAACATGTCAAGTTTCTGCTGCCAGC	960
OY	961	CGGGGGGAACCAATGCAACCAATGCGGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGA	1020
Db	961	CGGGGGGAACCAATGCAACCAATGCGGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGA	1020
OY	1021	GCATGCAATTGAGGGCTTCAAGAGTACGAAACCAAGCATGAGAGCTCATTTATGAAAAGTGT	1080
Db	1021	GCATGCAATTGAGGGCTTCAAGAGTACGAAACCAAGCATGAGAGCTCATTTATGAAAAGTGT	1080
OY	1081	GATCCCATCTGAAGAAGGAAATTAACCTGTGTATGTGAAGATGAATACGGGTCCATCAA	1140
Db	1081	GATCCCATCTGAAGAAGGAAATTAACCTGTGTATGTGAAGATGAATACGGGTCCATCAA	1140
OY	1141	TCAACGTAACCACTGGAATGTTGTGAAGCATCGCTCAACGGGCCCATCTTCCAAAGCCGG	1200
Db	1141	TCAACGTAACCACTGGAATGTTGTGAAGCATCGCTCAACGGGCCCATCTTCCAAAGCCGG	1200
OY	1201	ACTGCGGGCAATGCTTCCACAGTGTGGAGAGACGTAAAGTTTGTCTGCAAGTTTAA	1260
Db	1201	ACTGCGGGCAATGCTTCCACAGTGTGGAGAGACGTAAAGTTTGTCTGCAAGTTTAA	1260

Dd	1201	ACTGCCGCGCAATGCCCTCCACAGTGGTCCGAGAGAGAGTGAAGTTTGTCTGCAAGGTTTA	1260
Qy	1261	CAGTGATGCCCAAGCCCCACATCCAGTGGATCAAGCATGTGAAAAAGACGGCAGTAATA	1320
Dd	1261	CAGTGATGCCCAAGCCCCACATCCAGTGGATCAAGCATGTGAAAAAGACGGCAGTAATA	1320
Qy	1321	CGGGCCCCGAGGGGTGGCTTCACTCAAGGTTCTCAACACTCGGGGAGTTAAATAGTCCAA	1380
Dd	1321	CGGGCCCCGAGGGGTGGCTTCACTCAAGGTTCTCAACACTCGGGGAGTTAAATAGTCCAA	1380
Qy	1381	TGCAGAGTGTGCTCTGTTCATATGACCGAGGGCGAGATGCTGGGAGATATATATGTAA	1440
Dd	1381	TGCAGAGTGTGCTCTGTTCATATGACCGAGGGCGAGATGCTGGGAGATATATATGTAA	1440
Qy	1441	GGTCTCCAAATTATATAGGGCAGGCCAACAGTGTGCTGCTGCTCACTGTCTGCAAAAACA	1500
Dd	1441	GGTCTCCAAATTATATAGGGCAGGCCAACAGTGTGCTGCTGCTCACTGTCTGCAAAAACA	1500
Qy	1501	GCAAGCCGCTGGAAGAGAAAAAGAGATTACAGCTTCCCCAGACTACCTCGAGATAGCCAT	1560
Dd	1501	GCAAGCCGCTGGAAGAGAAAAAGAGATTACAGCTTCCCCAGACTACCTCGAGATAGCCAT	1560
Qy	1561	TTACTGCAATAGGGGTCTTCTTAATCCGCTGTATGGTGTAAACGTCACTCCTGTGCCGAT	1620
Dd	1561	TTACTGCAATAGGGGTCTTCTTAATCCGCTGTATGGTGTAAACGTCACTCCTGTGCCGAT	1620
Qy	1621	GAAGAACCGACCAAGAACCCAGACTTCAAGACCGACCGCTGTGTCAAACTGTACCAA	1680
Dd	1621	GAAGAACCGACCAAGAACCCAGACTTCAAGACCGACCGCTGTGTCAAACTGTACCAA	1680
Qy	1681	ACGTATCCCCCTGGCGAGACAGGTAAACGTTTCGCTGAAGTCCAGCTCTCCATGAATCTC	1740
Dd	1681	ACGTATCCCCCTGGCGAGACAGGTAAACGTTTCGCTGAAGTCCAGCTCTCCATGAATCTC	1740
Qy	1741	CAACACCCCGCTGGTGGAGATTAACAACGCTCTCTTCAACCGGCAACCCCCCATGCT	1800
Dd	1741	CAACACCCCGCTGGTGGAGATTAACAACGCTCTCTTCAACCGGCAACCCCCCATGCT	1800
Qy	1801	GGCAGGGGTCTCCGAGTATGAATCTTCCAGAGAACCCAAATGGAGTTTCCAGAGATTA	1860
Dd	1801	GGCAGGGGTCTCCGAGTATGAATCTTCCAGAGAACCCAAATGGAGTTTCCAGAGATTA	1860
Qy	1861	GCTGACACTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAATGTGTCATGTGGGGAAGC	1920
Dd	1861	GCTGACACTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAATGTGTCATGTGGGGAAGC	1920
Qy	1921	AGTGGGAATTGACAAAGACAAAGCCCAAGAGGCGGTACACGTTGCCGTGAAGATGTTGAA	1980
Dd	1921	AGTGGGAATTGACAAAGACAAAGCCCAAGAGGCGGTACACGTTGCCGTGAAGATGTTGAA	1980
Qy	1981	AGATGATGCCACAGAGAAAGACTTTCTGATCTGTGTCAAGATGTGATGAAGAT	2040
Dd	1981	AGATGATGCCACAGAGAAAGACTTTCTGATCTGTGTCAAGATGTGATGAAGAT	2040
Qy	2041	GATTGGGAAACAACAAGATATCATTAATCTTCTTGAGACCTGTCAACAGATGGGCCCTCT	2100
Dd	2041	GATTGGGAAACAACAAGATATCATTAATCTTCTTGAGACCTGTCAACAGATGGGCCCTCT	2100
Qy	2101	CTATGTCAATATTAGATATGCTCTCTTAAGGCAACTCCGAGAAATACCTCCGAGCCGGAG	2160
Dd	2101	CTATGTCAATATTAGATATGCTCTCTTAAGGCAACTCCGAGAAATACCTCCGAGCCGGAG	2160
Qy	2161	GCCACCCCGGAGTGAATCTCTTAATGACATTAACCGTATGCTCTAGAGACAGATGACTT	2220
Dd	2161	GCCACCCCGGAGTGAATCTCTTAATGACATTAACCGTATGCTCTAGAGAGCAGATGACTT	2220
Qy	2221	CAAGGACTTGTGTATCACTTACAGCTGGCAAGCATGTGAATCTTGGCTTCCCA	2280
Dd	2221	CAAGGACTTGTGTATCACTTACAGCTGGCAAGCATGTGAATCTTGGCTTCCCA	2280
Qy	2281	AAATGTATATATGAGATTTAGACCGCAAAATGTTTGGTAAACAGAAAACAATGTAT	2340
Dd	2281	AAATGTATATATGAGATTTAGACCGCAAAATGTTTGGTAAACAGAAAACAATGTAT	2340

Db 2281 AAAATGATTCATCGAGATTAGACGCCGAAATGTTTGGTAACGAAAACAATGTCT 2340
QY 2341 GAAAAATAGCAGACTTTGACCTGCCAGAGATATCAACAAATATAGACTATTAACAAAAAGAC 2400
Db 2341 GAAAAATAGCAGACTTTGACCTGCCAGAGATATCAACAAATATAGACTATTAACAAAAAGAC 2400
QY 2401 CACCAATGGCGCGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATAGATATA 2460
Db 2401 CACCAATGGCGCGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATAGATATA 2460
QY 2461 CACTCATCAGAGATGATCTGGGCTCCTGGGGGTGTAATGGGAGATCTTCACTTTAG 2520
Db 2461 CACTCATCAGAGATGATCTGGGCTCCTGGGGGTGTAATGGGAGATCTTCACTTTAG 2520
QY 2521 GGGCTCGCCCTACCCAGGAGATCCCGTGAAGAACTTTTAACTGCTGAAGAGAGACA 2580
Db 2521 GGGCTCGCCCTACCCAGGAGATCCCGTGAAGAACTTTTAACTGCTGAAGAGAGACA 2580
QY 2581 CAGATGATTAAGCCAGCCCACTGCAACCAACCTGATCATATATATAGAGAGACTGTTG 2640
Db 2581 CAGATGATTAAGCCAGCCCACTGCAACCAACCTGATCATATATATAGAGAGACTGTTG 2640
QY 2641 GGATGAGTGGCCCTCCAGAGACCAAGTTCAAGCAGATTGATGATGAGAGAGAGAT 2700
Db 2641 GGATGAGTGGCCCTCCAGAGACCAAGTTCAAGCAGATTGATGATGAGAGAGAT 2700
QY 2701 TCTCACTCTACAAACCAATGAGGATATCTTGAACCTCAAGCAACCTCTGAAACAGATTTC 2760
Db 2701 TCTCACTCTACAAACCAATGAGGATATCTTGAACCTCTGAAACAGATTTC 2760
QY 2761 ACTTGAATACCTCTGA 2775
Db 2761 AAGTGCAAACTCTGA 2775

RESULT 4
US-09-954-556-21
Sequence 21, Application US/09954556
Patent No. 6900053
GENERAL INFORMATION:
APPLICANT: Susan M. Monia
APPLICANT: Brett P. Freier
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
FILE REFERENCE: RTS-0250
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 21
LENGTH: 2826
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (419)...(2725)
US-09-954-556-21

Query Match 87.7%; Score 2723.4; DB 3; Length 2826;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2724; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCGCGAGCAAAAGTTGGTGGAGGCAACGCAAGCTGATGCTTTCTTCTCTCTGTTCCC 60
Db 1 CCCGCGAGCAAAAGTTGGTGGAGGCAACGCAAGCTGATGCTTTCTTCTCTCTGTTCCC 60
QY 61 CAAATCCGAGGAGAGCCCGGGGGCGTCAATGGCGCTCTCCGAGCCCGGGGTACGGGTGA 120
Db 61 CAAATCCGAGGAGAGCCCGGGGGCGTCAATGGCGCTCTCCGAGCCCGGGGTACGGGTGA 120
QY 121 AGCCCGGAGGCTTGGCGCGGCGAAGACCAAGACCACTTCTTCTGCGTTTGAAGTTGC 180
Db 121 AGCCCGGAGGCTTGGCGCGGCGAAGACCAAGACCACTTCTTCTGCGTTTGAAGTTGC 180

QY 181 TCCCCGCAACCCCGGGGCTCGTGGCTTCTCCATCCCGACCCACGCGGGGCGGGGCAAC 240
Db 181 TCCCCGCAACCCCGGGGCTCGTGGCTTCTCCATCCCGACCCACGCGGGGCGGGGCAAC 240
QY 241 ACAGGTCCGAGAGAGCGCTTGCATTCAAGTACTGACAGACAGACGAGCGCTCGTT 300
Db 241 ACAGGTCCGAGAGAGCGCTTGCATTCAAGTACTGACAGACAGACGAGCGCTCGTT 300
QY 301 CCTGAGCCCAACCGCACTGAAAGGCAATGGCGGTATCCATGCCCCGTATAGAGAGTGTCA 360
Db 301 CCTGAGCCCAACCGCACTGAAAGGCAATGGCGGTATCCATGCCCCGTATAGAGAGTGTCA 360
QY 361 GATGGAGTTAAGTCCACATGGAGATATGGAAGAGACCGGGGATTTGGTACCGTAAACAT 420
Db 361 GATGGAGTTAAGTCCACATGGAGATATGGAAGAGACCGGGGATTTGGTACCGTAAACAT 420
QY 421 GGTGACGTGGGTCCTTTCATCTGCTGGTGTGTGTCACATGGCAACTTGTCTTGGC 480
Db 421 GGTGACGTGGGTCCTTTCATCTGCTGGTGTGTGTCACATGGCAACTTGTCTTGGC 480
QY 481 CCGGCCCTCTTCACTTATGTTGAGAGATCCACATTAAGCCGAGAGCCCAACCA 540
Db 481 CCGGCCCTCTTCACTTATGTTGAGAGATCCACATTAAGCCGAGAGCCCAACCA 540
QY 541 ATACCAATCTCTCAACCAAGATGATAGTGGCTGCGCCAGGGGAGTGGCTAGAGTGG 600
Db 541 ATACCAATCTCTCAACCAAGATGATAGTGGCTGCGCCAGGGGAGTGGCTAGAGTGG 600
QY 601 CTGCTGTTGAAAGATGCGCGGTGATCACTTGAATGAAGATGGGGTGTGCACTTGGGGCC 660
Db 601 CTGCTGTTGAAAGATGCGCGGTGATCACTTGAATGAAGATGGGGTGTGCACTTGGGGCC 660
QY 661 CAACAAATAGACAGTGTCTTATTTGGGAGTACTTGGAGATTAAGGGCGCCACCTTAGAGA 720
Db 661 CAACAAATAGACAGTGTCTTATTTGGGAGTACTTGGAGATTAAGGGCGCCACCTTAGAGA 720
QY 721 CTCGGGCTCTATGCTGTGATCTGCACTGAGAGATGATGATGATGATGATGATGATGAT 780
Db 721 CTCGGGCTCTATGCTGTGATCTGCACTGAGAGATGATGATGATGATGATGATGATGAT 780
QY 781 GGTGATGTCACAGATGCGCATCTCATCCGAGATGATGATGATGATGATGATGATGATGAT 840
Db 781 GGTGATGTCACAGATGCGCATCTCATCCGAGATGATGATGATGATGATGATGATGATGAT 840
QY 841 AGATTTTGTGATGAGAGAGATTAACAAACAAAGAGACCACTTCTGAGCCAAACAGAAAA 900
Db 841 AGATTTTGTGATGAGAGAGATTAACAAACAAAGAGACCACTTCTGAGCCAAACAGAAAA 900
QY 901 GATGAAAAAGCGGCTCATGCTGTGCTGCGGCAACACTGTCAAGTTTCGCTGCCAGC 960
Db 901 GATGAAAAAGCGGCTCATGCTGTGCTGCGGCAACACTGTCAAGTTTCGCTGCCAGC 960
QY 961 CCGGGGGAACCAATGCCCAACCATGCGGTGCTGAAAAACGGGAAAGAGATTAAAGCAGA 1020
Db 961 CCGGGGGAACCAATGCCCAACCATGCGGTGCTGAAAAACGGGAAAGAGATTAAAGCAGA 1020
QY 1021 GCATGCGATTGAGGCTTCAAGGTACGAAGTACGAAGCTGAGACCTTCATTATGAAAGTGT 1080
Db 1021 GCATGCGATTGAGGCTTCAAGGTACGAAGTACGAAGCTGAGACCTTCATTATGAAAGTGT 1080
QY 1081 GGTCCCATCTGACAAAGGAAATTTATCTGTGTAGTGAAGTGAATGAGGTCTCA 1140
Db 1081 GGTCCCATCTGACAAAGGAAATTTATCTGTGTAGTGAAGTGAATGAGGTCTCA 1140
QY 1141 TCACAGTACCACTGATGTTGTGAGAGGATGCTCAACGGGCCATCTTCAAGCCGG 1200
Db 1141 TCACAGTACCACTGATGTTGTGAGAGGATGCTCAACGGGCCATCTTCAAGCCGG 1200
QY 1201 ACTGCGGCAAAATGCTTCAACAGTGTGGAGAGACGTAAGATTGTCTGCAAGTTTA 1260
Db 1201 ACTGCGGCAAAATGCTTCAACAGTGTGGAGAGACGTAAGATTGTCTGCAAGTTTA 1260
QY 1261 CAGTATGCCAGGCCCAATCAAGTGAATCAAGACGTAAGAAAGAAACGGCAGTAATA 1320

DB 1261 CAGTATGCCCCAGCCCACTCCAGTGCATCAAGCACTGAGAAAAGACGGCAGTAAAT 1320
QY 1321 CGGGCCCGACGGGCTGCGCTTACCTCAAGGTTCTCAAGCACTCGGGGATTAATAGTCCAA 1380
DB 1321 CGGGCCCGACGGGCTGCGCTTACCTCAAGGTTCTCAAGCACTCGGGGATTAATAGTCCAA 1380
QY 1381 TGCAGAAAGTCTGCTCTCTGTTCAATGTGACCCGAGCGGATGTGGGAAATATATGTAA 1440
DB 1381 TGCAGAAAGTCTGCTCTCTGTTCAATGTGACCCGAGCGGATGTGGGAAATATATGTAA 1440
QY 1441 GGTCTCAATTAATATAGGAGGAGCCAAACAGTCTGCTGCTCACTGTCTGCGCAAAACA 1500
DB 1441 GGTCTCAATTAATATAGGAGGAGCCAAACAGTCTGCTGCTCACTGTCTGCGCAAAACA 1500
QY 1501 GCAAGCGCTGGAAGAAAAGAGATTACAGCTTCCCAAGTACTCTGAGATAGCCAT 1560
DB 1501 GCAAGCGCTGGAAGAAAAGAGATTACAGCTTCCCAAGTACTCTGAGATAGCCAT 1560
QY 1561 TTAATGATAGGGGCTCTTCTTAATCGCTGTATGTGTAAAGTCACTCTGTGCGAAT 1620
DB 1561 TTAATGATAGGGGCTCTTCTTAATCGCTGTATGTGTAAAGTCACTCTGTGCGAAT 1620
QY 1621 GAAGAACAGCAAGAACAGCAGCTTACAGCAGCGGCTGTGCAAGAGTCAAA 1680
DB 1621 GAAGAACAGCAAGAACAGCAGCTTACAGCAGCGGCTGTGCAAGAGTCAAA 1680
QY 1681 ACCTATCCCCCTCGAGAGAGGTAACAGTTTCCGCTAGTCCAGCTCTCATGAATC 1740
DB 1681 ACCTATCCCCCTCGAGAGAGGTAACAGTTTCCGCTAGTCCAGCTCTCATGAATC 1740
QY 1741 CAACACCCGCTGCTGAGTAACACAGCCTCTCTTCAACGCGCAGACACCCCATGCT 1800
DB 1741 CAACACCCGCTGCTGAGTAACACAGCCTCTCTTCAACGCGCAGACACCCCATGCT 1800
QY 1801 GCGAGGGGCTCCGAGTATGAACTTCCAGAGAACCCAAATGGAAGTTTCCAGAGATA 1860
DB 1801 GCGAGGGGCTCCGAGTATGAACTTCCAGAGAACCCAAATGGAAGTTTCCAGAGATA 1860
QY 1861 GCTGACACTGGGAGAGCCCTGAGGAGAGGTTGCTTGGCAGAGTGTCAATGGCGAAGC 1920
DB 1861 GCTGACACTGGGAGAGCCCTGAGGAGAGGTTGCTTGGCAGAGTGTCAATGGCGAAGC 1920
QY 1921 AGTGGGAATTGACAAAGACAGCCCAAGAGGCGGTACCGTGGCCGTGAAGATGTGAA 1980
DB 1921 AGTGGGAATTGACAAAGACAGCCCAAGAGGCGGTACCGTGGCCGTGAAGATGTGAA 1980
QY 1981 AGATGATGCCACAGAGAAACCTTCTGATCTGTGTCAAGATGAGATGAAGAT 2040
DB 1981 AGATGATGCCACAGAGAAACCTTCTGATCTGTGTGTCAAGATGAGATGAAGAT 2040
QY 2041 GATTGGGAAACACAAAGATATCAATCTTCTTGAAGCTGCAACAGATGGGCTCT 2100
DB 2041 GATTGGGAAACACAAAGATATCAATCTTCTTGAAGCTGCAACAGATGGGCTCT 2100
QY 2101 CTATGTCATATGATGATGCTCTTAAAGCCAACTTCCAGAAATACCTCCGAGCCGAG 2160
DB 2101 CTATGTCATATGATGATGCTCTTAAAGCCAACTTCCAGAAATACCTCCGAGCCGAG 2160
QY 2161 GCCACCGGAGATGAGATCTCTATGACATTAACCGGTCTCTGAGAGAGAGATGACCT 2220
DB 2161 GCCACCGGAGATGAGATCTCTATGACATTAACCGGTCTCTGAGAGAGAGATGACCT 2220
QY 2221 CAAGAGCTTGGTGCATGACCTTACAGCTGCGCAGAGAGATGAGTGTGCTTCCA 2280
DB 2221 CAAGAGCTTGGTGCATGACCTTACAGCTGCGCAGAGAGATGAGTGTGCTTCCA 2280
QY 2281 AAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGTGTAACAGAAACAATGTGAT 2340
DB 2281 AAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGTGTAACAGAAACAATGTGAT 2340
QY 2341 GAAATAGCAGACTTGGAGCTGCGCAGAGATCAATATAGATTAACAAAAGAC 2400
DB 2341 GAAATAGCAGACTTGGAGCTGCGCAGAGATCAATATAGATTAACAAAAGAC 2400

DB 2341 GAAATAGCAGACTTGGAGCTGCGCAGAGATCAATATAGATTAACAAAAGAC 2400
QY 2401 CACCAATGGGCGGCTTCCAGTAAGTGAATGGCTCCAGAGACCTGTTTGAATGAGTATA 2460
DB 2401 CACCAATGGGCGGCTTCCAGTAAGTGAATGGCTCCAGAGACCTGTTTGAATGAGTATA 2460
QY 2461 CACTCATCAGAGATGATGTCTGCTCTTCCGGGTGTAAATGTGGAGATCTTCACTTAA 2520
DB 2461 CACTCATCAGAGATGATGTCTGCTCTTCCGGGTGTAAATGTGGAGATCTTCACTTAA 2520
QY 2521 GGGCTGCGCTTACCCAGGATTCCTCGTGAAGAACTTTTAAGCTCTGAAGAGACA 2580
DB 2521 GGGCTGCGCTTACCCAGGATTCCTCGTGAAGAACTTTTAAGCTCTGAAGAGACA 2580
QY 2581 CAGATGATTAAGCCAGCCCACTGACCAACGAACTGTACATGATGAGGAGCTGTTG 2640
DB 2581 CAGATGATTAAGCCAGCCCACTGACCAACGAACTGTACATGATGAGGAGCTGTTG 2640
QY 2641 GCATGAGTGCCTTCCAGAGACCAAGCTTCAAGCAGTGTGTAAGACTTGTGATCGAAT 2700
DB 2641 GCATGAGTGCCTTCCAGAGACCAAGCTTCAAGCAGTGTGTAAGACTTGTGATCGAAT 2700
QY 2701 TCTCACTTCAACCAATGAGAA 2725
DB 2701 TCTCACTTCAACCAATGAGTAA 2725

RESULT 5
US-09-954-556-19
Sequence 19, Application US/09954556
Patent No. 690053
GENERAL INFORMATION:
APPLICANT: Brett P. Morita
APPLICANT: Susan W. Freiler
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXP
FILE REFERENCE: RTS-0250
CURRENT APPLICATION NUMBER: US/09/954,556
NUMBER OF SEQ ID NOS: 108
LENGTH: 2868
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (419)...(2734)
US-09-954-556-19

Query Match 87.6%; Score 2722; DB 3; Length 2868;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCGAGCAAGTTTGTGAGAGCAACGCAAGCTGAGTCTTCTCTCTCTGTTCC 60
DB 1 CCGCGAGCAAGTTTGTGAGAGCAACGCAAGCTGAGTCTTCTCTCTCTGTTCC 60
QY 61 CAAATCGAGGAGCGCCGCGGCGGTGATGCGCTCTTCCGACGCTGAGGTACGCTGA 120
DB 61 CAAATCGAGGAGCGCCGCGGCGGTGATGCGCTCTTCCGACGCTGAGGTACGCTGA 120
QY 121 AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTTTCGCGTTGAGATTG 180
DB 121 AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTTTCGCGTTGAGATTG 180
QY 181 TCCCGCAACCCCGGCGTGTGCTTCTCATTCGCAACCGCGGCGCGGAGCAAC 240
DB 181 TCCCGCAACCCCGGCGTGTGCTTCTCATTCGCAACCGCGGCGCGGAGCAAC 240
QY 241 ACAGGTGCGAGAGCGTTGCCATTCAAGTACTGACAGAGCAGGCGAGCGCTGCTT 300
DB 241 ACAGGTGCGAGAGCGTTGCCATTCAAGTACTGACAGAGCAGGCGAGCGCTGCTT 300

301 CCTGAGCCCAACGAGCTGAGAGGCAATGCGCGCTAGTCCATGCCCCGTAGAGGAAGTGTGCA 360
|
|
|
Db 301 CTTGAGCCCAACGAGCTGAGAGGCAATGCGCGCTAGTCCATGCCCCGTAGAGGAAGTGTGCA 360
|
|
|
Qy 361 GATGGGATTAAGTCCACATGAGATATGGAAGAGGACCGGGGATTTGGTACCGTAACAT 420
|
|
|
Db 361 GATGGGATTAAGTCCACATGAGATATGGAAGAGGACCGGGGATTTGGTACCGTAACAT 420
|
|
|
Qy 421 GGTCACTGGGGTCTGTTTCATCTGCTGGTGTGTCAACATGGCAACCTTGTCCCTGGC 480
|
|
|
Db 421 GGTCACTGGGGTCTGTTTCATCTGCTGGTGTGTCAACATGGCAACCTTGTCCCTGGC 480
|
|
|
Qy 481 CCGGCCCTCTTCAAGTTTAGTGAAGATACCAATTAGAGCCAGAGAACCCACCA 540
|
|
|
Db 481 CCGGCCCTCTTCAAGTTTAGTGAAGATACCAATTAGAGCCAGAGAACCCACCA 540
|
|
|
Qy 541 AATCCAAATCTCTCAACCAAGATGTACGTGGCTGGCCAGGGGAGTGGCTAGAGGTGG 600
|
|
|
Db 541 AATCCAAATCTCTCAACCAAGATGTACGTGGCTGGCCAGGGGAGTGGCTAGAGGTGG 600
|
|
|
Qy 601 CTGCTGTTGAAGAATGCCGCGTGATCAGTTGGAATAAGATGGGGTCACTTGGGGCC 660
|
|
|
Db 601 CTGCTGTTGAAGAATGCCGCGTGATCAGTTGGAATAAGATGGGGTCACTTGGGGCC 660
|
|
|
Qy 661 CAACAATAGACAATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCCACCTAGAGA 720
|
|
|
Db 661 CAACAATAGACAATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCCACCTAGAGA 720
|
|
|
Qy 721 CTCGGCCCTTATGCTTGTATCTGCCAGTAGAGCTGTAGACAGTGAACCTTGGTACTTCA 780
|
|
|
Db 721 CTCGGCCCTTATGCTTGTATCTGCCAGTAGAGCTGTAGAGCTGTAGAACCTTGGTACTTCA 780
|
|
|
Qy 781 GGTGAATGTCAAGATGCAATCTCATCCGAGATGTAGATGACACCGATGTGCGGA 840
|
|
|
Db 781 GGTGAATGTCAAGATGCAATCTCATCCGAGATGTAGATGACACCGATGTGCGGA 840
|
|
|
Qy 841 AGATTTTGTCACTGAGACATGTAAACAAGAGAGCAACCTACTGACCAACAAGAAA 900
|
|
|
Db 841 AGATTTTGTCACTGAGACATGTAAACAAGAGAGCAACCTACTGACCAACAAGAAA 900
|
|
|
Qy 901 GATGAGAAAGCGGCTCATGCTGTGCTGGCCCAACATGTCAAGTTTGGCTGCCACG 960
|
|
|
Db 901 GATGAGAAAGCGGCTCATGCTGTGCTGGCCCAACATGTCAAGTTTGGCTGCCACG 960
|
|
|
Qy 961 CCGGGGGAACCCAAATGCCAACATGCGGTGGCTGAAGAAACGGGAAAGATTAAAGCAGA 1020
|
|
|
Db 961 CCGGGGGAACCCAAATGCCAACATGCGGTGGCTGAAGAAACGGGAAAGATTAAAGCAGA 1020
|
|
|
Qy 1021 GCATGCGATTTGAGGCTACAAAGTACGAAACCAAGCACTGAGAGCTCAATTATGAAAAGTGT 1080
|
|
|
Db 1021 GCATGCGATTTGAGGCTACAAAGTACGAAACCAAGCACTGAGAGCTCAATTATGAAAAGTGT 1080
|
|
|
Qy 1081 GGTCCCATCTGACAAAGGAAATTAATACCTGTGTAGTGAAGATGAATACGGGTCCATCA 1140
|
|
|
Db 1081 GGTCCCATCTGACAAAGGAAATTAATACCTGTGTAGTGAAGATGAATACGGGTCCATCA 1140
|
|
|
Qy 1141 TCAACAGTACCACTGGATTTGTGAGCGATGCGCTCAACGGGCCCATCTCCAGCCGG 1200
|
|
|
Db 1141 TCAACAGTACCACTGGATTTGTGAGCGATGCGCTCAACGGGCCCATCTCCAGCCGG 1200
|
|
|
Qy 1201 ACTGCGGCAAAATGCTTCCACAGTGTGCGAGAGAGAGTGAAGTGTGTCTGCAAGGTTTA 1260
|
|
|
Db 1201 ACTGCGGCAAAATGCTTCCACAGTGTGCGAGAGAGAGTGAAGTGTGTCTGCAAGGTTTA 1260
|
|
|
Qy 1261 CAGTGAATGCCAGCCCCACATCCAGTGGATCAAGCACTGAGAAAAGAAACGGCAGTAAATA 1320
|
|
|
Db 1261 CAGTGAATGCCAGCCCCACATCCAGTGGATCAAGCACTGAGAAAAGAAACGGCAGTAAATA 1320
|
|
|
Qy 1321 CCGGCGCGACGCGGCTGCTTACCTCAAGGTTTCTCAAGCACTCGGGGATTAATATGTTCAA 1380
|
|
|
Db 1321 CCGGCGCGACGCGGCTGCTTACCTCAAGGTTTCTCAAGCACTCGGGGATTAATATGTTCAA 1380
|
|
|
Qy 1381 TGCAGAAATGCTGCTGTGTTCAATGTACCGAGGCGGATGCTGGGAAATATATATGTAA 1440
|
|
|

1381 TGCAGAAATGCTGCTGTGTTCAATGTACCGAGGCGGATGCTGGGAAATATATATGTAA 1440
|
|
|
Db 1381 TGCAGAAATGCTGCTGTGTTCAATGTACCGAGGCGGATGCTGGGAAATATATATGTAA 1440
|
|
|
Qy 1441 GGTCTCCAAATTAATATAGGGCAGGCCAACCACTGCTGCTGCTCACTGTCTGCCAAAACA 1500
|
|
|
Db 1441 GGTCTCCAAATTAATATAGGGCAGGCCAACCACTGCTGCTGCTCACTGTCTGCCAAAACA 1500
|
|
|
Qy 1501 GCAAGCGCTGGAAGAGAAAAGAGATTAACAGCTTCCCGACACTACGTGAGATAGCCAT 1560
|
|
|
Db 1501 GCAAGCGCTGGAAGAGAAAAGAGATTAACAGCTTCCCGACACTACGTGAGATAGCCAT 1560
|
|
|
Qy 1561 TTAATGCAATAGGGGCTCTTAAATGCTGTATGCTGTGTAAACAGTCACTGTGCGAAT 1620
|
|
|
Db 1561 TTAATGCAATAGGGGCTCTTAAATGCTGTATGCTGTGTAAACAGTCACTGTGCGAAT 1620
|
|
|
Qy 1621 GAAAGAACAGCAAGAAAGCCAGACTTACAGACAGCCGCGTGTGCAACAGTACCA 1680
|
|
|
Db 1621 GAAAGAACAGCAAGAAAGCCAGACTTACAGACAGCCGCGTGTGCAACAGTACCA 1680
|
|
|
Qy 1681 AGGTATCCCCCTGCGGAGACAGGTAAAGTTTCCGCTGAGTCCAGCTCTCCATGAACTC 1740
|
|
|
Db 1681 AGGTATCCCCCTGCGGAGACAGGTAAAGTTTCCGCTGAGTCCAGCTCTCCATGAACTC 1740
|
|
|
Qy 1741 CAACACCCCGCTGAGGATTAACAACGCTCTCTTCAACGCGACACACCCCATGCT 1800
|
|
|
Db 1741 CAACACCCCGCTGAGGATTAACAACGCTCTCTTCAACGCGACACACCCCATGCT 1800
|
|
|
Qy 1801 GGCAGGGGTCTTCGAGTATGAACCTTCCAGAGAGCCCAAAATGGGATTTCCAAAGATTA 1860
|
|
|
Db 1801 GGCAGGGGTCTTCGAGTATGAACCTTCCAGAGAGCCCAAAATGGGATTTCCAAAGATTA 1860
|
|
|
Qy 1861 GGTGACACTGGGCAAGCCCTGGGAGAGGTTGCTTGGGCAAGTGTCACTGGCGGAAGC 1920
|
|
|
Db 1861 GGTGACACTGGGCAAGCCCTGGGAGAGGTTGCTTGGGCAAGTGTCACTGGCGGAAGC 1920
|
|
|
Qy 1921 AGTGGAAATTTGCAAAAGCAACAGCCCAAGAGGCGGTCAACGCTGACCGTGAAGTGTGA 1980
|
|
|
Db 1921 AGTGGAAATTTGCAAAAGCAACAGCCCAAGAGGCGGTCAACGCTGACCGTGAAGTGTGA 1980
|
|
|
Qy 1981 AGATATGCTCACAGAGAAAGACCTTTCTGATCTGCTGTACAGATGAGATGAAGAT 2040
|
|
|
Db 1981 AGATATGCTCACAGAGAAAGACCTTTCTGATCTGCTGTACAGATGAGATGAAGAT 2040
|
|
|
Qy 2041 GATTTGGGAAACCAAGAAATATATATATCTTCTGAGGCTGACACAGATGGGCTCT 2100
|
|
|
Db 2041 GATTTGGGAAACCAAGAAATATATATATCTTCTGAGGCTGACACAGATGGGCTCT 2100
|
|
|
Qy 2101 CTATGCTATGATTTGAGTATGCTCTTAAAGGCAACCTCCGAGAAATCTCCGAGCCGGAG 2160
|
|
|
Db 2101 CTATGCTATGATTTGAGTATGCTCTTAAAGGCAACCTCCGAGAAATCTCCGAGCCGGAG 2160
|
|
|
Qy 2161 GCCACCCGGGATGAGATCTCCTATGACATTAACCGTGTCTGTAGAGACATGACCTT 2220
|
|
|
Db 2161 GCCACCCGGGATGAGATCTCCTATGACATTAACCGTGTCTGTAGAGACATGACCTT 2220
|
|
|
Qy 2221 CAAAGACTGGTGTATGACACCTACAGCTGGCCAGACGAGTGAATCTTGGCTTCCCA 2280
|
|
|
Db 2221 CAAAGACTGGTGTATGACACCTACAGCTGGCCAGACGAGTGAATCTTGGCTTCCCA 2280
|
|
|
Qy 2281 AAAATGTATTCATCGATTTTAGCAGCCGAAATGTTTGTGTACAGAAAACAATGTAT 2340
|
|
|
Db 2281 AAAATGTATTCATCGATTTTAGCAGCCGAAATGTTTGTGTACAGAAAACAATGTAT 2340
|
|
|
Qy 2341 GAAATATAGCAACTTTGACTGCGCAGAGATATCAACAATATAGATATTAAGAAAAGAC 2400
|
|
|
Db 2341 GAAATATAGCAACTTTGACTGCGCAGAGATATCAACAATATAGATATTAAGAAAAGAC 2400
|
|
|
Qy 2401 CACCAATGGCGGCTTCCAGTAAAGTATGCTCCAGAAAGCCGTGTGTATGATGATATA 2460
|
|
|
Db 2401 CACCAATGGCGGCTTCCAGTAAAGTATGCTCCAGAAAGCCGTGTGTATGATGATATA 2460
|
|
|
Qy 2461 CACTCATCAGAGATGTCTGTGCTCTCGGGGTGTAAATGTGGAGATCTTCACTTTAGG 2520
|
|
|

Accession	Sequence	Length
Db	CACTCATCAGAGTATGTCTGTCTCTCGGGGTGTATGTGGAGATCTTCACTTTAGG	2520
Qy	GGGCTCGCCCTACCAAGGATTCCTGTGAGAACTTTTAAGCTCTGAAGAGACA	2580
Db	GGGCTCGCCCTACCAAGGATTCCTGTGAGAACTTTTAAGCTCTGAAGAGACA	2580
Qy	CAGATGGATTAAGCAGCCAACTGCAACCAAGAACTGTACATGATGATGAGGACTGTG	2640
Db	CAGATGGATTAAGCAGCCAACTGCAACCAAGAACTGTACATGATGATGAGGACTGTG	2640
Qy	GCATGCAGTGCCTCTCCAGAGACCAAGCTTCAAGCACTGTGTAGAAAGCTTGCATCGAAT	2700
Db	GCATGCAGTGCCTCTCCAGAGACCAAGCTTCAAGCACTGTGTAGAAAGCTTGCATCGAAT	2700
Qy	TCTCACTCTCAACCAATGAG	2722
Db	TCTCACTCTCAACCAATGAG	2722

```

US-09-954-556-18
: Sequence 18, Application US/09954556
: Patent No. 6900053
: GENERAL INFORMATION:
: APPLICANT: Brett P. Monia
: APPLICANT: Susan M. Freier
: APPLICANT: Scott Cooper
: TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
: FILE REFERENCE: RFS-0250
: CURRENT APPLICATION NUMBER: US/09/954,556
: CURRENT FILING DATE: 2001-09-14
: NUMBER OF SEQ ID NOS: 108
: SEQ ID NO 18
: LENGTH: 2941
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (419)...(2878)
US-09-954-556-18

Query Match      87.6%; Score 2722; DB 3; Length 2941;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      CCCGAGCAAGTTTGATGAGCGCAAGCGCTGATCTCTTCTCTCTGTTCCC      60
DB      1      CCCCAGCAAGTTTGATGAGCGCAAGCGCTGATCTCTTCTCTCTGTTCCC      60

QY      61      CAATTCGAGGGGAGCCCGCGGGGGGTCAATGCGCTCTCCGCAACCTGGGGGTACGGGTGA      120
DB      61      CAATTCGAGGGGAGCCCGCGGGGGGTCAATGCGCTCTCCGCAACCTGGGGGTACGGGTGA      120

QY      121     AGCCCGGAGGCTTGGCGCCGCGCAGAGCCCAAGACCACTCTTCTCGGTTGGAGTTGC      180
DB      121     AGCCCGGAGGCTTGGCGCGCGCGCAGAGCCCAAGACCAACTCTTCTCGGTTGGAGTTGC      180

QY      181     TCCCCGCAACCCCGGGCTCGTGGCTTTCTCATCCCAACCGCGGGGGCGGGGAGCAAC      240
DB      181     TCCCCGCAACCCCGGGCTCGTGGCTTTCTCATCCCAACCGCGGGGGCGGGGAGCAAC      240

QY      241     ACAGGTGCGGAGGAGGCGGTTGCGCATTCAGATGACTGACGACGACGCGAGCGCTCGGTT      300
DB      241     ACAGGTGCGGAGGAGGCGGTTGCGCATTCAGATGACTGACGACGACGCGAGCGCTCGGTT      300

QY      301     CCTGAGCCACCGGAGCTGAGGCAATTCGCGTAGTCCATGCCCCGTAGAGGAACTGTGCA      360
DB      301     CCTGAGCCACCGGAGCTGAGGCAATTCGCGTAGTCCATGCCCCGTAGAGGAACTGTGCA      360

QY      361     GATGGAGTTAAAGTTCACATGAGATATGAGAAAGACCGGGGAAATGGTACACCTAACAT      420
DB      361     GATGGAGTTAAAGTTCACATGAGATATGAGAAAGACCGGGGAAATGGTACACCTAACAT      420

```

QY	421	GGTCA	GCTGG	GGTGGTT	CATCTG	CCCTGGTGGTCA	CCATGGCA	CCTTGTCCTGGC	480
DB	421	GGTCA	GCTGG	GGTGGTT	CATCTG	CCCTGGTGGTCA	CCATGGCA	CCTTGTCCTGGC	480
QY	481	CGGGCC	CTCTT	CACTT	AGTGA	GTATCA	CTTAGAC	CAAGAGCCACCA	540
DB	481	CGGGCC	CTCTT	CACTT	AGTGA	GTATCA	CTTAGAC	CAAGAGCCACCA	540
QY	541	ATTA	CAATCT	CTTCA	CCAG	AGTGA	CGTGG	CCGACAGGGAGT	600
DB	541	ATTA	CAATCT	CTTCA	CCAG	AGTGA	CGTGG	CCGACAGGGAGT	600
QY	601	CTG	CTCTT	GAAG	ATGCC	CGGTG	ATCAG	TTGAGTGGGTGCA	660
DB	601	CTG	CTCTT	GAAG	ATGCC	CGGTG	ATCAG	TTGAGTGGGTGCA	660
QY	661	CAACA	ATATG	AGAC	ATGCTT	ATTTGGG	AGTCTTG	CAATAAGGCGCCAC	720
DB	661	CAACA	ATATG	AGAC	ATGCTT	ATTTGGG	AGTCTTG	CAATAAGGCGCCAC	720
QY	721	CTCCG	CCCTAT	GCTCT	GTACTG	CCAGT	AGGAC	CTTGAGAACTTGGT	780
DB	721	CTCCG	CCCTAT	GCTCT	GTACTG	CCAGT	AGGAC	CTTGAGAACTTGGT	780
QY	781	GCTGA	ATGTCA	CAGAT	GCATCT	CTCCG	AGATG	ATGAGATGAC	840
DB	781	GCTGA	ATGTCA	CAGAT	GCATCT	CTCCG	AGATG	ATGAGATGAC	840
QY	841	AGATTT	GTCA	GTAG	AGAA	CGTGA	CA	CAAGAGCCAT	900
DB	841	AGATTT	GTCA	GTAG	AGAA	CGTGA	CA	CAAGAGCCAT	900
QY	901	GATG	AAAAAG	GGGCT	CATG	CTG	GCTGG	GGCCAA	960
DB	901	GATG	AAAAAG	GGGCT	CATG	CTG	GCTGG	GGCCAA	960
QY	961	CGGGGG	AGAC	CCCA	ATG	CCCA	CA	TGCGGTG	1020
DB	961	CGGGGG	AGAC	CCCA	ATG	CCCA	CA	TGCGGTG	1020
QY	1021	GCA	TGCA	TTTGG	AGAG	CCCTA	AGGA	AGCTTAT	1080
DB	1021	GCA	TGCA	TTTGG	AGAG	CCCTA	AGGA	AGCTTAT	1080
QY	1081	GGTCC	CACT	CTTGA	CAAG	GGAA	TTTAT	CTGTGT	1140
DB	1081	GGTCC	CACT	CTTGA	CAAG	GGAA	TTTAT	CTGTGT	1140
QY	1141	TCACA	CGTACA	CCCTG	AGTGT	TGTG	AGAC	ATGCGCT	1200
DB	1141	TCACA	CGTACA	CCCTG	AGTGT	TGTG	AGAC	ATGCGCT	1200
QY	1201	ACTG	CCGG	CAAA	TGCTT	CTTCA	CA	TG	1260
DB	1201	ACTG	CCGG	CAAA	TGCTT	CTTCA	CA	TG	1260
QY	1261	CAGT	GATG	CCCA	GGCCCA	CACT	CA	GTG	1320
DB	1261	CAGT	GATG	CCCA	GGCCCA	CACT	CA	GTG	1320
QY	1321	CGGG	CCCG	ACG	GGCTG	CCCTA	CTTCA	GA	1380
DB	1321	CGGG	CCCG	ACG	GGCTG	CCCTA	CTTCA	GA	1380
QY	1381	TGCA	GAAG	TGCTG	CTCTT	CA	TG	1440	
DB	1381	TGCA	GAAG	TGCTG	CTCTT	CA	TG	1440	
QY	1441	GGTCC	CAATTA	TATAT	GGGCA	GGCCCA	CA	GTG	1500
DB	1441	GGTCC	CAATTA	TATAT	GGGCA	GGCCCA	CA	GTG	1500
QY	1501	GCA	AGCG	CTTGA	AGAA	GAATTA	CA	GCTT	1560
DB	1501	GCA	AGCG	CTTGA	AGAA	GAATTA	CA	GCTT	1560

```
Db 1501 GGAAGGCTGGAGAGAGAGAGATACAGCTTCCAGACTACCTGAGATACCCAT 1560
    |||
Qy 1561 TTACTGATAGAGGCTTCTTATCGCTGTATGTGTAAAGTCATCTGTCCGAAT 1620
    |||
Db 1561 TTACTGATAGAGGCTTCTTATCGCTGTATGTGTAAAGTCATCTGTCCGAAT 1620
    |||
Qy 1621 GAAAGACGACCAAGAGCCAGACTTCAGCAGCCAGCCGGCTGTGCAAGCTGACCA 1680
    |||
Db 1621 GAAAGACGACCAAGAGCCAGACTTCAGCAGCCAGCCGGCTGTGCAAGCTGACCA 1680
    |||
Qy 1681 AGGTATCCCTGCGGAGACAGGTACAGTTTCAGGTGAGTCCAGCTCCATGAATC 1740
    |||
Db 1681 AGGTATCCCTGCGGAGAGAGGTACAGTTTCAGGTGAGTCCAGCTCCATGAATC 1740
    |||
Qy 1741 CAACACCCCGCTGTGTAGATTAACAACGCTCTCTTCAACGAGACACCCCAATGCT 1800
    |||
Db 1741 CAACACCCCGCTGTGTAGATTAACAACGCTCTCTTCAACGAGACACCCCAATGCT 1800
    |||
Qy 1801 GGGAGGGGTCTCCGAGTATGAATTCAGAGGACCCAAATGGAGTTTCCAGAGATTA 1860
    |||
Db 1801 GGGAGGGGTCTCCGAGTATGAATTCAGAGGACCCAAATGGAGTTTCCAGAGATTA 1860
    |||
Qy 1861 GGTGACACTGGGGCAACCCCTGGGAGAGAGGTTGCTTTGGCAAGTGTATGGCGGAGC 1920
    |||
Db 1861 GGTGACACTGGGGCAACCCCTGGGAGAGAGGTTGCTTTGGCAAGTGTATGGCGGAGC 1920
    |||
Qy 1921 AGTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTCACTGGTCCGTGAAGTGTGA 1980
    |||
Db 1921 AGTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTCACTGGTCCGTGAAGTGTGA 1980
    |||
Qy 1981 AGATGATGCCAGAGAGAAAGACTTTCTGATCTGTGTCAAGATGTGAATGTGAAGT 2040
    |||
Db 1981 AGATGATGCCAGAGAGAAAGACTTTCTGATCTGTGTCAAGATGTGAATGTGAAGT 2040
    |||
Qy 2041 GATTTGGGAAACCAAGATATATCAATCTTTGAGAGCTGACACAGAGTGGGCTCT 2100
    |||
Db 2041 GATTTGGGAAACCAAGATATATCAATCTTTGAGAGCTGACACAGAGTGGGCTCT 2100
    |||
Qy 2101 CTATGTCAATAGTTGAGTATGCTCTTAAAGCACTTCAGAGATACCTCCAGCCCGAG 2160
    |||
Db 2101 CTATGTCAATAGTTGAGTATGCTCTTAAAGCACTTCAGAGATACCTCCAGCCCGAG 2160
    |||
Qy 2161 GCCACCCGGGATGAGTACTCTCTATGACATTAACCGTGTCTGTAGAGACAGATGACTT 2220
    |||
Db 2161 GCCACCCGGGATGAGTACTCTCTATGACATTAACCGTGTCTGTAGAGACAGATGACTT 2220
    |||
Qy 2221 CAAGACTTGTGTGATGACCTTACAGCTGAGCGGCGAGAGCGATGAGTACTTGGCTTCCA 2280
    |||
Db 2221 CAAGACTTGTGTGATGACCTTACAGCTGAGCGGCGAGAGCGATGAGTACTTGGCTTCCA 2280
    |||
Qy 2281 AAAATGTATTCATGAGATTTAGACAGCCAGAAATGTTTGTGAACAGAAACATATGTAT 2340
    |||
Db 2281 AAAATGTATTCATGAGATTTAGACAGCCAGAAATGTTTGTGAACAGAAACATATGTAT 2340
    |||
Qy 2341 GAAATATGACAGACTTTGAGCTGCGCAGAGATTAACAATATGACTTAAACAAAAGAC 2400
    |||
Db 2341 GAAATATGACAGACTTTGAGCTGCGCAGAGATTAACAATATGACTTAAACAAAAGAC 2400
    |||
Qy 2401 CACCAATGGGCGGCTTCAAGTGAAGTGAAGTGTGCAAGAAAGCCCTGTTGATGAGTATTA 2460
    |||
Db 2401 CACCAATGGGCGGCTTCAAGTGAAGTGAAGTGTGCAAGAAAGCCCTGTTGATGAGTATTA 2460
    |||
Qy 2461 CACTCATCAGAGTATGTCTGTCTTCCGGGTGTATATGTGGAGATCTTCACTTTAGG 2520
    |||
Db 2461 CACTCATCAGAGTATGTCTGTCTTCCGGGTGTATATGTGGAGATCTTCACTTTAGG 2520
    |||
Qy 2521 GGGCTGCGCTTACCCAGGAGATTCCTGCGAGGAACTTTTAACTGTGAGAGAGACA 2580
    |||
Db 2521 GGGCTGCGCTTACCCAGGAGATTCCTGCGAGGAACTTTTAACTGTGAGAGAGACA 2580
    |||
Qy 2581 CAGATGATTAACCGAGCCAACTGCAACAAGAACTGATCATGATGAGGAGCTGTTC 2640
    |||
```

```
Db 2581 CAGATGATTAACCGAGCCAACTGCAACAAGAACTGATCATGATGAGGAGCTGTTC 2640
    |||
Qy 2641 GCATCACTGCTCCAGAGACCAAGCTTCAAGAGTGTGTGAAGACTTGGATTCGAT 2700
    |||
Db 2641 GCATCACTGCTCCAGAGACCAAGCTTCAAGAGTGTGTGAAGACTTGGATTCGAT 2700
    |||
Qy 2701 TCTCACTCTCAACCAATGAG 2722
    |||
Db 2701 TCTCACTCTCAACCAATGAG 2722
    |||

RESULT 7
US-08-451-822A-15
; Sequence 15, Application US/08451822A
; Patent No. 5863888
; GENERAL INFORMATION:
; APPLICANT: Dione, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlesinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,822A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,430
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,372
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-451-822A-15

Query Match 87.4%; Score 2714.2; DB 2; Length 3416;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2790; Conservative 0; Mismatches 68; Indels 15; Gaps 2;

Qy 240 CACAGGTGCGGAGAGAGCTTCCATTAAGTGAAGTGAAGAGCGGAGCGCTCGGT 299
    |||
Db 2 CCCAGGTGCGGAGAGAGCTTCCATTAAGTGAAGTGAAGAGCGGAGCGCTCGGT 61
    |||
Qy 300 TCTGAGCCCAACGAGCTGAAGGATTCGCGGTAGTCCATCCGTAGAGAGAGTGTGC 359
    |||
```

Db 62 TCCGAGCCCAACCGAGCTGAGGCAATTGGCGGTAAGTCATGCCCGGTAGAGAGATGTGC 121
Qy 360 AGATGGAGATTAAAGTCCATATGAGATATGGAAGAGACCGGGATTTGGTACCGTAAACA 419
Db 122 AGATGGAGATTAAAGTCCATATGAGATATGGAAGAGACCGGGATTTGGTACCGTAAACA 181
Qy 420 TGGTCAAGCTGGGGGTGCTTCAATGCTGGTGGGTGACCATAGGCAACCTTGGCTTGG 479
Db 182 TGGTCAAGCTGGGGGTGCTTCAATGCTGGTGGGTGACCATAGGCAACCTTGGCTTGG 241
Qy 480 CCGGCGCTCTCTCACTTATAGTGAAGATACCATATAGAGCCAGAAAGCCCAACA 539
Db 242 CCGGCGCTCTCTCACTTATAGTGAAGATACCATATAGAGCCAGAAAGCCCAACA 301
Qy 540 AATACCAATCTCTCAACCAAGAGTGAAGTGGTGGCCAGAGGGAGTGGCTAGAGTGC 599
Db 302 AATACCAATCTCTCAACCAAGAGTGAAGTGGTGGCCAGAGGGAGTGGCTAGAGTGC 361
Qy 600 GCTGCGCTGTAAGAAAGATGCGCGCGGTATGAGTGAATAGATGGGGTGCATTTGGGGC 659
Db 362 GCTGCGCTGTAAGAAAGATGCGCGCGGTATGAGTGAATAGATGGGGTGCATTTGGGGC 421
Qy 660 CCAACATAGGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCCAACCTTAGAG 719
Db 422 CCAACATAGGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCCAACCTTAGAG 481
Qy 720 ACTCGGCGCTCTATGCTTTGTACTGCAAGTGAAGTGTGAACAAGTGAATCTTGGTCTTCA 779
Db 482 ACTCGGCGCTCTATGCTTTGTACTGCAAGTGAAGTGTGAACAAGTGAATCTTGGTCTTCA 541
Qy 780 TGGTGAATATGCAAGAGATGCAATCTCATCCGAGATGATAGAGATGACACCGATGGTGC 839
Db 542 TGGTGAATATGCAAGAGATGCAATCTCATCCGAGATGATAGAGATGACACCGATGGTGC 601
Qy 840 AAGATTTTGTCAAGTGAAGACGTAAACAACAAGAGACCACTATCTGACCAACAAGAAA 899
Db 602 AAGATTTTGTCAAGTGAAGACGTAAACAACAAGAGACCACTATCTGACCAACAAGAAA 661
Qy 900 AGATGAAAAAGCGGCTCCATGCTGTGCTGGCGCAACCTGTCAAGTTTGGCTGGCCAG 959
Db 662 AGATGAAAAAGCGGCTCCATGCTGTGCTGGCGCAACCTGTCAAGTTTGGCTGGCCAG 721
Qy 960 CCGGCGGGGAAACCCATGCCCAACCATGGGCTGGCTGAAAAACGGGAAGAGTTTAAAGAG 1019
Db 722 CCGGCGGGGAAACCCATGCCCAACCATGGGCTGGCTGAAAAACGGGAAGAGTTTAAAGAG 781
Qy 1020 AGCATGCAATTGAGGCTCAAGAGTACAGAAACAGCACTGGAGGCTCATTTATGAAAAAGT 1079
Db 782 AGCATGCAATTGAGGCTCAAGAGTACAGAAACAGCACTGGAGGCTCATTTATGAAAAAGT 841
Qy 1080 TGGTCCCATCTGACAAAGGAAATTAACCTGTGTATGAGAGATGAATACGGGCTCCATCA 1139
Db 842 TGGTCCCATCTGACAAAGGAAATTAACCTGTGTATGAGAGATGAATACGGGCTCCATCA 901
Qy 1140 ATCAACGATACACCTGATGTGTGAGAGCATGGCTCAACCGGCCCATCTCTCAACCGC 1199
Db 902 ATCAACGATACACCTGATGTGTGAGAGCATGGCTCAACCGGCCCATCTCTCAACCGC 961
Qy 1200 GACTGCGGGGAAATGCTCCCAAGTGGTGGAGAGACGTAGAGTTTGTGCAAGGTTT 1259
Db 962 GACTGCGGGGAAATGCTCCCAAGTGGTGGAGAGACGTAGAGTTTGTGCAAGGTTT 1021
Qy 1260 ACACTGATGCCCAAGCCCAACATCCAGTGGATCAAGACGTTGAAAAAGAACGGCGATTAAT 1319
Db 1022 ACACTGATGCCCAAGCCCAACATCCAGTGGATCAAGACGTTGAAAAAGAACGGCGATTAAT 1081
Qy 1320 ACGGCGCCGAGAGGCTGCTCACTCAAGTGTCTCAAGCACTCGGGGATAAATAGTTTCCA 1379
Db 1082 ACGGCGCCGAGAGGCTGCTCACTCAAGTGTCTCAAGGCTCGGGGATAAATAGTTTCCA 1141
Qy 1380 ATGCAAGAGTGTGGCTGTGT-----TCAATGTGACCGAGGCGGATGCTGGGAAATATA 1433
Db 1142 ACAAGAGATTTGAGGTTCTATATATGGAATGTAACTTTGAGAGAGCTGGGAAATATA 1201

Qy 1434 TATGTAGGCTTCCATTAATATAGGAGAGCCAAACAGTCTGCTGCTCATCTGTCTGC 1493
Db 1202 CGTGTGGCGGGGTAATTTATTTGGGATATCTTTTCACTGTGATGTTGACAGTTCTGC 1261
Qy 1494 CAAGAACGAGAGGCTGGAAGAAAGAGATTAACGTTTCCCAAGCTTACTGAGAGA 1553
Db 1262 C-----AGGCTCGAAGAGAAAGAGATTAACGTTTCCCAAGCTTACTGAGAGA 1312
Qy 1554 TACCATTTATCTGCAATAGGGGTCTTTTAAATGSCCTGATAGGTGATACAGTACCTGT 1613
Db 1313 TACCATTTATCTGCAATAGGGGTCTTTTAAATGSCCTGATAGGTGATACAGTACCTGT 1372
Qy 1614 GCCGAATGAAGAACAGCAAGCAAGAACCCAGACTTACAGAGCCAGCCGCTGTGCAAGC 1673
Db 1373 GCCGAATGAAGAACAGCAAGAACCCAGACTTACAGAGCCAGCCGCTGTGCAAGC 1432
Qy 1674 TGAACCAAGGTATCCCTGCGGAGACAGTAAACGTTTGGCTGATGCTCTCTCCA 1733
Db 1433 TGAACCAAGGTATCCCTGCGGAGACAGTAAACGTTTGGCTGATGCTCTCTCCA 1492
Qy 1734 TGAATCTCAACACCCGCTGTGTAGAGTAAACAACGCTCTCTTCAACCGGAGACACC 1793
Db 1493 TGAATCTCAACACCCGCTGTGTAGAGTAAACAACGCTCTCTTCAACCGGAGACACC 1552
Qy 1794 CCAATGCTGGAGGGGTCTCCAGATGAACCTTCAGAGGACCCAAATGGGAGTTTCCA 1853
Db 1553 CCAATGCTGGAGGGGTCTCCAGATGAACCTTCAGAGGACCCAAATGGGAGTTTCCA 1612
Qy 1854 GAGATTAAGTGAACACTGAGGCAAGCCCTGTGGAGAGTTTCTTGGGCAAGTGTCA 1913
Db 1613 GAGATTAAGTGAACACTGAGGCAAGCCCTGTGGAGAGTTTCTTGGGCAAGTGTCA 1672
Qy 1914 CGAAGCAGTGGGAATTTGACAAAGACAGCCCAAGAGGGGTGACCGTGGCCGTGAAGA 1973
Db 1673 CGAAGCAGTGGGAATTTGACAAAGACAGCCCAAGAGGGGTGACCGTGGCCGTGAAGA 1732
Qy 1974 TGTGTAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGAGAGATGAGATGA 2033
Db 1733 TGTGTAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTGAGAGATGAGATGA 1792
Qy 2034 TGAAGATATTGGGAAACACAAAGATATCAATTAATCTTCTTGAAGCTGTGACAAGATG 2093
Db 1793 TGAAGATATTGGGAAACACAAAGATATCAATTAATCTTCTTGAAGCTGTGACAAGATG 1852
Qy 2094 GGCCTCTATATGTCATATGTTGATGATGCTCTTAAAGCAACCTCCAGATACCTTCGAG 2153
Db 1853 GGCCTCTATATGTCATATGTTGATGATGCTCTTAAAGCAACCTCCAGATACCTTCGAG 1912
Qy 2154 CCGGAGGCGCAACCGGAGTGAAGTACCTCATAGCAATTAACCGGTTCTGAGAGAGAGA 2213
Db 1913 CCGGAGGCGCAACCGGAGTGAAGTACCTCATAGCAATTAACCGGTTCTGAGAGAGAGA 1972
Qy 2214 TGAACCTTCAAGAGCTTGTGTCACTGACCTTACAGAGCTGGCCAGACGATGAGTACTTGG 2273
Db 1973 TGAACCTTCAAGAGCTTGTGTCACTGACCTTACAGAGCTGGCCAGAGGATGAGTACTTGG 2032
Qy 2274 CTTCCAAAATATGATTCATGAGATTTAGACGACGAGAAATGTTTGTGTAACGAAAAACA 2333
Db 2033 CTTCCAAAATATGATTCATGAGATTTAGACGACGAGAAATGTTTGTGTAACGAAAAACA 2092
Qy 2334 ATGTGATGAATTAAGAGACTTTGAGACTGGCCAGAGATATCAACAATATATGACTATTA 2393
Db 2093 ATGTGATGAATTAAGAGACTTTGAGACTGGCCAGAGATATCAACAATATATGACTATTA 2152
Qy 2394 AAAAGACCAACAAATGGCGGCTTCAAGTCAAGTGAATGAGTCAAGAACCCCTGTTGATA 2453
Db 2153 AAAAGACCAACAAATGGCGGCTTCAAGTCAAGTGAATGAGTCAAGAACCCCTGTTGATA 2212
Qy 2454 GAGATTAACCTCATGAGATGATGTGTGCTTGGGGGTGTTAAATGTGGAGATCTTCA 2513
Db 2213 GAGATTAACCTCATGAGATGATGTGTGCTTGGGGGTGTTAAATGTGGAGATCTTCA 2272

OY		2514	CCTTAAGGGGCGCTGCCTCACCACAGGAATTCGCCGTGAGAACTTTTAACTGCTGAAG	2573
Db		2273	CTTTAAGGGGCGCTGCCTCACCAAGGAATTCCCGTGAGAACCTTTTTAACTGCTGAAG	2332
OY		2574	AAGAACA CAGAAATGATAAGCCAAGCCA CTGCA CCMA CGAA CTGTACA TGA TGA AGG	2633
Db		2333	AAGACAC A GAAATGATAAGCCAAGCCA CTGCA CCMA CGAA CTGTACA TGA TGA AGG	2392
OY		2634	ACTGTGGCATGCA GTGCCCCCTTCCCAGAGACCAA GCTTCAAGCAGTTTGTTAGAA ACTTGG	2693
Db		2393	ACTGTGGCATGCA GTGCCCCCTTCCCAGAGACCAA GCCTTCAACAGTTTGTTAGAA ACTTGG	2452
OY		2694	ATCGAATTC TCAC TCTCA CAACCAA TGAGSAA TA CTC TTGA C CTGAC GA ACCTCTCGAAC	2753
Db		2453	ATCGAATTC TCAC TCTCA CAACCAA TGAGSAA TA CTC TTGA C CTGAC GA ACCTCTCGAAC	2512
OY		2754	AGTAATTCAC TAGTTAAC CCTGACACA MAAGA GTTCTTGTCTCTTCA GSAANTATTCTGT	2813
Db		2513	AGTAATTCAC TAGTTAAC CCTGACACA MAAGA GTTCTTGTCTCTTCA GSAANTATTCTGT	2572
OY		2814	TTTCTCCAGAC CCCATGCTTTACGA ACCATGCTTCTCA GTA TTCACA CATPAAA CGSCA	2873
Db		2573	TTTCTCCAGAC CCCATGCTTTACGA ACCATGCTTCTCA GTA TTCACA CATPAAA CGSCA	2632
OY		2874	GTCGTTAAAA CA ATGAA TGA CTGTGTGCTGTGCCCTGCCCCA AA CAGA CAGCA CTGGGAACCTA	2933
Db		2633	GTCGTTAAAA CA ATGAA TGA CTGTGTGCTGTGCCCTGCCCCA AA CAGA CAGCA CTGGGAACCTA	2692
OY		2934	GCTACACTGAGCA GGAGGAGCA CAGCTCCCA GAGCTGTGTGCTGTCA CTTGTATATATG	2993
Db		2693	GCTACACTGAGCA GGAGGAGCA CAGCTCCCA GAGCTGTGTGCTGTCA CTTGTATATATG	2752
OY		2994	ATCAGAGAGATPAATTAATTGGAAAAATACAGCA TATGTGTAAAGATTATACAGTTGA	3053
Db		2753	ATCAGAGAGATPAATTAATTGGAAAAATACAGCA TATGTGTAAAGATTATACAGTTGA	2812
OY		3054	AAACTGTGAATCTTCCCCCAGAGAGGAAAGAGCTTTCGAGCAGTAGCACTGC	3106
Db		2813	AAACTGTGAATCTTCCCCCAGAGAGGAAAGAGCTTTCGAGCAGTAGCACTGC	2865
 RESULT 8 US-08-323-430-15 ; Sequence 15, Application US /08323430 ; Patent No. 6344546 GENERAL INFORMATION: APPLICANT: Dionne, Craig A APPLICANT: Crumley, Greg APPLICANT: Jeye, Michael C APPLICANT: Schlessinger, Joseph TITLE OF INVENTION: Fibroblast Growth Factor Receptors NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: Rhone-Poulenc Rorer Legal Department STREET: 500 Arcola Road CITY: Collegeville STATE: PA COUNTRY: USA ZIP: 19426 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/323, 430 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US to be assigned FILING DATE: 21-AUG-1992 APPLICATION NUMBER: US 07/549,587 FILING DATE: 06-JUL-1990				

Query	Match	87.4%	Score 2714.2	DB 3	Length 3416
Db	240	CACAGGTCGGGAGGAGCGTTGGCATTCAGATGACCTGCAGACGACGCGCGCTGGT	299		
Db	2	CCCGAGTCGGGAGGAGCGTTGGCATTCAGATGACCTGCAGACGACGCGCGCTGGT	61		
Qy	300	TCCGAGCCCAACGCGACCTGAGAGCATTTGGCGCGTATCCATGCCCCGTAGAGAAAGTGTG	359		
Db	62	TCCGAGCCCAACGCGACCTGAGAGCATTTGGCGCGTATCCATGCCCCGTAGAGAAAGTGTG	121		
Qy	360	AGATGGGATTAACGTCACATGAGATATGAGAGAGACCGGGGATTTGGTACCCTAACCA	419		
Db	122	AGATGGGATTAACGTCACATGAGATATGAGAGAGACCGGGGATTTGGTACCCTAACCA	181		
Qy	420	TGTCACGTCGGGGTCGTTTATCTGCGTGGTCGTCATCCATGGCAACCTGTCCCTGG	479		
Db	182	TGTCACGTCGGGGTCGTTTATCTGCGTGGTCGTCATCCATGGCAACCTGTCCCTGG	241		
Qy	480	CCCCGCCCTCTTCAGATTATGTTGAGATACACATTAGAGCCAGAAAGCCACCAACA	539		
Db	242	CCCCGCCCTCTTCAGATTATGTTGAGATACACATTAGAGCCAGAAAGCCACCAACA	301		
Qy	540	AATAACAATCTCTCAACAGAGATGTACGTGCTGGCCAGGGGAGTCCCTTAGAGTGC	599		
Db	302	AATAACAATCTCTCAACAGAGATGTACGTGCTGGCCAGGGGAGTCCCTTAGAGTGC	361		
Qy	600	GCTGCTGTGTAAGAATGCGCCGCTGATCAGTTGGACCTAAGAGATGGGTGCACTTGGGGC	659		
Db	362	GCTGCTGTGTAAGAATGCGCCGCTGATCAGTTGGACCTAAGAGATGGGTGCACTTGGGGC	421		
Qy	660	CCAAACAATAGACAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGGGCCACACTAGAG	719		
Db	422	CCAAACAATAGACAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGGGCCACACTAGAG	481		
Qy	720	ACTCGGCGCTTATGCTTGTATCTGCCAATGAGACTGTAGACAGTGAACCTTGGTACTTCA	779		
Db	482	ACTCGGCGCTTATGCTTGTATCTGCCAATGAGACTGTAGACAGTGAACCTTGGTACTTCA	541		
Qy	780	TGTTGATATGTACAGATGCTCATCTTCATTCGGAGATGATGAGAGATGACACCGATGCTGG	839		
Db	542	TGTTGATATGTACAGATGCTCATCTTCATTCGGAGATGATGAGAGATGACACCGATGCTGG	601		
Qy	840	AAGATTTTGTGAGTGAAGAACAGTAAACAACAAGAGAGCCATTAATGACCAACAAGAA	899		
Db	602	AAGATTTTGTGAGTGAAGAACAGTAAACAACAAGAGAGCCATTAATGACCAACAAGAA	661		
Qy	900	AGATGGAAGAACCGGCTCCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCCTGCCAG	959		
Db	662	AGATGGAAGAACCGGCTCCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCCTGCCAG	721		
Qy	960	CCGGGGGGAAACCAATGCAACATGCGGTGGCTGAAAAACGGGAAGAGATTTAAGCAAG	1019		
Db	722	CCGGGGGGAAACCAATGCAACATGCGGTGGCTGAAAAACGGGAAGAGATTTAAGCAAG	781		
Qy	1020	AGCATGCAATTGGAGCTTACAAAGTACGAAACAGCACTGGAAGCTCTATTAGAAAGTG	1079		

Db 1572 GAGATAGCTGACCTGGGCAAGCCCTGGGAGAGGTTGCTTGGGCAAGTGTCAAG 1631
Qy 1914 CGAGAGAGTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCCTGAAGA 1973
Db 1632 CGAGAGAGTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCCTGAAGA 1691
Qy 1974 TGTGAAAGATGATGCGCACAGAGAAAGCCTTTCGATCTGGTCTCAGAGATGAGATGA 2033
Db 1692 TGTGAAAGATGATGCGCACAGAGAAAGCCTTTCGATCTGGTCTCAGAGATGAGATGA 1751
Qy 2034 TGAAGATGATTTGGGAAACAAAGAAATATCATAAATCTTCTTGGAGCCCTGCACAGAGATG 2093
Db 1752 TGAAGATGATTTGGGAAACAAAGAAATATCATAAATCTTCTTGGAGCCCTGCACAGAGATG 1811
Qy 2094 GGGCTCTTATGTCATAGTGTGATGATGCTCTTAAAGGCACTTCGAGAAATCTCCGAG 2153
Db 1812 GGGCTCTTATGTCATAGTGTGATGATGCTCTTAAAGGCACTTCGAGAAATCTCCGAG 1871
Qy 2154 CCGGAGAGCCCAACCGGAGATGAGATGCTCTTAAAGGCACTTCGAGAAATCTCCGAG 2213
Db 1872 CCGGAGAGCCCAACCGGAGATGAGATGCTCTTAAAGGCACTTCGAGAAATCTCCGAG 1931
Qy 2214 TGACCTTCAAGAGACTTGGTGTCAATGCACTACAGCTGGCCAGACGAGATGAGATCTTG 2273
Db 1932 TGACCTTCAAGAGACTTGGTGTCAATGCACTACAGCTGGCCAGAGGCAATGAGATCTTG 1991
Qy 2274 CTTCCCAAAAATGATATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACAGAAAACA 2333
Db 1992 CTTCCCAAAAATGATATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACAGAAAACA 2051
Qy 2334 ATGTGATGAAATATGACAGACTTTGAGACTGCGCAGAGATATCAAAATTAATTAATTA 2393
Db 2052 ATGTGATGAAATATGACAGACTTTGAGACTGCGCAGAGATATCAAAATTAATTAATTA 2111
Qy 2394 AAAAGACCAAAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAACCTCTGTTGATA 2453
Db 2112 AAAAGACCAAAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAACCTCTGTTGATA 2171
Qy 2454 GAGATATCACTCATCAGATGATGATCTGGTCTTGGGGGTGTAATGTGGAGATCTTCA 2513
Db 2172 GAGATATCACTCATCAGATGATGATCTGGTCTTGGGGGTGTAATGTGGAGATCTTCA 2231
Qy 2514 CTTTAAAGGGGCTGCGCCCTTACCAAGAGATTTCCCTGGAGAGAACTTTTAAAGCTGCGAGAG 2573
Db 2232 CTTTAAAGGGGCTGCGCCCTTACCAAGAGATTTCCCTGGAGAGAACTTTTAAAGCTGCGAGAG 2291
Qy 2574 AAGGACAGATGATGATGAGCAAGCACTGCAACCAAGAACTGATGATGATGAGAG 2633
Db 2292 AAGGACAGATGATGATGAGCAAGCACTGCAACCAAGAACTGATGATGATGAGAG 2351
Qy 2634 ACTGTTGAGATGAGATGAGCTTCCAGAGACCAAGCTTCAAGCAAGTTGATGAGAGCTTGG 2693
Db 2352 ACTGTTGAGATGAGATGAGCTTCCAGAGACCAAGCTTCAAGCAAGTTGATGAGAGCTTGG 2411
Qy 2694 ATCGAATTTCTCATCTCAACCAATGAGATATCTTGAAGCTTCAAGCTTCTGCAAC 2753
Db 2412 ATCGAATTTCTCATCTCAACCAATGAGATATCTTGAAGCTTCAAGCTTCTGCAAC 2471
Qy 2754 AGTATTCACCTAGTAACTGCTGCAACAGAAAGTTCTTGTCTTCAAGAGATGATGATGAT 2813
Db 2472 AGTATTCACCTAGTAACTGCTGCAACAGAAAGTTCTTGTCTTCAAGAGATGATGATGAT 2531
Qy 2814 TTTCTCCAGAGCCCAATGCTTACGAACCAATGCTTCTCAAGTATCCACATTAACGGCA 2873
Db 2532 TTTCTCCAGAGCCCAATGCTTACGAACCAATGCTTCTCAAGTATCCACATTAACGGCA 2591
Qy 2874 GTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2933
Db 2592 GTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2651
Qy 2934 GCTACACTGAGAGAGAGACATGCTCCAGAGCTTGTGTCTCACTTGTATATATG 2993
Db 2652 GCTACACTGAGAGAGAGACATGCTCCAGAGCTTGTGTCTCACTTGTATATATG 2711

Qy 2994 ATCAGAGAGTAAATATTTGAAAGATATCAGATATGATGATGATGATGATGATGATGATGAT 3053
Db 2712 ATCAGAGAGTAAATATTTGAAAGATATCAGATATGATGATGATGATGATGATGATGATGAT 2771
Qy 3054 AAACCTGTAATCTTCCCAAG 3106
Db 2772 AAACCTGTAATCTTCCCAAG 2824

RESULT 10
US-09-954-556-28
; Sequence 28, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Bret P. Monia
; APPLICANT: Susan M. Preter
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXP
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 28
; LENGTH: 2650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-556-28

Query Match 74.7%; Score 2320; DB 3; Length 2650;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2323; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 395 GAGCCGGGAGTTGGTACCGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
Db 1 GAGCCGGGAGTTGGTACCGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Qy 455 GTCAACATGCGCACTTGTCCCTGCGCGCCCTCTTCAAGTTAGTTAGAGATACCA 514
Db 61 GTCAACATGCGCACTTGTCCCTGCGCGCCCTCTTCAAGTTAGTTAGAGATACCA 120
Qy 515 TTAGAGCAGAGAGCCACCAACCAATATCTTCAACCAAGATGATGATGATGATGATGATGATGAT 574
Db 121 TTAGAGCAGAGAGCCACCAACCAATATCTTCAACCAAGATGATGATGATGATGATGATGATGAT 180
Qy 575 GCGCCAGGAGTGTCTAGAGTGTGCTGCTGTTGAAAGATGCGCGCTGATCAAGTTGG 634
Db 181 GCGCCAGGAGTGTCTAGAGTGTGCTGCTGTTGAAAGATGCGCGCTGATCAAGTTGG 240
Qy 635 ACTAAGATGAGGAGTGTGCTGCGCGCCCAACCAATAGCAAGTCTTATTTGGGAGTACTTG 694
Db 241 ACTAAGATGAGGAGTGTGCTGCGCGCCCAACCAATAGCAAGTCTTATTTGGGAGTACTTG 300
Qy 695 CAGATTAAGGCGCCACACTAGAGACTCCGCGCTTATGCTTATGCTGCAAGTACCTGAGTAC 754
Db 301 CAGATTAAGGCGCCACACTAGAGACTCCGCGCTTATGCTTATGCTGCAAGTACCTGAGTAC 360
Qy 755 GTAGACAGTGAACCTTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
Db 361 GTAGACAGTGAACCTTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 815 GATAGAGATGACACCGATGAGGAGATTTTCTCAGTGAAGACAGTAAACAAAGAGA 874
Db 421 GATAGAGATGACACCGATGAGGAGATTTTCTCAGTGAAGACAGTAAACAAAGAGA 480
Qy 875 GCACCATATCTGACCAACAGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 934
Db 481 GCACCATATCTGACCAACAGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 935 AAACCTGCAAGTTTGTGCTGCGCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
Db 541 AAACCTGCAAGTTTGTGCTGCGCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

FILED DATE: US 07/743369
APPLICATION NUMBER: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..2331
US-08-471-570-7

Query Match 74.7%; Score 2320; DB 2; Length 2676;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2323; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 395 GAGCCGGGAGTTGGTACCGTAAACCATGTCAGCTGGGGTGTTCATCTGCTGTCGTG 454
DB 1 GAGCCGGGAGTTGGTACCGTAAACCATGTCAGCTGGGGTGTTCATCTGCTGTCGTG 60
QY 455 GTTACCATGGCAACCTTTGTCCTGCGCCGCCCTCTTCACTTAACTTAACTTAACTTAA 514
DB 61 GTTACCATGGCAACCTTTGTCCTGCGCCGCCCTCTTCACTTAACTTAACTTAACTTAA 120
QY 515 TTAGAGCCGAGAAAGCCACCAACCAATCAATCTCTCAACAGAGTGAAGTGAAGTGA 574
DB 121 TTAGAGCCGAGAAAGCCACCAACCAATCAATCTCTCAACAGAGTGAAGTGAAGTGA 180
QY 575 GCGCCAGGGAGTCTGCTAGAGTGTGCGCTGCTGTGAAAGAGTCCGCCGTGATCACTTGG 634
DB 181 GCGCCAGGGAGTCTGCTAGAGTGTGCGCTGCTGTGAAAGAGTCCGCCGTGATCACTTGG 240
QY 635 ACTAAGATGGGTGCACTTTGGGCGCCCAATAGACAGTCTTATTTGGGAGTACTTGG 694
DB 241 ACTAAGATGGGTGCACTTTGGGCGCCCAATAGACAGTCTTATTTGGGAGTACTTGG 300
QY 695 CAGATTAAGGGGCGCACCTAGAGACTCGGCGCTCTATGCTGTACTGCGCAGTGAAGT 754
DB 301 CAGATTAAGGGGCGCACCTAGAGACTCGGCGCTCTATGCTGTACTGCGCAGTGAAGT 360
QY 755 GTAGACAGTGAACCTTGTACTTCACTGATATGTCAAGATGCACTGATCCGAGAT 814
DB 361 GTAGACAGTGAACCTTGTACTTCACTGATATGTCAAGATGCACTGATCCGAGAT 420
QY 815 GATGAGATGACACCGATGCTGGGAAAGATTTTGTCACTGAGAAACAGTAAACAAGAGA 874
DB 421 GATGAGATGACACCGATGCTGGGAAAGATTTTGTCACTGAGAAACAGTAAACAAGAGA 480
QY 875 GCAACCTACTGAGCAACAGAAAGATGAAAGAGGCTCCATGCTGTGCGTGGCGGC 934
DB 481 GCAACCTACTGAGCAACAGAAAGATGAAAGAGGCTCCATGCTGTGCGTGGCGGC 540
QY 935 AACACTGTCAAGTTTCTGCTCCAGCCGCGGGGAAACCAATGCAACCATGCGTGGCTG 994
DB 541 AACACTGTCAAGTTTCTGCTCCAGCCGCGGGGAAACCAATGCAACCATGCGTGGCTG 600
QY 995 AAAAAACGGAAGAGTTTAAAGCAGAGACATGCACTTGAAGCTTAAAGGTAACGAAACAG 1054
DB 601 AAAAAACGGAAGAGTTTAAAGCAGAGACATGCACTTGAAGCTTAAAGGTAACGAAACAG 660
QY 1055 CACTGAGCTCATTTATGAAAGTGTGCTCATCTGACAAGGGAATTTACTCTGTGA 1114

DB 661 CACTGAGCTCATTTATGAAAGTGTGCTCATCTGACAAGGAAATTTACTCTGTG 720
QY 1115 GTGGAATGATTAAGGGTCCATCATCAACAGTACCACTGGATTTGAGCGATG 1174
DB 721 GTGGAATGATTAAGGGTCCATCATCAACAGTACCACTGGATTTGAGCGATG 780
QY 1175 CCTCAACCGGCCATCTCCAGCCGAGCTGCGGCAATGCTCCACATGCTGAGAGA 1234
DB 781 CCTCAACCGGCCATCTCCAGCCGAGCTGCGGCAATGCTCCACATGCTGAGAGA 840
QY 1235 GACGTAGATTTGTCTGCAAGTTTACAGTATGCCAGCCCACTCAGTGAATCAAG 1294
DB 841 GACGTAGATTTGTCTGCAAGTTTACAGTATGCCAGCCCACTCAGTGAATCAAG 900
QY 1295 CACGTGGAATAAGGCAATTAACGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 1354
DB 901 CACGTGGAATAAGGCAATTAACGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 1355 AAGCACTCGGGATTAATAGTTCATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1414
DB 961 AAGCACTCGGGATTAATAGTTCATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1415 GCGGATGCTGGGAAAT 1474
DB 1021 GCGGATGCTGGGAAAT 1080
QY 1475 GCTGCTCATCTGCTCTGCAAAACAGAGGCGCTGGAAGAAAGGATTAACGCT 1534
DB 1081 GCTGCTCATCTGCTCTGCAAAACAGAGGCGCTGGAAGAAAGGATTAACGCT 1140
QY 1535 TCCCGAGCTACCTGAGATATACATTTACTGATAGGGTCTTCTTAAATGCTGTATG 1594
DB 1141 TCCCGAGCTACCTGAGATATACATTTACTGATAGGGTCTTCTTAAATGCTGTATG 1200
QY 1595 GTGTTAAGCATCTCTGTGCGGAATGAAGAACAGACCAAGACCAAGCTTCAAGAC 1654
DB 1201 GTGTTAAGCATCTCTGTGCGGAATGAAGAACAGACCAAGACCAAGCTTCAAGAC 1260
QY 1655 CAGCGGCTGTGCAAGAGTGAACCAAGCTATCCCTGCGGAGACAGGTAACAGTTTG 1714
DB 1261 CAGCGGCTGTGCAAGAGTGAACCAAGCTATCCCTGCGGAGACAGGTAACAGTTTG 1320
QY 1715 GCTGATCAGCTCTCCATGAACTCAACACCCGCTGTGAGATTAACAACGCTT 1774
DB 1321 GCTGATCAGCTCTCCATGAACTCAACACCCGCTGTGAGATTAACAACGCTT 1380
QY 1775 TCTTCAACGAGACACCCCATGCTGCGAGGGTCTCCGATGTAACCTTCAAGAGAC 1834
DB 1381 TCTTCAACGAGACACCCCATGCTGCGAGGGTCTCCGATGTAACCTTCAAGAGAC 1440
QY 1835 CCAAAATGGAAGTTTCAAGAGATTAAGTGAACCTGAGGCAAGCCCTGGGAGAGGTTG 1894
DB 1441 CCAAAATGGAAGTTTCAAGAGATTAAGTGAACCTGAGGCAAGCCCTGGGAGAGGTTG 1500
QY 1895 TTTGGGCAAGTGTCACTGCGAAGAGTGGAAATTGCAAAAGCAAGCCCAAGAGGG 1954
DB 1501 TTTGGGCAAGTGTCACTGCGAAGAGTGGAAATTGCAAAAGCAAGCCCAAGAGGG 1560
QY 1955 GTCAACGTGGCGGTGAAGTGTGAAGATGAATGCCAGAGAAAGCTTTCTGATCTG 2014
DB 1561 GTCAACGTGGCGGTGAAGTGTGAAGATGAATGCCAGAGAAAGCTTTCTGATCTG 1620
QY 2015 GTGTCAAGATGGAATGAATGAAGATTTGGGAAACAAGAAATATCAATCTTCTT 2074
DB 1621 GTGTCAAGATGGAATGAATGAAGATTTGGGAAACAAGAAATATCAATCTTCTT 1680
QY 2075 GGAGCTTGCAACAGATGGGCTCTCTATGCTATGATGATGATGATGATGATGATGATG 2134
DB 1681 GGAGCTTGCAACAGATGGGCTCTCTATGCTATGATGATGATGATGATGATGATGATG 1740
QY 2135 CTCGAGAAATACCTCGAGCCCGGAGGCAACCCGAGATGAGTCTCTATGATCACTTAA 2194
DB 1741 CTCGAGAAATACCTCGAGCCCGGAGGCAACCCGAGATGAGTCTCTATGATCACTTAA 1800

QY 2195 CGTGTCTGAGAGCAGATGACCTTCAAGACCTTGTGTGATGCACTTACCACTGAGCC 2254
| | | | |
Db 1801 CGTGTCTGAGAGCAGATGACCTTCAAGACCTTGTGTGATGCACTTACCACTGAGCC 1860
| | | | |
QY 2255 AGACGGATGAGTACTTGGCTTCCAAAATGATTTATTCAGATTTGACGGCAAGAT 2314
| | | | |
Db 1861 AGACGGATGAGTACTTGGCTTCCAAAATGATTTATTCAGATTTGACGGCAAGAT 1920
| | | | |
QY 2315 GTTTGTGTAACAGAAAACAATGTGATGAAAAATAGACACTTGTGACTGCGCAGATATC 2374
| | | | |
Db 1921 GTTTGTGTAACAGAAAACAATGTGATGAAAAATAGACACTTGTGACTGCGCAGATATC 1980
| | | | |
QY 2375 AACATATATGACTTATTAACAAAAAGCACCAATGCGCGCTTCAATGCAATGTGATGCT 2434
| | | | |
Db 1981 AACATATATGACTTATTAACAAAAAGCACCAATGCGCGCTTCAATGCAATGTGATGCT 2040
| | | | |
QY 2435 CCAAGAACCTTGTGTGATGATATACATCTCATCAGATGATGTCTGTGCTTGGGGTG 2494
| | | | |
Db 2041 CCAAGAACCTTGTGTGATGATATACATCTCATCAGATGATGTCTGTGCTTGGGGTG 2100
| | | | |
QY 2495 TTAATGTGAGATCTTCACTTTAAGGGGCTGCGCTTACCCAGGATTCGCGTGAAGAA 2554
| | | | |
Db 2101 TTAATGTGAGATCTTCACTTTAAGGGGCTGCGCTTACCCAGGATTCGCGTGAAGAA 2160
| | | | |
QY 2555 CTTTTTAAGCTGCTGAAGAGACACAGATGATTAAGCCAGCACTGACCAACAA 2614
| | | | |
Db 2161 CTTTTTAAGCTGCTGAAGAGACACAGATGATTAAGCCAGCACTGACCAACAA 2220
| | | | |
QY 2615 CTGTACATGATGATGAGGACCTGTTGGCATGAGGCGCTCCAGAGACCAACGTTCAAG 2674
| | | | |
Db 2221 CTGTACATGATGATGAGGACCTGTTGGCATGAGGCGCTCCAGAGACCAACGTTCAAG 2280
| | | | |
QY 2675 CAGTGTGAGAGACTTGTGATGAAATCTCACTCTCAACCAACGATGAG 2722
| | | | |
Db 2281 CAGTGTGAGAGACTTGTGATGAAATCTCACTCTCAACCAACGATGAG 2328
| | | | |

RESULT 12
US-09-954-556-10
; Sequence 10, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freiler
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954, 556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 10
; LENGTH: 3306
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (607)...(3072)
US-09-954-556-10

Query Match 70.9%; Score 2201; DB 3; Length 3306;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2613; Conservative 0; Mismatches 420; Indels 90; Gaps 7;

QY 1 CCGCGAGGAAAGTTGTGAGGAGCAACGAAAGCTGAGTCTTTCTCTCGTTGCC 60
| | | | |
Db 142 CTGCGAGCAAGTTGTGAGGAGCAACGAAAGCTGAGTCTTTCTCTCGTTGCC 201
| | | | |
QY 61 CAATTCGAGGAGCGCGCGCGCTCATGCGCTCTCCGACGCTGAGGATACGGGTGA 120
| | | | |
Db 202 AATTCGAGGAGCGCGCGCTCATGCGCTCTCCGACGCTGAGGATACGGGTGA 258
| | | | |
QY 121 AGCCGAGGAGGCTTGGCGCGCGCAAGACCAAGACCACTCTTGTGCTTGGATGCG 180
| | | | |

Db 259 AGCTTCGAACTTGGCGCGCGCTGCTACCAAGAAATCGTTCTTTTGAAGTTTCC 318
| | | | |
QY 181 TCCCGCAACCCCGGGCTCGTGGCTTTCTCCATCCCAACCGCGGCGC-CCGGAGCA 239
| | | | |
Db 319 T-----CCGAGATCATCGCTGCTCCATCCCATCACTCTGGGCTCCGCGCAG 368
| | | | |
QY 240 CACAGTTCGCGAGAGAGCTTGGCCATTCAAGTGCATGACAGAGAGCGAGCGC----- 293
| | | | |
Db 369 CACGAGGAGAGAGAGCGCTGCATTCAAGTGCATGACAGAGAGAGAGAGAGCA 428
| | | | |
QY 294 -----CTCGGTT 300
| | | | |
Db 429 GTGGAGAGAGAACAGCATTAACACAGCAACAGAGACAGCGGCTCAGAGCTTGGCT 488
| | | | |
QY 301 CCTGAGCCACCGAGCTGAAGAGCATTCGCGTATGCTCAATCCCGTGAAGAGATGCA 360
| | | | |
Db 489 CCGTGAAGCTGCTGAGGCTGAAGGCAATGCAAGTGAAGCCATGCTCAGAGAGATGCA 548
| | | | |
QY 361 GATGGATTTAAGTTCACATGAGATATGAAAGAGACCGGGGATTTGGTACCGTACAT 420
| | | | |
Db 549 GATGGATTTAAGTTCACATGAGATATGAAAGAGACCGGGGATTTGGTACCGTACAT 608
| | | | |
QY 421 GATGAGCTGGGATGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
| | | | |
Db 609 GATGAGCTGGGATGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
| | | | |
QY 481 CCGGCTCTCTTCAAGTTTGAAGATACCAATTGAGCCAGAGAGCCACCAACCA 540
| | | | |
Db 669 CCGGCTCTCTTCAAGTTTGAAGATACCAATTGAGCCAGAGAGCCACCAACCA 728
| | | | |
QY 541 ATACCAATCTCTCAACCAAGATGATAGTGGCTGGCCAGGGAGTGGCTAGAGTGG 600
| | | | |
Db 729 ATACCAATCTCTCAACCAAGATGATAGTGGCTGGCCAGGGAGTGGCTAGAGTGG 788
| | | | |
QY 601 CTGCTGTTGAAGATGCGCGCTGATCATGTTGACCTAAGATGAGGCTGCACTTGGGCGC 660
| | | | |
Db 789 GTGCTGTTGAAGATGCGCGCTGATCATGTTGACCTAAGATGAGGCTGCACTTGGGCGC 848
| | | | |
QY 661 CAACATATGAGCAGTCTTATTTGGGAGTACTTGCATTAAGGGCGCCACACTAGAGA 720
| | | | |
Db 849 CAACATATGAGCAGTCTTATTTGGGAGTACTTGCATTAAGGGCGCCACACTAGAGA 908
| | | | |
QY 721 CTGCGGCTCTATGCTTGTATCTGCCAGTGAAGCTGTGAAGTGAATCTTGGTACTCAT 780
| | | | |
Db 909 CTGCGGCTCTATGCTTGTATCTGCCAGTGAAGCTGTGAAGTGAATCTTGGTACTCAT 968
| | | | |
QY 761 GGTGAATGTCAAGATGCTATCTCATCCGAGATGATGAGATGACACGATGTGCGGA 840
| | | | |
Db 969 GGTGAATGTCAAGATGCTATCTCATCCGAGATGATGAGATGACACGATGTGCGGA 1028
| | | | |
QY 841 AGATTTGTCAAGTGAAGACAGTAAACACAGAGACCACTATCTGAGCAACAGAAAA 900
| | | | |
Db 1029 AGATTTGTCAAGTGAAGACAGTAAACACAGAGACCACTATCTGAGCAACAGAAAA 1088
| | | | |
QY 901 GATGAAAAAGGGCTTCATGCTGTGCCCTGCGGCAACCTGCAAGTTCCGTGCCAGC 960
| | | | |
Db 1089 GATGAAAAAGGGCTTCATGCTGTGCCCTGCGGCAACCTGCAAGTTCCGTGCCAGC 1148
| | | | |
QY 961 CCGGGGAAACCAATGCAACCAATGCGGTGCTGAAAAACGGAGAGATTAAAGCAGA 1020
| | | | |
Db 1149 TGGGGGAAATCCAGCTCAACATGAGGTGTGTAATAACGGAGAGATTAAAGCAGA 1208
| | | | |
QY 1209 GCATGCAATGGAAGCTATTAAGTGAAGAACAGACCTGAGACCTTATTAAGAAAGGT 1268
| | | | |
Db 1081 GGTCCCATCTGACAAAGGAATTAACCTGTGTGAGTGAAGTGAATGAAATCGGTCATCA 1140
| | | | |
QY 1269 GGTCCCATCTGACAAAGGAATTAACCTGTGTGAGTGAAGTGAATGAAATCGGTCATCA 1328
| | | | |
Db 1141 TCACAGTACCACTGATGTTGTGAGAGATGCTGCTGACCGGCTCTCAAGCCGG 1200
| | | | |

Db 1329 CCAACCTAACCACTGGATGCTGTTGAAGTTCAACCAACCGTCCACTCTCAAGCTGG 1388
 QY 1201 ACTGCGGAAATGCTCTCAAGTGTGGAGAGAGAGTAAAGTTTGTCTGAAGTTTA 1260
 Db 1389 ACTGCTGGAATGCTCCACGGTGTGGAGAGAGTGAAGTTTGTCTGAAGTTTA 1448
 QY 1261 CAGTATGCGGAGCCGACATCAAGTGTCAAGCAAGTGAAGAAAGAGTAAATA 1320
 Db 1449 CAGCAATGCGGAGCCGACATCAAGTGTCAAGCAAGTGAAGAAAGAGTAAATA 1508
 QY 1321 CCGGCGCGGAGCTGCTCTCAAGTGTCTCAAGCAAGTGAAGAAAGAGTAAATA 1380
 Db 1509 CCGGCTGGAATGCTCTCAAGTGTCTCAAGCAAGTGAAGAAAGAGTAAATA 1568
 QY 1381 TCGAGAGTGTGCTCTGT-----TCAATGTACCGAGCGGAGTCTGGGAAATAT 1434
 Db 1569 CAAAGAGATTTGAGTTCTCTAATTTGGAATGTAACTTTTGAAGATGCTGGGAAATAT 1628
 QY 1435 ATGTAAAGTCTCCATTAATATAGGAGAGCCAAACAGTGTGCTGCTCACTGTCTGC 1494
 Db 1629 GTGCTTGGGAGTAAATCTATCGGAGATCTTTCACTGTGATGTGAAGTGTCTGC 1688
 QY 1495 AAAACAGCAAGCGCTGGAAGAGAAAGAGATTAAGCTTCCCAAGTCTGAGAT 1554
 Db 1689 -----AGCGCTGTGAGAGAGAGATCAAGCTTCCCAAGTCTGAGAT 1739
 QY 1555 AGCCATTTAATCTGATAGGGGCTCTTAAATCGCTGTATGTGTAAAGTCAATCTGTG 1614
 Db 1740 AACTATTTACTGATAGGGGCTCTTAAATCGCTGTATGTGTAAAGTCAATCTGTG 1799
 QY 1615 CCGAATGAAGAACAGCAACCAAGAGCAAGTTCAGACAGCGCGGTGTGCAAGAGT 1674
 Db 1800 CCGAATGAAGAACAGCAACCAAGAGCAAGTTCAGACAGCGGTGTGCAAGAGT 1859
 QY 1675 GACCAAAAGTATCCCTGCTGAGAGAGAGTAAAGAGTTCAGTCCAGTCTCTCAT 1734
 Db 1860 GACCAAGCGCATTCCTCTGAGAGAGAGTAAAGAGTTCAGTCCAGTCTCTCAT 1919
 QY 1735 GAACTTCACACCCGCTGTGTGAGATTAACAAGCTCTTCAACGCGAGACACCC 1794
 Db 1920 GAACTTCACACCCGCTGTGTGAGATTAACAAGCTCTTCAACGCGAGACACCC 1979
 QY 1795 CATGCTGAGAGGGGTCTCCGAGTAAAGTTCAGAGAGACCAAAATGGAAGTTCCAG 1854
 Db 1980 GATGCTAGAGAGGGGTCTCCGAGTAAAGTTCAGAGAGATCCAAATGGAAGTTCCAG 2039
 QY 1855 AGTAAAGTGAAGCTGAGAGAGCCCTGGAGAGAGTTCCTTGGCAAGTGGTCAATGC 1914
 Db 2040 AGTAAAGTGAAGCTGAGAGAGCCCTGGAGAGAGTTCCTTGGCAAGTGGTCAATGC 2099
 QY 1915 GGAAGCAATGGGAATTTGACAAAGACAAAGCCCAAGAGCGGTCAAGTGGCGGTGAAGT 1974
 Db 2100 TGAAGCAATGGGAATTTGACAAAGACAAAGCCCAAGAGCGGTCAAGTGGCGGTGAAGT 2159
 QY 1975 GTTGAAGAGTGAATGCAAGAGAAAGACCTTCTGATCTGTGTCAAGATGAAGTGAAT 2034
 Db 2160 GTTGAAGAGTGAATGCAAGAGAAAGACCTTCTGATCTGTGTCAAGATGAAGTGAAT 2219
 QY 2035 GAAGATGATTTGGAAACAAAGAAATATCAATATCTTCTGAGCTGCAACAGAGATG 2094
 Db 2220 GAAGATGATTTGGAAACAAAGAAATATCAATATCTTCTGAGCTGCAACAGAGATG 2279
 QY 2095 GCCTCTATATGTCATATGATGATGCTCTTAAAGGCAACTTCGAAGAAATCTCGAGC 2154
 Db 2280 AACTCTCTATATGTCATATGATGATGCTCTTAAAGGCAACTTCGAAGAAATCTCGAGC 2339
 QY 2155 CCGAGAGCCACCGGAGATGAAGTCTCTATGAATTAACCGTGTCTCGAAGAGAGAT 2214
 Db 2340 CCGAGAGCCACCGGAGATGAAGTCTCTATGAATTAACCGTGTCTCGAAGAGAGAT 2399
 QY 2215 GACCTTCAAGAGACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2274
 Db 2400 GACCTTCAAGAGACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2459

QY 2275 TTTCCAAAATGATATTCATGAGATTTAGACCCAGAAATGTTTGGTAAAGAAAACA 2334
 Db 2460 TTTCCAAAATGATATTCATGAGATTTAGACCCAGAAATGTTTGGTAAAGAAAACA 2519
 QY 2335 TGTGATGAAGATAGAGACTTTGGACTGCGAGATATCAACATATAGCTATTACA 2394
 Db 2520 TGTGATGAAGATAGAGACTTTGGACTGCGAGATATCAACATATAGCTATTACA 2579
 QY 2395 AAAGACCAATGAGGCGCTTCCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2454
 Db 2580 AAAGACCAATGAGGCGCTTCCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2639
 QY 2465 AGTATGACCTGATGAGAT 2514
 Db 2640 AGTATGACCTGATGAGAT 2699
 QY 2515 TTTAGGGGCTGCGCTTCCAGAGATTCGGTGAAGAACTTTTAAAGCTGCAAGGA 2574
 Db 2700 TTTAGGGGCTGCGCTTCCAGAGATTCGGTGAAGAACTTTTAAAGCTGCAAGGA 2759
 QY 2575 AGGACACAGATGATTAAGCCAGCTGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2634
 Db 2760 GGGACACAGATGATTAAGCCAGCTGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2819
 QY 2635 CTGTTGGAT 2694
 Db 2820 CTGTTGGAT 2879
 QY 2695 TCGAATTCATCTCTCAACCAATGAGAAATCTTGAAGCTCAAGCTCTGCAACA 2754
 Db 2880 TCGAATTCATCTCTCAACCAATGAGAAATCTTGAAGCTCAAGCTCTGCAACA 2939
 QY 2755 GTATTCAGCTGAT 2814
 Db 2940 GTATTCAGCTGAT 2999
 QY 2815 TTTCTCAGACCCAGCTTTCAGAAAGCAAGCTTCTCAAGTATCAACATTAAGGAG 2874
 Db 3000 TTTCTCAGACCCAGCTTTCAGAAAGCAAGCTTCTCAAGTATCAACATTAAGGAG 3059
 QY 2875 TGTAAACATGAT 2934
 Db 3060 TGTAAACATGAT 3119
 QY 2935 CTACCTAGAGAGGAGACCATGCTCCAGAGCTTG--TTGTCTCACTTGTATATATG 2992
 Db 3120 CTACCTAGAGAGGAGACCATGCTCCAGAGCTTG--TTGTCTCACTTGTATATATG 3179
 QY 2993 GATCAGAGAGTAAATTAATGGAAGATATGAT 3052
 Db 3180 GATCAGAGAGTAAATTAATGGAAGATATGAT 3239
 QY 3053 AAA 3055
 Db 3240 GAA 3242
 QY 3240 GAA 3242

RESULT 13
 US-09-954-556-23
 ; Sequence 23, Application US/09954556
 ; Patent No. 690053
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Susan M. Freiler
 ; APPLICANT: Scott Cooper
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
 ; FILE REFERENCE: RTS-0250
 ; CURRENT APPLICATION NUMBER: US/09/954,556
 ; CURRENT FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 108
 ; SEQ ID NO 23
 ; LENGTH: 3025

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (595)...(2643)
US-09-954-556-23

Query Match      66.7%; Score 2072.2; DB 3; Length 3025;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 13; Indels 280; Gaps 7;

Oy 1 CCCCGAGCAAAAGTTGGTGAAGGCAAG-CAGGCTGAGTCTTTCTTCTCTCTCC 59
Db 170 CTCGGAGCAAAAGTTGGTGAAGGCAAGCCCAAGCTTGAATCTTTCTCTCTCTCC 229
Oy 60 CCAATTCGAGGGGCAAGCCCGGGGGGCTGATG---GCGCTCTCGAGCCTTGGGTAAGC 116
Db 230 CCAATTCGAGGGGCAAGCCCGGGGGGCTGATG---GCGCTCTCGAGCCTTGGGTAAGC 289
Oy 117 GTGAGCCCGGAGGCTTGGCGCCGCGAGAGACCCAGAGACCACTTTCTGCGTTGAG 176
Db 290 GTGAGCCCGGAGGCTTGGCGCCGCGAGAGACCCAGAGACCACTTTCTGCGTTGAG 349
Oy 177 TTGCTCCCGCAACCCCGGGGCTGTCGCTTTCTCAATCCCAACCGCGGGGCG--CGGG 235
Db 350 TTGCTCCCGCAACCCCGGGGCTGTCGCTTTCTCAATCCCAACCGGGGCGGGGG 409
Oy 226 ACAACAAGGTGCGGAGAGGCTTGGCCATTCAAGTGAAGTGAAGAGAGC-GCAGCGCC 294
Db 410 ACAACAAGGTGCGGAGAGGCTTGGCCATTCAAGTGAAGTGAAGAGAGAGAGAGAG 469
Oy 295 TCGGTTCTGAGACCCCAACGCA-GCTGAAGGCAATTCGCGGTAGTCAATGCGGTAGAGAA 353
Db 470 TCGGTTCTGAGACCCCAACGCAAGGCTGAAGGCAATTCGCGGTAGTCAATGAGAGAA 529
Oy 354 GTGTGAGATGGGATTAAGTTCACATGAGATATGAGAAAGAGACCGGGGATTTGTAACG 413
Db 530 GTGTGAGATGGGATTAAGTTCACATGAGATATGAGAAAGAGACCGGGGATTTGTAACG 589
Oy 414 TAAACATGGTCAAGTGGGGTCTGTTTCACTGCTGGTCTGGTCAACATGCAACCTTGT 473
Db 590 TAAACATGGTCAAGTGGGGTCTGTTTCACTGCTGGTCTGGTCAACATGCAACCTTGT 649
Oy 474 CCTGGCCCGGCGCTCTTCAAGTTTATGTTAGAGATACCAATTAAAGCCAAAGCCAC 533
Db 650 CCTGGCCCGGCGCTCTTCAAGTTTATGTTAGAGATACCAATTAAAGCCACAG----- 701
Oy 534 CAACCAATATCAAAATCTCTCAACCAAGAGTGAAGTGGCTGGCCAGGGAGTGGCTAG 593
Db 702 ----- 701
Oy 594 AGGTGGCTGCTGTTGAAAGATGCGCGGTGATCAGTTGGAATAAGATGGGGTGCAT 653
Db 702 ----- 701
Oy 654 TGGGGCCCAACATAGACAGTGTATTGGGAGTACTTGACATTAAGGGCGCCACAC 713
Db 702 ----- 701
Oy 714 CTAGAGACTCCGGCTCTATGCTTGTACTGCCAGTAGAGCTGTAGACATGAAACTTTGCT 773
Db 702 ----- 701
Oy 774 ACTTCAATGTAATGTCAAGATGCAATCTATCCGAGATGATGAGATGACACCGATG 833
Db 702 -----AGATGCAATCTCAATCCGAGATGATGAGATGACACCGATG 742
Oy 834 GTGCGGAAAGATTTTGTCAGTAGAACAGTAAACAAGAGAGACCAATCTGACCAACA 893
Db 743 GTGCGGAAAGATTTTGTCAGTAGAACAGTAAACAAGAGAGACCAATCTGACCAACA 802
Oy 894 CAGAAAAGATGAAAGAGGGCTCAATGCTGTGCTGGCCCAACTGTCAAGTTTCTGCT 953
Db 894 CAGAAAAGATGAAAGAGGGCTCAATGCTGTGCTGGCCCAACTGTCAAGTTTCTGCT 953
```

```
Db 803 CAGAAAAGATGAAAGAGGGCTCAATGCTGTGCTGGCCCAACTGTCAAGTTTCTGCT 862
Oy 954 GCCCAGCCGGGGGAAACCAATGCCAACCAATGGGCTGGCTGAAAGAGGAAAGATTTA 1013
Db 863 GCCCAGCCGGGGGAAACCAATGCCAACCAATGGGCTGGCTGAAAGAGGAAAGATTTA 922
Oy 1014 AGCAGAGACATTCGATTTGGAGGGCTACAAAGGTAAGAAACAGACCTGAGCCTCATTAAG 1073
Db 923 AGCAGAGACATTCGATTTGGAGGGCTACAAAGGTAAGAAACAGACCTGAGCCTCATTAAG 982
Oy 1074 AAGTGTGTCTCCATCTGACAAAGGAAATTATACCTGTGTATGAGATGAAATACGGGT 1133
Db 983 AAGTGTGTCTCCATCTGACAAAGGAAATTATACCTGTGTGTGAGAAATACCGGT 1042
Oy 1134 CCATCAATCAACGTAACCTGGAATGTTGTGAGGCAATGGCTTCAACCGGCCATCTCTCC 1193
Db 1043 CCATCAATCAACGTAACCTGGAATGTTGTGAGGCAATGGCTTCAACCGGCCATCTCTCC 1102
Oy 1194 AAGCGGAGCTGGCCAAATGCTTCCACAGTGTGAGAGAGAGCTAGAGTTTGTCTGCA 1253
Db 1103 AAGCGGAGCTGGCCAAATGCTTCCACAGTGTGAGAGAGAGCTAGAGTTTGTCTGCA 1162
Oy 1254 AGTTTACAGTGAATGCCAGGCCCAATCAAGTGAATCAAGCAGTGAAGAAAGAGCGCA 1313
Db 1163 AGTTTACAGTGAATGCCAGGCCCAATCAAGTGAATCAAGCAGTGAAGAAAGAGCGCA 1222
Oy 1314 GTAATATCGGGCCCGAGCGGCTGCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 1373
Db 1223 GTAATATCGGGCCCGAGCGGCTGCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 1282
Oy 1374 GTTCCAAATGAGAGATGCTGCTCTGTTCAATGTAACGAGGCGGATGCTGGGGAATATA 1433
Db 1283 GTTCCAAATGAGAGATGCTGCTCTGTTCAATGTAACGAGGCGGATGCTGGGGAATATA 1342
Oy 1434 TATGTAAGTCTCAATTAATATAGGCAAGGCCAAACAGTCTGCTCACTGTCTCTGC 1493
Db 1343 TATGTAAGTCTCAATTAATATAGGCAAGGCCAAACAGTCTGCTCACTGTCTCTGC 1402
Oy 1494 CAATAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCGAGACTACCTGAGAG 1553
Db 1403 CAATAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCGAGACTACCTGAGAG 1462
Oy 1554 TAGCCATTATCGATAGGGGCTCTTCAATGCTGCTGATGATGATGATCACTGATCTGT 1613
Db 1463 TAGCCATTATCGATAGGGGCTCTTCAATGCTGCTGATGATGATGATCACTGATCTGT 1522
Oy 1614 GCCGATGAGAGACAGACCAAGAGCCAGACTTCAAGAGCCAGCGGCTGTGCAAAAGC 1673
Db 1523 GCCGATGAGAGACAGACCAAGAGCCAGACTTCAAGAGCCAGCGGCTGTGCAAAAGC 1582
Oy 1674 TGAACCAACGTAATCCCCCTGGGAGAGACG-----GTTTGGGCTGAGTCCAGCTCTTCA 1733
Db 1583 TGAACCAACGTAATCCCCCTGGGAGAGACG-----GTTTGGGCTGAGTCCAGCTCTTCA 1636
Oy 1734 TGAACCTCCAAACCCCGCTGGTGAAGATTAACAAGCCTCTTCAACGCGCAGACACC 1793
Db 1637 TGAACCTCCAAACCCCGCTGGTGAAGATTAACAAGCCTCTTCAACGCGCAGACACC 1696
Oy 1794 CCATGCTGGCAGGGGTCTCCGAGTATGAATTTCCAGAGAGACCAAAATGGGAGTTTCCAA 1853
Db 1697 CCATGCTGGCAGGGGTCTCCGAGTATGAATTTCCAGAGAGACCAAAATGGGAGTTTCCAA 1756
Oy 1854 GAGATTAAGCTGACATGCGGCAAGCCCGTGGGAGAAAGTTGCTTGGGGAAGTGGTCATGG 1913
Db 1757 GAGATTAAGCTGACATGCGGCAAGCCCGTGGGAGAAAGTTGCTTGGGGAAGTGGTCATGG 1816
Oy 1914 CGGAAAGTGGGAAATTGACAAAGACCAAGCCCAAGAGGCGTCAACGTTGCGCTGAAGA 1973
Db 1817 CGGAAAGTGGGAAATTGACAAAGACCAAGCCCAAGAGGCGTCAACGTTGCGCTGAAGA 1876
Oy 1974 TGTGAAAGATGATCCACAGAGAAAGACTTTCTGATCTGTGTCAAGATGAGATGA 2033
Db 1877 TGTGAAAGATGATCCACAGAGAAAGACTTTCTGATCTGTGTCAAGATGAGATGA 1936
```

2034 TGAAGATGATGGGAAACACAGATATCTAATCTCTGGAGGCTGCACAGAGATG 2093
DB 1937 TGAAGATGATGGGAAACACAGATATCTAATCTCTGGAGGCTGCACAGAGATG 1996
QY 2094 GGCCTCTATGTCATAGTGAATGCTCTTAAGGCAACTCCAGAAATACCTCCGAG 2153
DB 1997 GGCCTCTATGTCATAGTGAATGCTCTTAAGGCAACTCCAGAAATACCTCCGAG 2056
QY 2154 CCGGAGGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTCCAGAGCAGA 2213
DB 2057 CCGGAGGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTCCAGAGCAGA 2116
QY 2214 TGAACCTTCAAGAGCTTGCTGTCTATGACCTTACAGAGCTGCGACAGAGAGTACTCTG 2273
DB 2117 TGAACCTTCAAGAGCTTGCTGTCTATGACCTTACAGAGCTGCGACAGAGAGTACTCTG 2176
QY 2274 CTTCCCAAAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGTGTAAAGAAAAC 2333
DB 2177 CTTCCCAAAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGTGTAAAGAAAAC 2236
QY 2334 ATGTGATGAAAATAGACACTTTGGAAGCTGCGCAGAGATTAACAATATATGACTATTACA 2393
DB 2237 ATGTGATGAAAATAGACACTTTGGAAGCTGCGCAGAGATTAACAATATATGACTATTACA 2296
QY 2394 AAAAGACCAACATGCGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTGTGATA 2453
DB 2297 AAAAGACCAACATGCGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTGTGATA 2356
QY 2454 GAGTATTAACCTCATGAGATGATGTCTGCTTCCGGGGGTATTAATGTGGAGATCTTCA 2513
DB 2357 GAGTATTAACCTCATGAGATGATGTCTGCTTCCGGGGGTATTAATGTGGAGATCTTCA 2416
QY 2514 CTTTAAAGGGGCTGCGCTTACCCAGAGATTTCCGCTGAGAGAACTTTTAACTGCTGAGAG 2573
DB 2417 CTTTAAAGGGGCTGCGCTTACCCAGAGATTTCCGCTGAGAGAACTTTTAACTGCTGAGAG 2476
QY 2574 AAGGACACAGATGATGATAGCCCAAGCTGCAACCAAGCACTGTATCATATATATATAGAG 2633
DB 2477 AAGGACACAGATGATGATAGCCCAAGCTGCAACCAAGCACTGTATCATATATATAGAG 2536
QY 2634 ACTGTGGGATGAGAGGCTTCCCAAGAGCAAGCTTCAAGAGCTGTGTAGAGAGCTTGG 2693
DB 2537 ACTGTGGGATGAGAGGCTTCCCAAGAGCAAGCTTCAAGAGCTGTGTAGAGAGCTTGG 2596
QY 2694 ATCGAATTTCTCACTCTCAACAC 2716
DB 2597 ATCGAATTTCCCCCAACCTTCC 2619

RESULT 14
US-08-471-570-5
; Sequence 5, Application US/08471570
; Patent No. 5750371
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Koichi
; APPLICANT: SENOO, Masaharu
; APPLICANT: WATANABE, Tatsuya
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
; ADDRESSER: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:
APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STR UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1954 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 25..1953
; US-08-471-570-5

Query Match 62.7%; Score 1946; DB 2; Length 1954;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1949; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 395 GGAACCGGGGATGTTGATCCGTAAACATGTCAGCTGGGGTCTTTCATCTGCTGCTGCTG 454
DB 1 GGAACCGGGGATGTTGATCCGTAAACATGTCAGCTGGGGTCTTTCATCTGCTGCTGCTG 60
QY 455 GTACACATGAGCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 514
DB 61 GTACACATGAGCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 515 TTAGAGCCAGAGAGCCCAACCAACCAATCTCTCAACCAAGTGTATCGTGGCT 574
DB 121 TTAGAGCCAGAGAGCCCAACCAACCAATCTCTCAACCAAGTGTATCGTGGCT 180
QY 575 GCGCCAGGGAGCTGCTAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
DB 181 GCGCCAGGGAGCTGCTAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 635 ACTAAGGATGGGGTGCATTTGGGGGCCCAACATATAGGACAGTGTATTTGGGGAGTACTTG 694
DB 241 ACTAAGGATGGGGTGCATTTGGGGGCCCAACATATAGGACAGTGTATTTGGGGAGTACTTG 300
QY 695 CAGATTAAGGGGCGCACACCTAGAGACTCCGGCTCTATGCTTGTACTGCCAGTAGACT 754
DB 301 CAGATTAAGGGGCGCACACCTAGAGACTCCGGCTCTATGCTTGTACTGCCAGTAGACT 360
QY 755 GTAGACATGAACTTGTGATCTCATGTGTAATGTCAAGATGCCATCTCATCCGAGAT 814
DB 361 GTAGACATGAACTTGTGATCTCATGTGTAATGTCAAGATGCCATCTCATCCGAGAT 420
QY 815 GATGAGGATGACACCGATGCTGCGGAAATTTTTCAGTGAAGACAGTAAACAAGAGA 874
DB 421 GATGAGGATGACACCGATGCTGCGGAAATTTTTCAGTGAAGACAGTAAACAAGAGA 480
QY 875 GACACATATGAGACCAACAGAAAAAGATGAAAAAGCGCTCCATGCTGCTGCTGCGCC 934
DB 481 GACACATATGAGACCAACAGAAAAAGATGAAAAAGCGCTCCATGCTGCTGCTGCGCC 540
QY 935 AACCTGTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
DB 541 AACCTGTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY	995	AAAAACGGGAAGAGCTTTAAACAGAGACATCGCATTTGGGGCTTACAAGGTAAACGAAC	1054
Db	601	AAAAACGGGAAGAGCTTTAAACAGAGATCGCATTTGGAGCTTCAAGGTACGAAC	660
QY	1055	CACGTGAGCCCTCATTTAGGAAGTGTGGTCCCATCTGTGACAAGGGAAATTATACCTGTGTA	1114
Db	661	CACGTGAGCCCTCATTTAGGAAGTGTGGTCCCATCTGTGACAAGGGAAATTATACCTGTGTG	720
QY	1115	GTGGAGATTGAATTACGGGTCCATCAATCAGACGTACCACTGGATGTTTGTGGACGATCG	1174
Db	721	GTGGAGATTGAATTACGGGTCCATCAATCAGACGTACCACTGGATGTTTGTGGACGATCG	780
QY	1175	CCTCACCGGGCCCATCTCTCCAAAGCCGGAGATGGCCGGGAAATGGCTCACAGTGTGTGGAGGA	1234
Db	781	CCTCACCGGGCCCATCTCTCCAAAGCCGGAGATGGCCGGGAAATGGCTCACAGTGTGTGGAGGA	840
QY	1235	GACGTAGAGTTTGTCTGCAAGGTTTACAGTATGCGCCAGCCCAATCCAGTGTGATCAAG	1294
Db	841	GACGTAGAGTTTGTCTGCAAGGTTTACAGTATGCGCCAGCCCAATCCAGTGTGATCAAG	900
QY	1295	CACGTGAAAAAAGACGGACGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGTTCTC	1354
Db	901	CACGTGAAAAAAGACGGACGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGTTCTC	960
QY	1355	AAGCACTGGGGGATTAATATGTTTCCATGCAATGCAAGATGCTGGCTCTGTTCAATGTACCCAG	1414
Db	961	AAGCACTGGGGGATTAATATGTTTCCATGCAAGATGCTGGCTCTGTTCAATGTACCCAG	1020
QY	1415	GGGAGTGGCGGGGAATATATATGTAAGGCTTCCATTTATATAGGCGAGGCCAACAGCT	1474
Db	1021	GGGAGTGGCGGGGAATATATATGTAAGGCTTCCATTTATATAGGCGAGGCCAACAGCT	1080
QY	1475	GCTGGCTCACTGTCTCTGCCAAACAGCAAGCGCTGTGAAGAAAGAGATTACGCT	1534
Db	1081	GCTGGCTCACTGTCTCTGCCAAACAGCAAGCGCTGTGAAGAAAGAGATTACGCT	1140
QY	1535	TCCCCAGACTACCTGAGATATAGCCATTTATCTGCATAGGGGTCCTTTATATGGCTGTATG	1594
Db	1141	TCCCCAGACTACCTGAGATATAGCCATTTATCTGCATAGGGGTCCTTTATATGGCTGTATG	1200
QY	1595	GTGGTAAAGTATCCTGTGGCCGAATGAAGAACAGACCAAGAACCCAGACTTACAGCAGC	1654
Db	1201	GTGGTAAAGTATCCTGTGGCCGAATGAAGAACAGACCAAGAACCCAGACTTACAGCAGC	1260
QY	1655	CAGCCGGCTGTGCAACAAGCTGACCAACGATATCCCTGTGGGAGCAGGTAAAGTTTCG	1714
Db	1261	CAGCCGGCTGTGCAACAAGCTGACCAACGATATCCCTGTGGGAGCAGGTAAAGTTTCG	1320
QY	1715	GCTGAGTCCAGCTCTCTCATGAACTTCACAACCCCGCTGTGTGAAGATTAACAACGCTTC	1774
Db	1321	GCTGAGTCCAGCTCTCTCATGAACTTCACAACCCCGCTGTGTGAAGATTAACAACGCTTC	1380
QY	1775	TCTTCAACGGCAGACCCGCCATGTCTGGCAGGGGTCCTCGATATGAATTCACAGAGAC	1834
Db	1381	TCTTCAACGGCAGACCCGCCATGTCTGGCAGGGGTCCTCGATATGAATTCACAGAGAC	1440
QY	1835	CCAAAATGGGAAGTTTCCAAAGATTAAGCTGACACTGTGGCAGCCCTGTGGAAAGTTTC	1894
Db	1441	CCAAAATGGGAAGTTTCCAAAGATTAAGCTGACACTGTGGCAGCCCTGTGGAAAGTTTC	1500
QY	1895	TTTGGGCAAGTGTCTATGGCGGAAGCATGTGGGATTTGACAAAGACAGCCCAAGAGAGCG	1954
Db	1501	TTTGGGCAAGTGTGTCTATGGCGGAAGCATGTGGGATTTGACAAAGACAGCCCAAGAGAGCG	1560
QY	1955	GTCACCGTGGCCGTGAAGATGTTGAAAGATGATCCACAGAAAGACCTTCTGATCTG	2014
Db	1561	GTCACCGTGGCCGTGAAGATGTTGAAAGATGATCCACAGAAAGACCTTCTGATCTG	1620
QY	2015	GTGTCAAGATGAGATGATGAAGATGATTGGGAAACACAAGAAATATCATTAATCTTCTT	2074
Db	1621	GTGTCAAGATGAGATGATGAAGATGATTGGGAAACACAAGAAATATCATTAATCTTCTT	1680
QY	2075	GGAGCTGCACACAGATGGGCTCTCTATGTCTATATGTTGAATATGCTTAAAGCAAC	2134

Accession	Sequence	Length
Db	1681 GGAGCCTTCACACAGGATGGGCTCTCTATGTCTATGTTAGTATGGCTCTAAAGGCAAC	1740
Qy	2135 CTCCGAGATACCTTCGAGCCCGGAGGCCACCCGGGATGAGTACTCTCTAAGAATTAAC	2139
Db	1741 CTCGAGAAATCTCTCCAGCCCGGAGGCCACCCGGGAGGATGATCTCTAAGAATTAAC	1800
Qy	2195 CGTGTTCCTCGAGAGCAGATAGCTTCAAGGACTTGGTGTCATGCACTTACCAAGCTGGCC	2254
Db	1801 CGTGTTCCTCGAGAGCAGATAGCTTCAAGGACTTGGTGTCATGCACTTACCAAGCTGGCC	1860
Qy	2255 AGACGATGAGATCTTGGCTTCCCAAAAATGTATTTCATCAGATTTAGCAGCAGAAAT	2314
Db	1861 AGACGATGAGATCTTGGCTTCCCAAAAATGTATTTCATCAGATTTAGCAGCAGAAAT	1920
Qy	2315 GTTTTGTAAAGAAAACATGTATGTAAGAAATAG	2348
Db	1921 GTTTTGTAAAGAAAACATGTATGTAAGAAATAG	1954

```

RESULT 15
US-09-949-016-3171
; Sequence 3171, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3171
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3171

```

Query Match	60.9%	Score 1890.4;	DB 3;	Length 2079;
Best Local Similarity	96.1%	Pred. No. 0;		
Matches 1998; Conservative	0;	Mismatches 61;	Indels 21;	Gaps 5

Qy	269	AAGTACTGAGAGAGAGC-GCAGCCCTCTGGTTCTCTGAGCCACCGCA-GCTGAAGGCAT	326
Db	9	AATTGACTGGAGCAGCAGGGGGCAGCGCTCTGGTTCTCTGAGCCACCGCAGGCTGAAGGCAT	68
Qy	327	TGCGCGTAATCCATATGCCCCGTAGAGGAACTGTGCATAATGGGATTAATACGTCCATATGAGAT	386
Db	69	TGCGCGTAATCCATATGCCCCGTAGAGGAACTGTGCATAATGGGATTAATACGTCCATATGAGAT	128
Qy	387	ATGGAAGAGAGACCGGGGATTTGGTACCGGTACCATGGTCACTAGCTGGGGTCTTTTCATCTGGC	446
Db	129	ATGGAAGAGAGACCGGGGATTTGGTACCGGTACCATGGTCACTAGCTGGGGTCTTTTCATCTGGC	188
Qy	447	TGCTCGTGTCAACATGCGAACCTTGTCCTCTGGCCCGGCGCTCTTCACTTAGTTAGTTAGG	506
Db	189	TGCTCGTGTCAACATGCGAACCTTGTCCTCTGGCCCGGCGCTCTTCACTTAGTTAGTTAGG	248
Qy	507	ATACCAATTAGAGCCAGAGAGCCACCAACCAATATCCAAATCTCTCAACAGAAAGTGT	566
Db	249	ATACCAATTAGAGCCAGAGAGCCACCAACCAATATCCAAATCTCTCAACAGAAAGTGT	308
Qy	567	ACGTGCTCCGCCAGGGGAGTGGCTAGAGAGTGGCGCTGTGTAAGAAAGATGGCCGCTGA	626
Db	309	ACGTGCTCCGCCAGGGGAGTGGCTAGAGAGTGGCGCTGTGTAAGAAAGATGGCCGCTGA	368

QY 627 TCAGTTGCACTAAGATGGGGTGCCTTGGGGCCCAACATAGGACAGTGTCTTATTTGGGG 686
 DB |||||
 DB 369 TCAGTTGCACTAAGATGGGGTGCCTTGGGGCCCAACATAGGACAGTGTCTTATTTGGGG 428
 QY 687 AGTACTTGAGATTAAGGGCGCCACACTAGAGACTCCGGCCTTATGCTTGTACTGCCA 746
 DB |||||
 DB 429 AGTACTTGAGATTAAGGGCGCCACACTAGAGACTCCGGCCTTATGCTTGTACTGCCA 488
 QY 747 GTAGACTGTAGACACTGTAACTTGTACTTCACTGTGTATGTCAAGATGCCATCTCAT 806
 DB |||||
 DB 489 GTAGACTGTAGACACTGTAACTTGTACTTCACTGTGTATGTCAAGATGCCATCTCAT 548
 QY 807 CCGGAGATGTATAGAGATTCACCCGATGTGCGGAAATTTGTCACTGTAGAACAGTAA 866
 DB |||||
 DB 549 CCGGAGATGTATAGAGATTCACCCGATGTGCGGAAATTTGTCACTGTAGAACAGTAA 608
 QY 867 ACNAGAGACACATCTGAGACCAACACAGAAAAGTGAAGAGCGGCTCACTGTCTGTC 926
 DB |||||
 DB 609 ACNAGAGACACATCTGAGACCAACACAGAAAAGTGAAGAGCGGCTCACTGTCTGTC 668
 QY 927 CTGCGGCAACACTGTCAAGTTTCTGCTGCCAGCCGGGGGAAACCAATGCCACATGC 986
 DB |||||
 DB 669 CTGCGGCAACACTGTCAAGTTTCTGCTGCCAGCCGGGGGAAACCAATGCCACATGC 728
 QY 987 GGTGGCTGAAAAACGGGAGAGATTAAAGAGAGATGCAATGGAGGCTCAAGTAC 1046
 DB |||||
 DB 729 GGTGGCTGAAAAACGGGAGAGATTAAAGAGAGATGCAATGGAGGCTCAAGTAC 788
 QY 1047 GAAACAGACCTGAGACCTCATATATGAAAAGTGTGCTCCATCTGCAAGAGAAATTATA 1106
 DB |||||
 DB 789 GAAACAGACCTGAGACCTCATATATGAAAAGTGTGCTCCATCTGCAAGAGAAATTATA 848
 QY 1107 CCTGTGTAGTGAAGATTAATGATGCGGTTCATCAATCAACAGTACCACTGGATGTTG 1166
 DB |||||
 DB 849 CCTGTGTGTGAGATTAATGATGCGGTTCATCAATCAACAGTACCACTGGATGTTG 908
 QY 1167 AGGATGCGCTCACCGGCCCATCTCTCAAGCCGGACTGCGCGGAAATGCTCTCAAGTGG 1226
 DB |||||
 DB 909 AGGATGCGCTCACCGGCCCATCTCTCAAGCCGGACTGCGCGGAAATGCTCTCAAGTGG 968
 QY 1227 TCGGAGAGACGATGAGATTGTCTGCAAGGTTTACAGTATGCCAGCCCAATCCAGT 1286
 DB |||||
 DB 969 TCGGAGAGACGATGAGATTGTCTGCAAGGTTTACAGTATGCCAGCCCAATCCAGT 1028
 QY 1287 GATCAAGACGATGAGAAAAGACGCAATTAATGCGGCGGAGCGGCTGCTTACTCA 1346
 DB |||||
 DB 1029 GATCAAGACGATGAGAAAAGACGCAATTAATGCGGCGGAGCGGCTGCTTACTCA 1088
 QY 1347 AGGTTCTCAAGCACTGGGGATTAATGTTCCATGCAAGTGTGGCTGTGT----- 1400
 DB |||||
 DB 1089 AGGTTCTCAAGCACTGGGGATTAATGTTCCATGCAAGTGTGGCTGTGT----- 1148
 QY 1401 TCAATGTGACCGAGGGGATGCTGGGGATATATATGTAAAGTCTCCAAATTATATAGGGC 1460
 DB |||||
 DB 1149 GGAATGTAACTTTTGAAGACGCTGGGGAATATACGTGCTTGGCGGTAATTTCTATTGGGA 1208
 QY 1461 AGGCCAACCAAGTCTGCTGCTCACTGTCTCTGCCAAAACAGCAAGCGCTGGAAGAAA 1520
 DB |||||
 DB 1209 TATCTTTTCACTGTGATGTGATCAAGTGTCTGCC-----AGCGCTGGAAGAAA 1259
 QY 1521 AGGAGATTACAGCTTCCCGAGACTTACTGTGAAGATAGCCATTTACTGATAGGGGTCTTCT 1580
 DB |||||
 DB 1260 AGGAGATTACAGCTTCCCGAGACTTACTGTGAAGATAGCCATTTACTGATAGGGGTCTTCT 1319
 QY 1581 TAATGCTGTATGTGTGTAAAGTCACTCTGTGCCGAATGAAGAACAGCAAGAAC 1640
 DB |||||
 DB 1320 TAATGCTGTATGTGTGTAAAGTCACTCTGTGCCGAATGAAGAACAGCAAGAAC 1379
 QY 1641 CAGACTTCAGACAGCCCGGCTGTGCAAGCTGACAAAGTATCTCTGCGGAGAC 1700
 DB |||||
 DB 1380 CAGACTTCAGACAGCCCGGCTGTGCAAGCTGACAAAGTATCTCTGCGGAGAC 1439
 QY 1701 AGGTAAC---AGTTTGGGCTGAGTCAAGTCTCTCCATGAATCTCAACACCCCGCTGGTG 1756

DB 1440 AGGTAACAGAAAGTTTGGGCTGAGTCCAGCTCTCTCAATGAATCCAAACCCCGCTGGTG 1499
 QY 1757 AGGATTAACACAGGCTCTCTTCAACCGGACACACCCCAATGCTGGGAGGGTCTCCAG 1816
 DB 1500 AGGATTAACACAGGCTCTCTTCAACCGGACACACCCCAATGCTGGGAGGGTCTCCAG 1559
 QY 1817 TATGAACCTTCAGAGAACCCAAATGGAGATTCCAGAGATTAAGCTGACACTGGGCAAG 1876
 DB |||||
 DB 1560 TATGAACCTTCAGAGAACCCAAATGGAGATTCCAGAGATTAAGCTGACACTGGGCAAG 1619
 QY 1877 CCCCTGGAGAGAGTTGCTTTGGGCAAGTGTCACTGGCGGAAGCAAGTGGAAATTGACAA 1936
 DB |||||
 DB 1620 CCCCTGGAGAGAGTTGCTTTGGGCAAGTGTCACTGGCGGAAGCAAGTGGAAATTGACAA 1679
 QY 1937 GACAGCCCAAGAGAGCGGCTCACCGTGGCCGTGAAGATGTTGAAGATATGCCACAG 1996
 DB |||||
 DB 1680 GACAGCCCAAGAGAGCGGCTCACCGTGGCCGTGAAGATGTTGAAGATATGCCACAG 1739
 QY 1997 AAGACCTTTCATCTGTGTGATGATGAGATGATGAAGATGATGGAAACACAG 2056
 DB |||||
 DB 1740 AAGACCTTTCATCTGTGTGATGATGAGATGATGAAGATGATGGAAACACAG 1799
 QY 2057 AATATCATTAATCTTCTTGAAGCTTGCACACAGATGGGCTCTCTATGTCAATGTTGAG 2116
 DB |||||
 DB 1800 AATATCATTAATCTTCTTGAAGCTTGCACACAGATGGGCTCTCTATGTCAATGTTGAG 1859
 QY 2117 TATGCTCTTAAGGCAACCTCCAGATATCTCCAGAGCCCGGAGGCAACCCCGGATGAG 2176
 DB |||||
 DB 1860 TATGCTCTTAAGGCAACCTCCAGATATCTCCAGAGCCCGGAGGCAACCCCGGATGAG 1919
 QY 2177 TATCTCTTATGATTAACCGTGTCTGAGAGAGATGATGATGATGATGATGATGATGAT 2236
 DB |||||
 DB 1920 TATCTCTTATGATTAACCGTGTCTGAGAGAGATGATGATGATGATGATGATGATGAT 1979
 QY 2237 TSCACTACAGCTGGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2296
 DB |||||
 DB 1980 TSCACTACAGCTGGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2039
 QY 2297 GATTTAGCAGCCAGAAATGTTTGTGTAAACAGAAAACATG 2336
 DB |||||
 DB 2040 GATTTAGCAGCCAGAAATGTTTGTGTAAACAGAAAACATG 2079

Search completed: October 2, 2006, 18:05:28
 Job time : 558 secs

This Page Blank (uspio)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:57:12 ; Search time 3249 Seconds
(without alignments)
11746.813 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaaaattgtgtg.....tttcgtgagcgtgacgc 3106

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues 37784340

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:**
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:**
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:**
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:**
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:**
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:**
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:**
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:**
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:**
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:**
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:**
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:**
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:**
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:**
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:**
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11E_PUBCOMB.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3013.2	97.0	4574	8 US-10-648-593-132	Sequence 132, App
2	3013.2	97.0	4574	10 US-10-956-157-2419	Sequence 2419, App
3	3013.2	97.0	4574	12 US-10-960-414-172	Sequence 172, App
4	3013.2	97.0	4574	13 US-11-019-829-39	Sequence 39, App
5	3013.2	97.0	4574	16 US-11-019-175-132	Sequence 132, App
6	2904.2	93.5	4587	13 US-11-019-829-38	Sequence 38, App
7	2849.4	91.7	4575	13 US-11-019-829-42	Sequence 42, App
8	2806.2	90.3	3080	3 US-09-954-556-25	Sequence 25, App
9	2781.8	89.6	4268	3 US-09-954-456-293	Sequence 293, App
10	2781.8	89.6	4268	3 US-09-954-456-1599	Sequence 1599, App
11	2781.8	89.6	4268	3 US-09-954-556-3	Sequence 3, App
12	2781.8	89.6	4268	3 US-09-968-007A-461	Sequence 461, App
13	2781.8	89.6	4268	10 US-10-843-641A-3320	Sequence 3320, App
14	2781.8	89.6	4268	10 US-10-843-641A-4626	Sequence 4626, App
15	2781.8	89.6	4268	10 US-10-843-641A-6931	Sequence 6931, App
16	2747.4	88.5	4667	7 US-10-007-926A-15	Sequence 15, App
17	2747.4	88.5	4667	13 US-11-019-829-47	Sequence 47, App

18	2747.4	88.5	4666	9 US-10-723-860-6953	Sequence 6953, App
19	2728.6	87.8	2923	3 US-09-954-556-20	Sequence 20, App
20	2723.4	87.7	2826	3 US-09-954-556-21	Sequence 21, App
21	2722	87.6	2868	3 US-09-954-556-19	Sequence 19, App
22	2722	87.6	2941	3 US-09-954-556-18	Sequence 18, App
23	2639.6	85.0	3219	13 US-11-019-829-44	Sequence 44, App
24	2556.8	82.3	3248	13 US-10-302-812-43	Sequence 43, App
25	2506	80.7	3216	13 US-11-019-829-43	Sequence 43, App
26	2475	79.7	4310	13 US-11-019-829-45	Sequence 45, App
27	2404.4	77.4	4222	13 US-11-019-829-49	Sequence 49, App
28	2382.4	76.7	4216	13 US-11-019-829-50	Sequence 50, App
29	2350.8	75.7	4305	13 US-11-019-829-48	Sequence 48, App
30	2327.4	74.9	2466	8 US-10-843-339C-85	Sequence 85, App
31	2327.4	74.9	3244	3 US-09-954-556-24	Sequence 24, App
32	2327.4	74.9	3244	3 US-09-873-367C-171	Sequence 171, App
33	2327.4	74.9	3244	10 US-10-843-641A-171	Sequence 171, App
34	2327.4	74.9	3244	10 US-10-505-680-715	Sequence 715, App
35	2327.4	74.9	4223	13 US-11-019-829-40	Sequence 40, App
36	2320	74.7	2650	3 US-09-954-556-28	Sequence 28, App
37	2201	70.9	3306	3 US-09-954-556-10	Sequence 10, App
38	2185	70.3	2672	16 US-11-136-527-3514	Sequence 3514, App
39	2116.2	68.1	3011	10 US-10-956-157-4901	Sequence 4901, App
40	2072.2	66.7	3025	3 US-09-954-556-23	Sequence 23, App
41	1890.4	60.9	2079	6 US-10-087-192-1133	Sequence 1133, App
42	1677.8	54.0	2311	16 US-11-136-527-3513	Sequence 3513, App
43	1475.6	47.5	1978	6 US-10-087-192-1130	Sequence 1130, App
44	1468.4	47.3	1807	13 US-11-019-829-46	Sequence 46, App
45	1345	43.3	1475	3 US-09-954-556-27	Sequence 27, App

ALIGNMENTS

RESULT 1
US-10-648-593-132
; Sequence 132, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-132

Query Match	97.0%	Score 3013.2:	DB 8:	Length 4574:
Best Local Similarity	99.5%	Pred. No. 0:		
Matches 3097:	Conservative	0:	Mismatches	8:
			Indels	9:
			Gaps	7:
QY	1	CCCGAGGAAAGTTGTTGAGGCAACG-CAAGCTGAGTCTTCTCTCTCC	59	
DB	168	CTCGGAGCAAAAGTTGTTGAGGCAACGCAAGCTGAGTCTTCTCTCTCTCC	227	
QY	60	CCAAATCGAGGAGCGAGCGCGGCGTCAATG--GCGTCTCTCGGAGCTGGGTAACG	116	
DB	228	CCAAATCGCA-GGACGCGCGCGGCGTCAATGCGCGCTCTCGGAGCTGGGTAACG	286	
QY	117	G-TGAAGCCCGGAGGCTTGGCGCGGCGAAGCAACCAACCACTTCTGCTTGA	175	
DB	287	GCTGAAGCCCGGAGGCTTGGCGCGGCGAAGCAACCAACCACTTCTGCTTGA	346	
QY	176	GTTGCTCCCGGAGGCTTGGCGCGGCGTCTGCTTCTCTCATCCGACCGCGGAGC-CGAG	234	

Db	347	GTTCGTC	CCCAAC	CCCCGGG	GTGTCGCTTCTC	ATCCGAC	CCACG	CGCGG	CGG	346
Qy	235	GACAA	CA	GAGTCG	GAGAGAG	CGTTG	CCATTCA	AGTGA	CTGACG	293
Db	407	GACAA	CA	GAGTCG	CGGAGAG	CGTTG	CCATTCA	AGTGA	CTGACG	466
Qy	294	CTCGG	TTCTTA	AGCCCA	CCGCA - GCTGA	AGGGA	ATTGCGGTGTG	TCATCC	CGCTAG	352
Db	467	CTCGG	TTCTTA	AGCCCA	CCGCA - GCTGA	AGGGA	ATTGCGGTGTG	TCATCC	CGCTAG	526
Qy	353	AGTGG	CAGATGG	ATTAACT	CA	CATGAG	ATATGA	AAAGAG	ACCGGGA	412
Db	527	AGTGG	CAGATGG	ATTAACT	CA	CATGAG	ATATGA	AAAGAG	ACCGGGA	586
Qy	413	GTAA	CCATGG	TCA	GCTGGGTG	CTTCA	TCGCTGTGTG	TCACAT	TGCA	472
Db	587	GTAA	CCATGG	TCA	GCTGGGTG	CTTCA	TCGCTGTGTG	TCACAT	TGCA	646
Qy	473	TCCCG	GGCCCG	CCCTCCTT	CA	GTTTAA	GTGAGAT	ACCA	CAATTAA	532
Db	647	TCCCG	GGCCCG	CCCTCCTT	CA	GTTTAA	GTGAGAT	ACCA	CAATTAA	706
Qy	533	CCAAC	AAATAC	CA	ATCTCTCA	ACCA	AGATAG	TGGCTG	CGCAGGGA	592
Db	707	CCAAC	AAATAC	CA	ATCTCTCA	ACCA	AGATAG	TGGCTG	CGCAGGGA	766
Qy	593	GAGGT	GCGCTG	CTGTGAA	AGATG	CGCGCTG	ATCATG	TTGA	CTAAGA	652
Db	767	GAGGT	GCGCTG	CTGTGAA	AGATG	CGCGCTG	ATCATG	TTGA	CTAAGA	826
Qy	653	TTGGG	GGCCCA	CA	ATGGA	CAGTGT	ATT	TTGGGGA	CTTGA	712
Db	827	TTGGG	GGCCCA	CA	ATGGA	CAGTGT	ATT	TTGGGGA	CTTGA	886
Qy	713	CCTAG	AGATC	CGGCTCTATG	CTTGT	TATCTG	CCAGTGA	CTGTAG	CAGTGA	772
Db	887	CCTAG	AGATC	CGGCTCTATG	CTTGT	TATCTG	CCAGTGA	CTGTAG	CAGTGA	946
Qy	773	TACTT	CATG	TATGTCA	CAGATG	CCATCTCA	TCCG	AGATG	ATGAGATGA	832
Db	947	TACTT	CATG	TATGTCA	CAGATG	CCATCTCA	TCCG	AGATG	ATGAGATGA	1006
Qy	833	GGTGG	GGAAG	ATTTTGT	CAGTGA	GAACATGA	CAACA	GAGAC	CCATCTG	892
Db	1007	GGTGG	GGAAG	ATTTTGT	CAGTGA	GAACATGA	CAACA	GAGAC	CCATCTG	1066
Qy	893	ACA	GA	AAAAATG	GA	AAAGCGCTCA	TGCTGTG	CTGGGCA	CACTG	952
Db	1067	ACA	GA	AAAAATG	GA	AAAGCGCTCA	TGCTGTG	CTGGGCA	CACTG	1126
Qy	953	TGCGC	AGCGGGG	GAACCA	ATG	CCATG	CCATG	CGGTG	CTGA	1012
Db	1127	TGCGC	AGCGGGG	GAACCA	ATG	CCATG	CCATG	CGGTG	CTGA	1186
Qy	1013	AAG	CAGAG	CATGTGA	TTGAGGCTCA	AGGTACGA	AAACAGCA	CTG	AGCTCAT	1072
Db	1187	AAG	CAGAG	CATGTGA	TTGAGGCTCA	AGGTACGA	AAACAGCA	CTG	AGCTCAT	1246
Qy	1073	GAA	AGTGTG	TCCCATCTG	CAAGGAAATTA	TA	CTGTGTATG	ATG	TA	1132
Db	1247	GAA	AGTGTG	TCCCATCTG	CAAGGAAATTA	TA	CTGTGTATG	ATG	TA	1306
Qy	1133	TCC	ATCAATCA	CGTACCA	CTGGAATG	TGTGAGGAT	CGCTCA	CGG	CCATCTC	1192
Db	1307	TCC	ATCAATCA	CGTACCA	CTGGAATG	TGTGAGGAT	CGCTCA	CGG	CCATCTC	1366
Qy	1193	CAAG	CCGACTG	CCGCAATG	CTCCACAG	TGCTGCA	AGTGTG	CTG		1252
Db	1367	CAAG	CCGACTG	CCGCAATG	CTCCACAG	TGCTGCA	AGTGTG	CTG		1426
Qy	1253	AAG	GTTCAG	TGATG	CCCA	CAATCA	GTGATCA			1312
Db	1427	AAG	GTTCAG	TGATG	CCCA	CAATCA	GTGATCA			1486

OY	1313	AGTAAATACGGGCGCCGACGGGCTGGCCCTTACCTCAAGGTTCTTCBAACACTCGGGGATAAT	1372
Db	1487	AGTAAATACGGGCGCCGACGGGCTGGCCCTTACCTCAAGGTTCTTCBAACACTCGGGGATAAT	1546
OY	1373	AGTTCCAAATGCAGAAAGTGTGGCTCTGTTCAAATGTGACCGAGGCGGATGTCTGGGAAATAT	1432
Db	1547	AGTTCCAAATGCAGAAAGTGTGGCTCTGTTCAAATGTGACCGAGGCGGATGTCTGGGAAATAT	1606
OY	1433	ATATGTAAAGTCTTCCAAATTATATAGGGCAGGCCAACACTCTGGCTCGCTGCTCATCTGTCCG	1492
Db	1607	ATATGTAAAGTCTTCCAAATTATATAGGGCAGGCCAACACTCTGGCTCGCTGCTCATCTGTCCG	1666
OY	1493	CCAAAACAGCAAGCGCGCTGGAGAGAAAAGAGATTACAGCTTCCCACTACCTGAG	1552
Db	1667	CCAAAACAGCAAGCGCGCTGGAGAGAAAAGAGATTACAGCTTCCCACTACCTGAG	1726
OY	1553	ATAGCCATTATCTGCAATAGGGAGTCTTCTTATGCGCTGTATGATGTGTAAACATCATCTCTG	1612
Db	1727	ATAGCCATTATCTGCAATAGGGAGTCTTCTTATGCGCTGTATGATGTGTAAACATCATCTCTG	1786
OY	1613	TGCGGAATGAAAGAACAGACCAAGAAAGCCAGACTTCAGAGGCAAGCGGCTGTGACAAAG	1672
Db	1787	TGCGGAATGAAAGAACAGACCAAGAAAGCCAGACTTCAGAGGCAAGCGGCTGTGACAAAG	1846
OY	1673	CTGACCAAAAGTATCCCGCTGCGAGACAGGTAAAGTTTGGCTGAGTCCAGCTCTCC	1732
Db	1847	CTGACCAAAAGTATCCCGCTGCGAGACAGGTAAAGTTTGGCTGAGTCCAGCTCTCC	1906
OY	1733	ATGAATCTCAACACCCCGCTGTGTGAGATTAACAACACGCTCTCTTCAACGGCACAACACC	1792
Db	1907	ATGAATCTCAACACCCCGCTGTGTGAGATTAACAACACGCTCTCTTCAACGGCACAACACC	1966
OY	1793	CCCATGTGCGAGGGGCTCCGAGTATGAATTCAGAGGACCCAAATGSGAGTTTCCA	1852
Db	1967	CCCATGTGCGAGGGGCTCCGAGTATGAATTCAGAGGACCCAAATGSGAGTTTCCA	2026
OY	1853	AGAGATTAAGTGAACACTGGGCAAGCCCTGGGGAAGAGTTGCTTTGGGCAATGTGTCATG	1912
Db	2027	AGAGATTAAGTGAACACTGGGCAAGCCCTGGGGAAGAGTTGCTTTGGGCAAGTGTGTCATG	2086
OY	1913	GCGAAGACGATGGGGAATTGACAAAGCAACGCCAAGAGAGCGGTCAACGTCGCGGTGAAG	1972
Db	2087	GCGAAGACGATGGGGAATTGACAAAGCAACGCCAAGAGAGCGGTCAACGTCGCGGTGAAG	2146
OY	1973	ATGTGTAAAGATGATGCGACAGAGAAAGACTTTTGTGATCTGTGTCAAGATGTGAGATG	2032
Db	2147	ATGTGTAAAGATGATGCGACAGAGAAAGACTTTTGTGATCTGTGTCAAGATGTGAGATG	2206
OY	2033	ATGAAGATGATTTGGGAAACACAGAAATATCATTAATCTTTGGAACCTGACACAGGAT	2092
Db	2207	ATGAAGATGATTTGGGAAACACAGAAATATCATTAATCTTTGGAACCTGACACAGGAT	2266
OY	2093	GGGCGCTCTATGTGCATAGTTGAGTATGCGCTTAAAGGCAACCTCGAGATTAACCTCCGA	2152
Db	2267	GGGCGCTCTCTATGTGCATAGTTGAGTATGCGCTTAAAGGCAACCTCGAGATTAACCTCCGA	2326
OY	2153	GCCCGAGAGCCACCCGGATGAGTACTCCTATGACATTAAACCTGTGTTCTCTGAGAGCAG	2212
Db	2327	GCCCGAGAGCCACCCGGATGAGTACTCCTATGACATTAAACCTGTGTCTCTGAGAGCAG	2386
OY	2213	ATGACCTTCAAGCACTTGCTGTCAATGACCTACAGCTGGCCGAGCGGATGAGTACTTG	2272
Db	2387	ATGACCTTCAAGCACTTGCTGTCAATGACCTACAGCTGGCCGAGCGGATGAGTACTTG	2446
OY	2273	GCTTCCCAAAATGTATTCATCGAGTTTATGACCCAGAAATGTTTGGTAAACAGAAAAC	2332
Db	2447	GCTTCCCAAAATGTATTCATCGAGTTTATGACCCAGAAATGTTTGGTAAACAGAAAAC	2506
OY	2333	AATGTGATGAAATATGACGACTTTGGACCTGCCAGAGATATCAACAATATAGACTTTAC	2392
Db	2507	AATGTGATGAAATATGACGACTTTGGACCTGCCAGAGATATCAACAATATATAGACTTTAC	2566

QY 2393 AAAAGACCAACCAATGGGGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTTANT 2452
DB 2557 AAAAGACCAACCAATGGGGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTTANT 2626
QY 2453 AGAGTATACACTCATCAGAGTATGTCTGTCTTCGCGGGTGTTAATGTGGAGATCTTC 2512
DB 2627 AGAGTATACACTCATCAGAGTATGTCTGTCTTCGCGGGTGTTAATGTGGAGATCTTC 2686
QY 2513 ACTTTAGGGGGGCTCCCTCAACCAAGGATTCCTGTGAGAGAACTTTTAACTGTCTGAAG 2572
DB 2687 ACTTTAGGGGGGCTCCCTCAACCAAGGATTCCTGTGAGAGAACTTTTAACTGTCTGAAG 2746
QY 2573 GAAAGACACAGATGGATTAAGCAAGCACTGCAACCAAGTGAATGAATGAAG 2632
DB 2747 GAAAGACACAGATGGATTAAGCAAGCACTGCAACCAAGTGAATGAATGAAG 2806
QY 2633 GACTGTGGCATGAGTGGCTCCCAAGAGACCAAGCTTCAAGCAATGGTGAAGACTTGG 2692
DB 2807 GACTGTGGCATGAGTGGCTCCCAAGAGACCAAGCTTCAAGCAATGGTGAAGACTTGG 2866
QY 2693 GATCGAATTTCTCACTCTCAACAATGAGAACTTGGAACTTCAAGCACTCTCGAA 2752
DB 2867 GATCGAATTTCTCACTCTCAACAATGAGAACTTGGAACTTCAAGCACTCTCGAA 2926
QY 2753 CAGTATTCACCTAATACCTTGAACAAGAACTTGTCTTCAAGAGATGAATCTGT 2812
DB 2927 CAGTATTCACCTAATACCTTGAACAAGAACTTGTCTTCAAGAGATGAATCTGT 2986
QY 2813 TTTTCTCCAGACCCCATGCTTACGAACCATGCTTCTCAATATCCACATTAACGAG 2872
DB 2987 TTTTCTCCAGACCCCATGCTTACGAACCATGCTTCTCAATATCCACATTAACGAG 3046
QY 2873 AGTGTAAACCAATGATGATGTGTCTGTCTGTCTTCCCAACAGAGACAGCACTGGAACT 2932
DB 3047 AGTGTAAACCAATGATGATGTGTCTGTCTGTCTTCCCAACAGAGACAGCACTGGAACT 3106
QY 2933 AGCTACATGAGACAGAGAGACCAATGCTTCCAGAGCTTGTCTTCACTGTATATATG 2992
DB 3107 AGCTACATGAGACAGAGAGACCAATGCTTCCAGAGCTTGTCTTCACTGTATATATG 3166
QY 2993 GATCAGAGAGTAAATTAATTTGAGAAAGTATGATGATGATTAAGATTTTACAGTTG 3052
DB 3167 GATCAGAGAGTAAATTAATTTGAGAAAGTATGATGATGATTAAGATTTTACAGTTG 3226
QY 3053 AAAAATTTGATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAAGCTGC 3106
DB 3227 AAAAATTTGATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAAGCTGC 3280

RESULT 2
US-10-956-157-2419
; Sequence 2419, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2419
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-2419

Query Match 97.0%; Score 3013.2; DB 10; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

QY 1 CCCCGAGCAAGATTGGTGAAGCAAG-CAAGCTGAGTCTTTCTTCTCTGTTCC 59
DB 168 CTCGAGAGCAAGATTGGTGAAGCAAGCAAGCTGAGTCTTTCTTCTCTGTTCC 227
QY 60 CCAATTCGAGGAGGAGCCCGCGGCTCATG--GCGTCTTCGCGAGCTTGGGTACG 116
DB 228 CCAATTCGAG-GGAGGCGCGGCGGCTCATGCGCGCTCTTCGCGAGCTTGGGTACG 286
QY 117 G-TGAAGCCCGGAGGAGCTTGGGCGCGGAGAGACCAAGAGCACTCTTCTGCGTTTGA 175
DB 287 GCTGAAGCCCGGAGGAGCTTGGGCGCGGAGAGACCAAGAGCACTCTTCTGCGTTTGA 346
QY 176 GTTGTCTCCCGCAACCCCGGCTCGTCTGCTTCTTCATCCGAGCCGAGCGGAGG-CCG 234
DB 347 GTTGTCTCCCGCAACCCCGGCTCGTCTGCTTCTTCATCCGAGCCGAGCGGAGG 406
QY 235 GACAAACAGGTGCGGAGAGAGCTTGCATTCAAGTGAATGCAAGCAGCAGC-AGAGCG 293
DB 407 GACAAACAGGTGCGGAGAGAGCTTGCATTCAAGTGAATGCAAGCAGCAGCAGCAGCG 466
QY 294 CTGCGTTCTTGAAGCCCAACCGCA-GCTGAAGGCAATTGCGGTATGTCATGCGGTAGA 352
DB 467 CTGCGTTCTTGAAGCCCAACCGCAAGCTGAAGGCAATTGCGGTATGTCATGCGGTAGA 526
QY 353 AGTGTGAGATGGATTAAGCTCAACATGAGATATGAGAGAGACCGGAGATTGGTACC 412
DB 527 AGTGTGAGATGGATTAAGCTCAACATGAGATATGAGAGAGACCGGAGATTGGTACC 586
QY 413 GTAACATGATGATGAGGTGCTTCACTGTGCTGTGCTGTGCTGATCAATGAGCACTTG 472
DB 587 GTAACATGATGATGAGGTGCTTCACTGTGCTGTGCTGTGCTGATCAATGAGCACTTG 646
QY 473 TCCCGGCGCGGCGCTCTTCAATTAATGATGAGATACCAATTAAGACCGAAGAGCA 532
DB 647 TCCCGGCGCGGCGCTCTTCAATTAATGATGAGATACCAATTAAGACCGAAGAGCA 706
QY 533 CCAACCAATTAATCAATCTCTCAACCAAGATGATGAGTGCAGCGGAGATGCTGA 592
DB 707 CCAACCAATTAATCAATCTCTCAACCAAGATGATGAGTGCAGCGGAGATGCTGA 766
QY 593 GAGGTGCGCTGCTGTGAGAAAGATGCGCGGTATCAATGAGATTAAGAGTGGGTGAC 652
DB 767 GAGGTGCGCTGCTGTGAGAAAGATGCGCGGTATCAATGAGATTAAGAGTGGGTGAC 826
QY 653 TTGGGCGCCCAACATATGAGACAGTGTATTTGGGAGATCTTGCAGATTAAGGCGCCCA 712
DB 827 TTGGGCGCCCAACATATGAGACAGTGTATTTGGGAGATCTTGCAGATTAAGGCGCCCA 886
QY 713 CCTAGAGACTCGGCTCTATGCTTGTACTGCAAGTGAAGATGAGATGAGTGAACCTTGG 772
DB 887 CCTAGAGACTCGGCTCTATGCTTGTACTGCAAGTGAAGATGAGATGAGTGAACCTTGG 946
QY 773 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
DB 947 TACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
QY 833 GGTGCGGAGAAATTTGTCAAGTGAAGACATTAACCAAGAGAGCACTTCTGAGCAAC 892
DB 1007 GGTGCGGAGAAATTTGTCAAGTGAAGACATTAACCAAGAGAGCACTTCTGAGCAAC 1066
QY 893 ACAGAAAGATGAGAAAGAGGCTCATGCTGTGCTGCGGCAACATGTCAGATTTGCG 952
DB 1067 ACAGAAAGATGAGAAAGAGGCTCATGCTGTGCTGCGGCAACATGTCAGATTTGCG 1126
QY 953 TGCCAGCGCGGAGAGACCAATGCAACATGCGGTGCTGAGAAACGAGAGAGTTT 1012
DB 1127 TGCCAGCGCGGAGAGACCAATGCAACATGCGGTGCTGAGAAACGAGAGAGTTT 1186
QY 1013 AAGCAGAGCATGCAATGAGAGCTTCAAGAGTGAAGCAACCAAGCACTGAGCTCAATTG 1072
DB 1187 AAGCAGAGCATGCAATGAGAGCTTCAAGAGTGAAGCAACCAAGCACTGAGCTCAATTG 1246
QY 1073 GAAAGTGTGCTCCATGCAAGAGGAAATTAACCTGTGATGAGATGAATGAATGAGG 1132

Db 1247 GAAAGTGTGTCCTCATCTGACAGAGGAATTAATCTGTGTGTGAGAAATATACGGG 1306
Oy 1133 TCCATCATCAAGCTACACCTGGATGTGTGAGGATGCGCTCACCGGCGCATCTC 1192
Db 1307 TCCATCATCAAGCTACACCTGGATGTGTGAGGATGCGCTCACCGGCGCATCTC 1366
Oy 1193 CAAGCCGAGCTGCGGCAATATGCTCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1252
Db 1367 CAAGCCGAGCTGCGGCAATATGCTCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1426
Oy 1253 AAGGTTTCACTGATGCTGCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1312
Db 1427 AAGGTTTCACTGATGCTGCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1486
Oy 1313 AGTAAATACGAGGCGGAGGAGTGTCTCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1372
Db 1487 AGTAAATACGAGGCGGAGGAGTGTCTCAAGTGTGTGAGGAGAGTGAAGTTGTCTGC 1546
Oy 1373 AGTTCATGAGAGAGTGTCTGTCTCAATGTGTGAGGAGGAGTGTGTGAGGAGTGT 1432
Db 1547 AGTTCATGAGAGAGTGTCTGTCTCAATGTGTGAGGAGGAGTGTGTGAGGAGTGT 1606
Oy 1433 ATATGATAGTGTCTCAATTTATATAGGAGGAGGAGTGTGTGAGGAGTGTGTGAGG 1492
Db 1607 ATATGATAGTGTCTCAATTTATATAGGAGGAGGAGTGTGTGAGGAGTGTGTGAGG 1666
Oy 1493 CCAAAACAGAGGCGCTGGAAGAGAGAGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGT 1552
Db 1667 CCAAAACAGAGGCGCTGGAAGAGAGAGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGT 1726
Oy 1553 ATAGCATTTATCTGATAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1612
Db 1727 ATAGCATTTATCTGATAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1786
Oy 1613 TGCCGATAG 1672
Db 1787 TGCCGATAG 1846
Oy 1673 CTGACCAACGATGCTGCTGCGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1732
Db 1847 CTGACCAACGATGCTGCTGCGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1906
Oy 1733 ATGAATCTCAACACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1792
Db 1907 ATGAATCTCAACACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1966
Oy 1793 CCGATGCTGCGAGGAGT 1852
Db 1967 CCGATGCTGCGAGGAGT 2026
Oy 1853 AGAGATTAAGCTGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1912
Db 2027 AGAGATTAAGCTGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
Oy 1913 GCGGAG 1972
Db 2087 GCGGAG 2146
Oy 1973 ATGTTGAAG 2032
Db 2147 ATGTTGAAG 2206
Oy 2033 ATGAAGATGATGAG 2092
Db 2207 ATGAAGATGATGAG 2266
Oy 2093 GGGGCTCTATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2152
Db 2267 GGGGCTCTATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
Oy 2153 GCGCGAGGAG 2212

Db 2327 GCGCGAGGAG 2386
Oy 2213 ATGACCTTCAAGAGCTTGT 2272
Db 2287 ATGACCTTCAAGAGCTTGT 2446
Oy 2273 GCTTCCCAAAAATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 2332
Db 2447 GCTTCCCAAAAATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 2506
Oy 2333 AATGTATGAAAATGATGAGCTTGT 2392
Db 2507 AATGTATGAAAATGATGAGCTTGT 2566
Oy 2393 AAAAAAGACCAATGAGGAGCTTGT 2452
Db 2567 AAAAAAGACCAATGAGGAGCTTGT 2626
Oy 2453 AGATATATCACTGATGAG 2512
Db 2627 AGATATATCACTGATGAG 2686
Oy 2513 ACTTAAAGGAGGCTGCGCTTCAAG 2572
Db 2687 ACTTAAAGGAGGCTGCGCTTCAAG 2746
Oy 2573 GAAGAGACAGAGATGATTAAG 2632
Db 2747 GAAGAGACAGAGATGATTAAG 2806
Oy 2633 GACGTGTGAGATGAG 2692
Db 2807 GACGTGTGAGATGAG 2866
Oy 2693 GATCGAATTTCTCACTCTCAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2752
Db 2867 GATCGAATTTCTCACTCTCAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2926
Oy 2753 CAGTATTCACCTGATGAG 2812
Db 2927 CAGTATTCACCTGATGAG 2986
Oy 2813 TTTTCTCCAG 2872
Db 2987 TTTTCTCCAG 3046
Oy 2873 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2932
Db 3047 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3106
Oy 2933 AGCTACACTGAG 2992
Db 3107 AGCTACACTGAG 3166
Oy 2993 GATCAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3052
Db 3167 GATCAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3226
Oy 3053 AAAAATTTGATTTTCCCAAG 3106
Db 3227 AAAAATTTGATTTTCCCAAG 3280

RESULT 3
US-10-960-414-172
; Sequence 172, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSEPH
; APPLICANT: VEGA, VINCENTIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; PROGNOSIS, AND DIAGNOSIS OF CANCERS

FILE REFERENCE: 38271-76067
CURRENT APPLICATION NUMBER: US/10/960,414
CURRENT FILING DATE: 2004-10-06
NUMBER OF SEQ ID NOS: 500
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 172
LENGTH: 4574
TYPE: DNA
ORGANISM: Homo sapiens
US-10-960-414-172

Query Match 97.0%; Score 3013.2; DB 12; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

1 CCCGAGAGCAAGTTTGTGTGAGGCAACG-CAAGCTGAGTCTTTCTCTCTGCTTC 59
168 CTCGGAGAGCAAGTTTGTGTGAGGCAACGCAAGCTGAGTCTTTCTCTCTGCTTC 227
60 CCAATTCGAGGCGAGCCCGCGGCGTCAATG--GCGCTCTCCGAGCTTGGGTAAGC 116
228 CCAATTCGAG-GGCAGCCCGCGGCGTCAATGCGCGCTCTCCGAGCTTGGGTAAGC 286
117 G-TGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCACTTTCTGAGTTTGA 175
287 GCTGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCACTTTCTGAGTTTGA 346
176 GTTGTCTCCCGCAACCCCGGCGTCTGCTTCTTCATCCGACCCGCGGAGC-CGAG 234
347 GTTGTCTCCCGCAACCCCGGCGTCTGCTTCTTCATCCGACCCGCGGAGC-CGAG 406
235 GACAAACAGGTGCGGAGAGCGTTTCCATTCAAGTGACTGACAGACGAC-CCAGCC 293
407 GACAAACAGGTGCGGAGAGCGTTTCCATTCAAGTGACTGACAGACGACGACGCG 466
294 CTCGGTCTGAGCCCAACGCA-CCGTAAGGCAATGCGGTAAGTCCATGCGGTAGAGA 352
467 CTCGGTCTGAGCCCAACGCAACGCAATGCGGTAAGTCCATGCGGTAGAGA 526
353 AGTGTGAGATGAGATTAACTGTCACATGAGATATGAGAGAGACCGGAGATTGGTAC 412
527 AGTGTGAGATGAGATTAACTGTCACATGAGATATGAGAGAGACCGGAGATTGGTAC 586
413 GTTACCATGTCAGCTGGGCGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472
587 GTTACCATGTCAGCTGGGCGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
473 TCCCTGCGCGCGCTCTCTCAAGTTTAACTGAGATACCACTTAAAGCCAGAGGCA 532
647 TCCCTGCGCGCGCTCTCTCAAGTTTAACTGAGATACCACTTAAAGCCAGAGGCA 706
533 CCAACCAATTAACAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGAT 592
707 CCAACCAATTAACAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGAT 766
593 GAGGTGCGCTGCTGTTGAAAGATGCGCGCTGATCACTTGAAGTGAAGTGAAGTGA 652
767 GAGGTGCGCTGCTGTTGAAAGATGCGCGCTGATCACTTGAAGTGAAGTGAAGTGA 826
653 TTGGGGCCCAACATGAGACAGTGTATTGAGGAGTACTTGAAGTGAAGTGAAGTGA 712
827 TTGGGGCCCAACATGAGACAGTGTATTGAGGAGTACTTGAAGTGAAGTGAAGTGA 886
713 CCTAGAGACTCGGCGCTTATGCTTATGCTGACAGTGAAGTGAAGTGAAGTGAAGTGA 772
887 CCTAGAGACTCGGCGCTTATGCTTATGCTGACAGTGAAGTGAAGTGAAGTGAAGTGA 946
773 TACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
947 TACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
833 GGTGGGGAAGATTTTGTGAGTGAAGACATTAACAAGAGACCAATCTGAGCAAC 892

1007 GGTGGGGAAGATTTTGTGAGTGAAGACATTAACAAGAGACCAATCTGAGCAAC 1066
893 AACAAGAGATGAGAAAGAGGCTCCATGCTGCTGCGGCAACATCTGCAAGTTTGC 952
1067 AACAAGAGATGAGAAAGAGGCTCCATGCTGCTGCGGCAACATCTGCAAGTTTGC 1126
953 TGCCAGCGCGGAGGAGAACCAATGCAACATGCGGTGCTGAAAACGGAGAGGTTT 1012
1127 TGCCAGCGCGGAGGAGAACCAATGCAACATGCGGTGCTGAAAACGGAGAGGTTT 1186
1013 AAGCAGAGCATTCGATTGAGGCTTCAAGATGCAAAACAGCATGAGCTTCAATATG 1072
1187 AAGCAGAGCATTCGATTGAGGCTTCAAGATGCAAAACAGCATGAGCTTCAATATG 1246
1073 GAATGTGTCCTTCACTGACAGGAGAAATTAATCTGTGTAGTGAAGTGAATGAGG 1132
1247 GAATGTGTCCTTCACTGACAGGAGAAATTAATCTGTGTAGTGAAGTGAATGAGG 1306
1133 TCCATCAATCAACATGACCACTGATGTTGAGAGCATGCTCACCGGCCATCTTC 1192
1307 TCCATCAATCAACATGACCACTGATGTTGAGAGCATGCTCACCGGCCATCTTC 1366
1193 CAAGCCGAGCTGCGGCAATGCTTCAAGTGTGAGAGAGAGTGAAGTTTGTCTGC 1252
1367 CAAGCCGAGCTGCGGCAATGCTTCAAGTGTGAGAGAGAGTGAAGTTTGTCTGC 1426
1253 AAGTTTACATGATGCTTCAAGTGTGAGAGAGAGTGAAGTTTGTCTGC 1312
1427 AAGTTTACATGATGCTTCAAGTGTGAGAGAGAGTGAAGTTTGTCTGC 1486
1313 AGTAATGCGGCGCGGAGGCTGCTTCAAGTGTGAGAGAGTGAAGTTTGTCTGC 1372
1487 AGTAATGCGGCGCGGAGGCTGCTTCAAGTGTGAGAGAGTGAAGTTTGTCTGC 1546
1547 AGTTCAATGCAAGAGTCTGCTGCTTCAAGTGTGAGAGAGTGAAGTTTGTCTGC 1606
1433 AATGTGAAGTCTTCAATTAATTAAGGAGGCAACAGTCTGCTGCTGCTGCTGCTG 1492
1607 AATGTGAAGTCTTCAATTAATTAAGGAGGCAACAGTCTGCTGCTGCTGCTGCTG 1666
1493 CCAAAACAGCAAGCCCTGAGAGAGAGAGATTAAGTCTTCCCAAGTGAAGTGA 1552
1667 CCAAAACAGCAAGCCCTGAGAGAGAGAGATTAAGTCTTCCCAAGTGAAGTGA 1726
1553 AATGCAATTAATGAGAGTCTTCTTAATGCTGATGATGATGATGATGATGATGAT 1612
1727 AATGCAATTAATGAGAGTCTTCTTAATGCTGATGATGATGATGATGATGATGAT 1786
1613 TGCCAGATGAGAGACAGACCAAGAGAGGCTTCAAGAGCAGCCGCTGCTGCAAG 1672
1787 TGCCAGATGAGAGACAGACCAAGAGAGGCTTCAAGAGCAGCCGCTGCTGCAAG 1846
1673 CTGACCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1732
1847 CTGACCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1906
1733 ATGAATCTCAACACCCGCTGATGAGATTAACAACGCTTCTTCAACGCGCAGAC 1792
1907 ATGAATCTCAACACCCGCTGATGAGATTAACAACGCTTCTTCAACGCGCAGAC 1966
1793 CCAATGCTGCGAGGCTTCCAGATGATTAATCTTCAAGAGAGCCCAAAATGGAAGTTTCA 1852
1967 CCAATGCTGCGAGGCTTCCAGATGATTAATCTTCAAGAGAGCCCAAAATGGAAGTTTCA 2026
1853 AAGAGATGAGTGAACCTGCGGCAAGCCCTGAGAGAGGTTGCTTGGGCAATGCTCATG 1912
2027 AAGAGATGAGTGAACCTGCGGCAAGCCCTGAGAGAGGTTGCTTGGGCAATGCTCATG 2086
1913 GCGGAGCAGTGGAGATTGAACAAGACAGCCCAAGAGAGGCGGTCACTGCGCGTGAAG 1972
2087 GCGGAGCAGTGGAGATTGAACAAGACAGCCCAAGAGAGGCGGTCACTGCGCGTGAAG 2146

OY	1973	ATGTTGAAAGATGATGGCCACAGAGAAAGACCTTTCGATCGTGTGTCAGAGATGGAGATG	2032
Db	2147	ATGTTGAAAGATGATGGCCACAGAGAAAGACCTTTCGATCGTGTGTCAGAGATGGAGATG	2206
OY	2033	ATGAAGATGATTTGGGAAACAACAAGAAATATATAAATCTTCTTGAGACCTGACACAGAT	2092
Db	2207	ATGAAGATGATTTGGGAAACAACAAGAAATATATAAATCTTCTTGAGACCTGACACAGAT	2266
OY	2093	GGGCGCTCTATGTTCATGCTTGAGTATGCTCTTAAAGGCAACCTCCGAGAAATACCTCCGA	2152
Db	2267	GGGCGCTCTATGTTCATGCTTGAGTATGCTCTTAAAGGCAACCTCCGAGAAATACCTCCGA	2326
OY	2153	GCCCGGAGGCCACCCGGGATGGAGTACCTCATATGACATTAACCGTGTCTCTGAGAGCAG	2212
Db	2327	GCCCGGAGGCCACCCGGGATGGAGTACCTCATATGACATTAACCGTGTCTCTGAGAGCAG	2386
OY	2213	ATGACCTTCAAGAGACTTGTGTCAATGACCTTACAGCTGCGCAGACGATGAGATCTTG	2272
Db	2387	ATGACCTTCAAGAGACTTGTGTCAATGACCTTACAGCTGCGCAGACGATGAGATCTTG	2446
OY	2273	GCTTCCCAAAATGATGATCATGAGATTGAGACCCGAAATGTTTGGTATACAGAAAC	2332
Db	2447	GCTTCCCAAAATGATGATCATGAGATTGAGACCCGAAATGTTTGGTATACAGAAAC	2506
OY	2333	AATGTGATGAAATAATGACAGACTTTTGAATCTGCGCAGAGATATCAACAATATATGACTATAC	2392
Db	2507	AATGTGATGAAATAATGACAGACTTTTGAATCTGCGCAGAGATATCAACAATATATGACTATAC	2566
OY	2393	AAAAAGACCAACAATGGGCGGCTTCCAGTAAAGTGAATGGCTCCAGAAAGCCGTGTTGAT	2452
Db	2567	AAAAAGACCAACAATGGGCGGCTTCCAGTAAAGTGAATGGCTCCAGAAAGCCGTGTTGAT	2626
OY	2453	AGAGATATCACTCATCAGAGTATGTGTGCTCTCTCGGGGTGTAAATGTGGAGATCTTC	2512
Db	2627	AGAGATATCACTCATCAGAGTATGTGTGCTCTCTCGGGGTGTAAATGTGGAGATCTTC	2686
OY	2513	ACTTTAGGGGGCTCGCCCTTACCCAGGGATTCCTCGTAGAGAACTTTTAAAGCTGCTGAA	2572
Db	2687	ACTTTAGGGGGCTCGCCCTTACCCAGGGATTCCTCGTAGAGAACTTTTAAAGCTGCTGAA	2746
OY	2573	GAAGGACACAGAAATGATTAAGCAGACCAAATGCAACAAGAACTGTACATGATGATGAG	2632
Db	2747	GAAGGACACAGAAATGATTAAGCAGACCAAATGCAACAAGAACTGTACATGATGATGAG	2806
OY	2633	GACTGTGGCATGTCAGTGCCTCCACAGACCAAAGTTCAGACAGTTGTGTGAAGAATTG	2692
Db	2807	GACTGTGGCATGTCAGTGCCTCCACAGACCAAAGTTCAGACAGTTGTGTGAAGAATTG	2866
OY	2693	GATCGAATTCATCTCTCAACAACAATGAGAAATCTTGGACCTCAGCAACCTCTGAA	2752
Db	2867	GATCGAATTCATCTCTCAACAACAATGAGAAATCTTGGACCTCAGCAACCTCTGAA	2926
OY	2753	CAGTATTCACATGATTACCTCTGACCAAGAAGTCTTGTCTTCCAGAGATGATCTGTT	2812
Db	2927	CAGTATTCACATGATTACCTCTGACCAAGAAGTCTTGTCTTCCAGAGATGATCTGTT	2986
OY	2813	TTTTCTCCAGACCCCAATGCTTTACGAAACATGCTTCTCAAGTATCCAACAATAAGGC	2872
Db	2987	TTTTCTCCAGACCCCAATGCTTTACGAAACATGCTTCTCAAGTATCCAACAATAAGGC	3046
OY	2873	AGGTGTTAAACATGATGATGCTGTGCTGCTCTCCCAAAACAGACACACACTGAGAACT	2932
Db	3047	AGGTGTTAAACATGATGATGCTGTGCTGCTCTCCCAAAACAGACACACACTGAGAACT	3106
OY	2933	AGCTACACTGAGACGGGAGACCATGCTCCAGACCTTGTGTCTCACTTGATATATG	2992
Db	3107	AGCTACACTGAGACGGGAGACCATGCTCCAGACCTTGTGTCTCACTTGATATATG	3166
OY	2993	GATCAGAGAGATTAATATTTGAAAAAGTAATAGCAATATGTGTAAAGATTTATACAGT	3052
Db	3167	GATCAGAGAGATTAATATTTGAAAAAGTAATAGCAATATGTGTAAAGATTTATACAGT	3226

```

QY      3053 AAAACTGTATCTTCCCGAGAGAGAAGGTTTCGTGAGCAGTGACCTGC 3106
        |||
DB      3227 AAACCTGTATCTTCCCGAGAGAGAAGGTTCTGGAGCATGGACTGC 3280

RESULT 4
US-11-019-829-39
; Sequence 39, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: fibroblast growth factor receptor 2 transcript variant 2
; LOCATION: (1)..(4574)
; OTHER INFORMATION: LocusID: 2263; NM_022369
US-11-019-829-39

Query Match          97.0%; Score 3013.2; DB 13; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7.
```

Qy	1	CCCGGAGGAAAGTTTGGGAGGGAAAG-CAGAGCTAGTCTTTCTCTCTGCTCC	59
Db	168	CTGCGAGCAAAAGTTTGGTGGAGGCAAGCCAAAGCTAGTCTTTCTCTCTGCTCC	227
Qy	60	CCAAATCCGAGGGCAGAGCCCGGAGCGTCAATG--GCGTCTCTCCGACGCTGGGTATAGC	116
Db	228	CCAAATCCGA-GGAGAGCCGCGGGGCGTATGCGCGCTCTCCGACGCTGGGGTACGC	286
Qy	117	G-TGAAGCCCGGAGGCTTGGGCGGAGCAAGCCAAAGACCATCTTCTTGCTTTGGGA	175
Db	287	GCTGAAGCCCGGAGGCTTGGCGCGGCGGAACCCAGAGACCATCTTCTTGCTTTGGGA	346
Qy	176	GTTGCTCCCCGCAACCCCGGAGCTGTCGCTTTCTCATCCGACCCAAGCGGGGC-CGGG	234
Db	347	GTTGCTCCCCACAACCCCGGAGCTGTCGCTTTCTCATCTCCAGCCAGCGGGAGCGGGG	406
Qy	235	GACAAACAAGTTCGCGGAGAGAGCGTTGGCAATCAAGTACATGACAGAGAGC-AGCAGCG	293
Db	407	GACAAACAAGTTCGCGGAGAGAGCGTTGGCAATCAAGTACTGACAGAGAGCGGAGCGC	466
Qy	294	CTCGGTTCTGAGCCACCGCA-GCTGAAGGCAATGCGGTAAGTCATGCCGTGAGGA	352
Db	467	CTCGGTTCTGAGCCACCGCAGGCTGAAGGCAATGCGGTAAGTCATGCCGTGAGGA	526
Qy	353	AGTGTGAGATGGGATTTAAGTCCACATGGAATATGGAAGGAGCCGGGAAATGGTACC	412
Db	527	AGTGTGAGATGGGATTTAAGTCCACATGGAATATGGAAGGAGCCGGGAAATGGTACC	586
Qy	413	GTAACATGATGAGCTGGGGTGGTTTCATCTGCTGGTGGTGCATCAATGGCAACTTGG	472
Db	587	GTAACATGATGAGCTGGGGTGGTTTCATCTGCTGGTGGTGCATCAATGGCAACTTGG	646
Qy	473	TCCCTGGCCCGGCGCTCTTCAGTTTAAGTTGAGGACACATTTGAGGCAAGAAGGCA	532
Db	647	TCCCTGGCCCGGCGCTCTTCAGTTTAAGTTGAGGATACACATTTGAGGCAAGAAGGCA	706
Qy	533	CAAACCAATATCAAATCTCTCAACCAAGAAGTACGTGAGTCGCGCAGGGAGTGGCTA	592
Db	707	CAAACCAATATCAAATCTCTCAACCAAGAAGTACGTGAGTCGCGCAGGGAGTGGCTA	766
Qy	593	GAGTGGCTGCTGTTGAAAGATGCCCGGATGATCAATTGAATCTAAGATGGAGGTGCAC	652

Db 767 GAGGTGCGTGTCTGTTGAAGAATGCCGCGTGATCATGTTGACCTAAGATGGGGTGCAAC 826
Qy 653 TTGGGGCCCAACATATGAGACATGCTTTATTTGGGAGTACTTGGAGATTAAGGGCCGCAAC 712
Db 827 TTGGGGCCCAACATATGAGACATGCTTTATTTGGGAGTACTTGGAGATTAAGGGCCGCAAC 886
Qy 713 CCTAGAGACTCCGGCCCTATGCTTGTATCTGCCAGTATGAGCTGTAGACATGTGAACCTTGG 772
Db 887 CCTAGAGACTCCGGCCCTATGCTTGTATCTGCCAGTATGAGCTGTAGACATGTGAACCTTGG 946
Qy 773 TACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
Db 947 TACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
Qy 833 GGTGCGGAAGATTTTGTCACTGATGAACATGTAACAACAAGAGACACCATATCTGAGACCAAC 892
Db 1007 GGTGCGGAAGATTTTGTCACTGATGAACATGTAACAACAAGAGACACCATATCTGAGACCAAC 1066
Qy 893 ACGAAGAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCGCAACACTGTCAAGTTTCCG 952
Db 1067 ACGAAGAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCGCAACACTGTCAAGTTTCCG 1126
Qy 953 TGCCACGCGGGGGGGAACCCATATGCAACCATATGCGGTGCTGAAAAACGGGAGAGATT 1012
Db 1127 TGCCACGCGGGGGGGAACCCATATGCAACCATATGCGGTGCTGAAAAACGGGAGAGATT 1186
Qy 1013 AAGCAGAGAGATGCAATTTGAGAGGCTCAAGGTACGAACCAAGCATGTGAGCTCATTTATG 1072
Db 1187 AAGCAGAGAGATGCAATTTGAGAGGCTCAAGGTACGAACCAAGCATGTGAGCTCATTTATG 1246
Qy 1073 GAAAGTGTGTCCATCTGACAAAGGAAATTAACCTGTGTATGAGAGATGAATATG 1132
Db 1247 GAAAGTGTGTCCATCTGACAAAGGAAATTAACCTGTGTGTATGAGAGATGAATATG 1306
Qy 1133 TCCATCAATCAACATGACCACTGATGTTGTGAGAGCATGCGCTCAACGCGCCATCTCTC 1192
Db 1307 TCCATCAATCAACATGACCACTGATGTTGTGAGAGCATGCGCTCAACGCGCCATCTCTC 1366
Qy 1193 CAAGCCGACTGCGGCAAAATGCTTCCACATGCTGTGAGAGAGAGATGAGATTGTCTCG 1252
Db 1367 CAAGCCGACTGCGGCAAAATGCTTCCACATGCTGTGAGAGAGAGATGAGATTGTCTCG 1426
Qy 1253 AAGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
Db 1427 AAGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
Qy 1313 AATTAATACGAGGCGCGGCTGCTTACCTCAAGGTTCTCAAGCACTCGGGATTAAT 1372
Db 1487 AATTAATACGAGGCGCGGCTGCTTACCTCAAGGTTCTCAAGCACTCGGGATTAAT 1546
Qy 1373 AGTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
Db 1547 AGTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
Qy 1433 ATATGTAAGTCTTCAATTTATATAGGAGAGGCAACATGCTGTGCTCACTGTCTCG 1492
Db 1607 ATATGTAAGTCTTCAATTTATATAGGAGAGGCAACATGCTGTGCTCACTGTCTCG 1666
Qy 1493 CCAAAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1552
Db 1667 CCAAAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1726
Qy 1553 ATAGCAATTTACTGATAGGGGTCTTCTTAATGCGCTGTATGATGATGATGATGATGATGATGATGAT 1612
Db 1727 ATAGCAATTTACTGATAGGGGTCTTCTTAATGCGCTGTATGATGATGATGATGATGATGATGATGAT 1786
Qy 1613 TGCCGATGAGAAACAGACCAAGAGAGGCACTTACAGCAGCGAGCGGTGTGCAAG 1672
Db 1787 TGCCGATGAGAAACAGACCAAGAGAGGCACTTACAGCAGCGAGCGGTGTGCAAG 1846
Qy 1673 CTGACCAAAAGTATCCCTGCGGAGAGACAGTTAAAGTTTCGCTGAGTCACTCTCTC 1732
Db 1847 CTGACCAAAAGTATCCCTGCGGAGAGACAGTTAAAGTTTCGCTGAGTCACTCTCTC 1906

Qy 1733 ATGAATCTCAACACCCGCTGTGAGATTAACAACGCTCTCTTCAACGGCAGACAC 1792
Db 1907 ATGAATCTCAACACCCGCTGTGTAGATTAACAACGCTCTCTTCAACGGCAGACAC 1966
Qy 1793 CCCATGCTGAGAGGGGTCTCCAGATGATGAACCTTCCAGAGAACCAAAATGGAGTTTCCA 1852
Db 1967 CCCATGCTGAGAGGGGTCTCCAGATGATGAACCTTCCAGAGAACCAAAATGGAGTTTCCA 2026
Qy 1853 AAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGGTCAAG 1912
Db 2027 AAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGGTCAAG 2086
Qy 1913 GGGGAAGAGTGGGAATTGACAAAGACAAGCCCAAGAGAGCGGTCAAGCTGGCCGTGAAG 1972
Db 2087 GGGGAAGAGTGGGAATTGACAAAGACAAGCCCAAGAGAGCGGTCAAGCTGGCCGTGAAG 2146
Qy 1973 ATGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2032
Db 2147 ATGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
Qy 2033 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
Db 2207 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2266
Qy 2093 GGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2152
Db 2267 GGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
Qy 2153 GCCCGAGGCGCACCGGGAGTGAAGTACTCTATGACATTAACCGTGTCTTGAGAGAGCAG 2212
Db 2327 GCCCGAGGCGCACCGGGAGTGAAGTACTCTATGACATTAACCGTGTCTTGAGAGAGCAG 2386
Qy 2213 ATGACCTTCAAGAGCTTGTGTATGACACTTACAGCTGCGCAGACGATGAGATCTTG 2272
Db 2387 ATGACCTTCAAGAGCTTGTGTATGACACTTACAGCTGCGCAGACGATGAGATCTTG 2446
Qy 2273 GCTTCCCAAAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2332
Db 2447 GCTTCCCAAAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2506
Qy 2333 AATGAT 2392
Db 2507 AATGAT 2566
Qy 2393 AAAAAACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGCTTCCAGAACCCCTGTTGAT 2452
Db 2567 AAAAAACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGCTTCCAGAACCCCTGTTGAT 2626
Qy 2453 AAGATTAACCTCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2512
Db 2627 AAGATTAACCTCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2686
Qy 2513 ACTTTAGGGGAGTCCGCTTACCAAGGATTCCTGAGAGAACTTTTAAGCTGTGAAG 2572
Db 2687 ACTTTAGGGGAGTCCGCTTACCAAGGATTCCTGAGAGAACTTTTAAGCTGTGAAG 2746
Qy 2573 GAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2632
Db 2747 GAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2806
Qy 2633 GACTGTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2692
Db 2807 GACTGTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2866
Qy 2693 GATGCAATTTCTCACTCTCAACAACATGAGAGATCTTGAAGCTGAGCCTGCAACCTCTCGAA 2752
Db 2867 GATGCAATTTCTCACTCTCAACAACATGAGAGATCTTGAAGCTGAGCCTGCAACCTCTCGAA 2926
Qy 2753 CAGTATTCACCTAGTTACCTTGAACAAGAGTTCTTGTCTTCAAGAGATGATTTCTGTT 2812
Db 2927 CAGTATTCACCTAGTTACCTTGAACAAGAGTTCTTGTCTTCAAGAGATGATTTCTGTT 2986

OY	2815	TTTTCTCCAGACCCCAGGCCCTTTAGAAACGAGCCCTCCTCAATATTCACAATAAAGGC	2872
Db	2987	TTTTCTCCAGACCCCAGGCCCTTTAGAACCAAGCCCTTCTCAATATTCACAATAAAGGC	3046
OY	2873	AGTGTTAAAAATGATGATGACTGTGTCTGTCTGTCCCCAAGAGAAGCACTGGAAAATT	2932
Db	3047	AGTGTTAAAAATGATGATGACTGTGTCTGTCTGTCCCCAAGAGAAGCACTGGAAAATT	3106
OY	2993	AGCTAACATGACGAGGAGACCAAGSCCTCCAGAGCTGTGTCTCCACTGTATATATG	2992
Db	3107	AGCTAACATGAGCGAGGAGACCATGSCCTCCAGAGCTGTGTGTCTCCACTGTATATATG	3166
OY	2993	GATCAGAGAGTAATAATTTGGAAAAAGTATCATCATATGTGTAAAGATTATACAGTTG	3052
Db	3167	GATCAGAGAGTAATAATTTGGAAAAAGTATCATCATATGTGTAAAGATTATACAGTTG	3226
OY	3053	AAAACTTGTAATCTTCCCGAGAGGAAGAAAGTTTGGAGCGAGTAGACATGC	3106
Db	3227	AAAACTTGTAATCTTCCCGAGAGGAAGAAAGTTTCTGGAGCATGTGACATGC	3280

```

RESULT 5
US-11-072-175-132
; Sequence 132, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-132

```

Query Match	97.0%;	Score 3013.2;	DB 16;	Length 4574;
-------------	--------	---------------	--------	--------------

Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7.

QY	1	CCCGGAGCAAGTTTGATGAGGCAAG-CAGAGCTGAGTCTTTCTCTCTGCTGC	59
Db	168	CTCGGAGCAAGTTTGGTGAAGGCAAGCCAAAGCTGAGTCTTTCTCTCTGTTCC	227
QY	60	CCAAATCCGAGGGCAAGCCCGGGGCGTATG--GAGCTCTCCGACGCTGGGGTAAAG	116
Db	228	CCAAATCCGA-GGAGAGCCCGCGAGGCGTATGCGCGGCTCTCCGAGCTGGGGTAAAGC	286
QY	117	G-TGAAGCCCGGAGGCTTGCGCGCGGCGCAAGCCAAAGACACACTCTTCTGCGTTTGA	175
Db	287	GCTGAAGCCCGGAGGCTTGCGCGCGGCGCAAGCCAAAGACACACTCTTCTGCGTTTGA	346
QY	176	GTTTGCTCCCGCAACCCCGGGCTCGTGCCTTTCTCATCCGACCCAGCGGGGGC-CGGG	234
Db	347	GTTTGCTCCCGCAACCCCGGGCTCGTGCCTTTCTCATCCGACCCAGCGGGGGCGCGGG	406
QY	235	GACAAACAAGTGGCGAGAGAGGTGCATTCAAGTGACTCAGACAGAGC-GCAGAGGC	293
Db	407	GACAAACAAGTGGCGAGAGAGGTGGCCATTCAAGTGACTCAGAGAGCAGAGGCGAGGC	466
QY	294	CTCGGTTCTGAAGCCACCGCA-GCTGAAGGCAATTGCGGTAGTCCATATCCCTGTAGAGA	352
Db	467	CTCGGTTCTGAAGCCACCGCAGGCTGAAGGCAATTGCGGTAGTCCATATCCCTGTAGAGA	526

OY		353	AGCTGTGAGATGGGATTAAAGTCCAAATGGAGAATAAGAAAGAGACCGGGGACTTTGGTACC	412
Db		527	AGGTGTGAGATGGGATTAAAGTCCTCAATGGAGATTATGAAGAGAACCGGGGATTTGGTACC	586
OY		413	GTAACCAATGGTACAGCTGGGGTGCTTTTCATCTGCCTGGTCTGTGTCAACAATGCAACTTGG	472
OY		473	TCCCTGGCCCCGCCCTCCTTCAAGTTTAGTTTAGAGATTACCATTTAAGCCAGAAAGGCCA	532
Db		647	TCCCTGGCCCCGCCCTCCTTCAAGTTTAGTTTAGAGATTACCATTTAAGCCAGAAAGGCCA	706
OY		533	CCAACCAAATAACCAATCTCTCAACCAAGAGTGAAGTGCCTGGCCAGGGGAGTGCCTA	592
Db		707	CCAAACCAAATAACCAATCTCTCAACCAAGAGTGAAGTGCCTGGCCAGGGGAGTGCCTA	766
OY		593	GAGGTGGCGTGCCTGTGTGAAAAGATGCCGCCGTGATCAGTTTGAATAAGATGGGGTGCAC	652
Db		767	GAGGTGGCGTGCCTGTGTGAAAAGATGCCGCCGTGATCAGTTTGAATAAGATGGGGTGCAC	826
OY		653	TTGGGGGCCCAACAAATAGACAGTGCCTTATTTGGGGAGTACTTTCAGATTAAGCGCGCCACA	712
Db		827	TTGGGGGCCCAACAAATAGACAGTGCCTTATTTGGGGAGTACTTTCAGATTAAGCGCGCCACA	886
OY		713	CCTTAGAGACTCCGCCCTCTATAGCTTTGTATCTGCCAGTATGAGACTGTAAACCTTGG	772
Db		887	CCTTAGAGACTCCGCCCTCTATAGCTTTGTATCTGCCAGTATGAGACTGTAAACCTTGG	946
OY		773	TACTTCAATGATGAATGTCAACAGATGCCATCTATCCGAGATGATGAGATGACACCGAT	832
Db		947	TACTTCAATGATGAATGTCAACAGATGCCATCTATCCGAGATGATGAGATGACACCGAT	1006
OY		833	GGTGGGAAAGATTTTGTCAGTGAGAACAGTAAACAACAAGAGACCACTACTTGGACCAAC	892
Db		1007	GGTGGGAAAGATTTTGTCAGTGAGAACAGTAAACAACAAGAGACCACTACTTGGACCAAC	1066
OY		893	AACAAAAAGATGAAAAAGCGGCTCAATGCTGTGCTGGCCCAACATCTCAAGTTTCCG	952
Db		1067	AACAAAAAGATGAAAAAGCGGCTCAATGCTGTGCTGGCCCAACATCTCAAGTTTCCG	1126
OY		953	TGCCCAAGCCGGGGGGGAAACCAATCCCAACCAATGCGGTGAGTGAATAACCGGAAAGAGTTT	1012
Db		1127	TGCCCAAGCCGGGGGGGAAACCAATCCCAACCAATGCGGTGAGTGAATAACCGGAAAGAGTTT	1186
OY		1013	AAGCAGAGCATCGCATTTGAGGCTACAAAGGTACGAAACGACACTGAGCTCTCATTAATG	1072
Db		1187	AAGCAGAGCATCGCATTTGAGGCTACAAAGGTACGAAACGACACTGAGCTCTCATTAATG	1246
OY		1073	GAAAGTGTGTCCATCTGTCAAGGAAATTTATCTGTGTATGTGAGAAATGAATAACGGG	1132
Db		1247	GAAAGTGTGTCCATCTGTCAAGGAAATTTATCTGTGTGTGAGAAATGAATAACGGG	1306
OY		1133	TCCATCAATCACAGSTACCACTGTGATTTGTGAGAGCATGCTCTCACCGGCCCATCTCTC	1192
Db		1307	TCCATCAATCACAGSTACCACTGTGATTTGTGAGAGCATGCTCTCACCGGCCCATCTCTC	1366
OY		1193	CAAGCCGAGCTTGC CGGCAAAATGCTCTCAACAGTGTGCGAGGAGACGTAGAATTGTCTGC	1252
Db		1367	CAAGCCGAGCTTGC CGGCAAAATGCTCTCAACAGTGTGCGAGGAGACGTAGAATTGTCTGC	1426
OY		1253	AAGTTTACATGATATGCCAGGCCCAATCTCAATCGATGTATCAAGCATCTGTGAAAACAAACCGC	1312
Db		1427	AAGTTTACATGATATGCCAGGCCCAATCTCAATCGATGTATCAAGCATCTGTGAAAACAAACCGC	1486
OY		1313	AGTAATAATACGGGCCCGGACGGGGCTGCCAATCAAGGTTCTCAAGCATCTGGGGGATAAT	1372
Db		1487	AGTAATAATACGGGCCCGGACGGGGCTGCCAATCAAGGTTCTCAAGCATCTGGGGGATAAT	1546
OY		1373	AGTTTCAATGACGAAGTGTGCTCTGTTCATGTATGACCGAGCGCGATGCTGGGGAAATAT	1432
Db		1547	AGTTTCAATGACGAAGTGTGCTCTGTTCATGTATGACCGAGCGCGATGCTGGGGAAATAT	1606
OY		1433	ATATGTAAAGTCTCCAAATTATATAGGAGCGCAACAGTCTGCTGCTCACTGT CCTG	1492

OY	117	GTGAAGCCCGGGAGAGCTTGGCGCGCGGGAGAACCCAAAGACCAACTCTTCTGCGCTTGGAG	176
Db	288	GTGAAGCCCGGGAGAGCTTGGCGCGCGGGAGAACCCAAAGACCAACTCTTCTGCGCTTGGAG	347
OY	177	TTTGCTCCCCGCAACCCCGGGGCTCGTGGCTTTCTTCATCCCGAACCAAGCGCGGAGC	235
Db	348	TTTGCTCCCCCAACCCCGGGGCTCGTGGCTTTCTTCATCCCGAACCAAGCGCGGAGC	407
OY	236	ACAAACAAGTCGCGAGAGACGTTTGCATTCAAGTACCTGCAGACAGC	294
Db	408	ACAAACAAGTCGCGAGAGAGCTTGGCATTCAGTACCTGCAGACAGCAGCGC	467
OY	295	TCGGTTCCTGAGCCCAACCGCA-GCTGAAGGACTTGGCGCTGATCCATGCCCCGTAAGAGAA	353
Db	468	TCGGTTCCTGAGCCCAACCGCAGGCTGAAGGACTTGGCGCTGATCCATGCCCCGTAAGAGAA	527
OY	354	GTGTCACAATGGGAATTAAAGTCCAATGGAGATATGGAAAGAGACCGGGGATTGTATCG	413
Db	528	GTGTCACAATGGGAATTAAAGTCCAATGGAGATATGGAAAGAGACCGGGGATTGTATCG	587
OY	414	TAACCATGTCAGCTGGGGTGGTTTCATCTGCGCTGCTGCTGATCCATGCGCAACTTGT	473
Db	588	TAACCATGTCAGCTGGGGTGGTTTCATCTGCGCTGCTGCTGATCCATGCGCAACTTGT	647
OY	474	CCCTGGCCCGGCGCTCTCTCACTTAACTTGAAGATACCACTTGAACCCAAAGACAC	533
Db	648	CCCTGGCCCGGCGCTCTCTCACTTAACTTGAAGATACCACTTGAACCCAAAGACAC	707
OY	534	CAACCAATACCAATCTCTCAACCAAGATGTACGTGGCTGCGCACGAGGAGTGGCTAG	593
Db	708	CAACCAATACCAATCTCTCAACCAAGATGTACGTGGCTGCGCACGAGGAGTGGCTAG	767
OY	594	AGGTGCGCTGCTGTGGAAGATGCGCGCTGATCACTTGGACTTAAGGATGGGTGACT	653
Db	768	AGGTGCGCTGCTGTGGAAGATGCGCGCTGATCACTTGGACTTAAGGATGGGTGACT	827
OY	654	TGGGCGCCCAATGACAGTGGCTTATTTGGGAGTACTTGCAGATTAAGGCGCCAC	713
Db	828	TGGGCGCCCAATGACAGTGGCTTATTTGGGAGTACTTGCAGATTAAGGCGCCAC	887
OY	714	CTAGAGACTCCGGGCTCTATGCTTATCTGCGCAGTGAAGCTGTGAACAGTAACTTGGT	773
Db	888	CTAGAGACTCCGGGCTCTATGCTTATCTGCGCAGTGAAGCTGTGAACAGTAACTTGGT	947
OY	774	ACTTCATGTCATGTCACAGATGTCATCTCATCCGAGATGATGAGATGACCGATG	833
Db	948	ACTTCATGTCATGTCACAGATGTCATCTCATCCGAGATGATGAGATGACCGATG	1007
OY	834	GTGCGAGATTTTGTCACTGAGAACAGTAAACAAACAAAGACCACTATCTGACCAACA	893
Db	1008	GTGCGAGATTTTGTCACTGAGAACAGTAAACAAACAAAGACCACTATCTGACCAACA	1067
OY	894	CAGAAAAGATGAAAAAGCGGCTCCATGCTGTCGCGGCGCAACCTGTCAAGTTTGCT	953
Db	1068	CAGAAAAGATGAAAAAGCGGCTCCATGCTGTCGCGGCGCAACCTGTCAAGTTTGCT	1127
OY	954	GCCACGCGGGGGAGAACCAATGCCCAACCATGCGGTGCTGAAAAACGGAGAGATTTA	1013
Db	1128	GCCACGCGGGGGAGAACCAATGCCCAACCATGCGGTGCTGAAAAACGGAGAGATTTA	1187
OY	1014	AGCAGAGCATGTCATTGGAGGCTACAGGTACGAACCAAGCACTGAGACCTCATTTATGG	1073
Db	1188	AGCAGAGCATGTCATTGGAGGCTACAGGTACGAACCAAGCACTGAGACCTCATTTATGG	1247
OY	1074	AAAGTCGTCCATCTGACAAAGGAAATTAACTGTGTGATGAGAAATATACGGGT	1133
Db	1248	AAAGTCGTCCATCTGACAAAGGAAATTAACTGTGTGATGAGAAATATACGGGT	1307
OY	1134	CCATCAATCAACGTACCACTGATGTGTGAGCGATCGCTTACCGGCTCATCTCC	1193
Db	1308	CCATCAATCAACGTACCACTGATGTGTGAGCGATCGCTTACCGGCTCATCTCC	1367
OY	1194	AAAGCGAGTCCCGCAATTCGCTCCACAGTGTGAGAGAGACGTAACTTGTCTCA	1253

Db	1368	AAGCCGACATGCGCGCAAAATGCTCCACAGTGGTCGAGGAGACGTAGAGTTGTCTGCA	1427
QY	1254	AGGTTTACAGTATGCGCCAGCCCAATCCAGTGGATCAAGCACTGTGAAAAGAACGGCA	1313
Db	1428	AGGTTTACAGTATGCGCCAGCCCAATCCAGTGGATCAAGCACTGTGAAAAGAACGGCA	1487
QY	1314	GTAAATACGGGCGCGGAGCTGCTCTGTCTCAAGGTTCTCAGACTCGGGATTAATA	1373
Db	1488	GTAAATACGGGCGCGGAGCTGCTCTGTCTCAAGGTTCTCAGACTCGGGATTAATA	1547
QY	1374	GTTCCATGCAAGTGTCTGTCTGT-----TCATGTGACCGAGCGGATGCTGAGG	1427
Db	1548	CCAGGACAAAGAAATGAGGTTCTCTAATTTCCGAATGTACTTTGAGAGCGTGGGG	1607
QY	1428	AATATATATGAAGTGTCTCCAAATATATAGGGCAGGCAACAGTGTGCTGCTCACTG	1487
Db	1608	AATATACGTGCTTGGCGGGATTTCTATGTGGAAATCTCTTCACTGTGCAATGTGACAG	1667
QY	1488	TCCTGCCAAAACAGCAAGCGCTTGGAAGAGAAAGAGATTACAGTTTCCCGACATACC	1547
Db	1668	TTCTGGC-----AGCGCTGGAAGAGAAAGAGATTACAGTTTCCCGACATACC	1718
QY	1548	TGAGATATGCCATTTACTGTCTATAGGGTCTTAAACGCTGTATATGTGTATACGTCA	1607
Db	1719	TGAGATATGCCATTTACTGTCTATAGGGTCTTAAACGCTGTATATGTGTATACGTCA	1778
QY	1608	TCCTGTGCCAATGAAAGAACAGCAACAAAGAACGACATTCAGACGACGCGCTGTGC	1667
Db	1779	TCCTGTGCCAATGAAAGAACAGCAACAAAGAACGACATTCAGACGACGCGCTGTGC	1838
QY	1668	ACAAAGCTGACCAAAAGTATCCCTCTGCGGAGACAGTAAAGTTTCGCTGATGTACCT	1727
Db	1839	ACAAAGCTGACCAAAAGTATCCCTCTGCGGAGACAGTAAAGTTTCGCTGATGTACCT	1898
QY	1728	CCTCATTAATCTCCAAACACCCCGCTGTGTGAAGATTAACAACGCGTCTTCAACGGCAG	1787
Db	1839	CCTCATTAATCTCCAAACACCCCGCTGTGTGAAGATTAACAACGCGTCTTCAACGGCAG	1958
QY	1788	ACACCCCATGCTGGCAGGGGTCTCCAGTATGTAACTTCAGAGGACCCAATATGGGAGT	1847
Db	1959	ACACCCCATGCTGGCAGGGGTCTCCAGTATGTAACTTCAGAGGACCCAATATGGGAGT	2018
QY	1848	TTCCAAAGATTAAGCTGACACTGTGGCAAGCCCTGTGGAGAAAGTTTCTTGGGCAATGG	1907
Db	2019	TTCCAAAGATTAAGCTGACACTGTGGCAAGCCCTGTGGAGAAAGTTTCTTGGGCAATGG	2078
QY	1908	TCATGGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCG	1967
Db	2079	TCATGGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCG	2138
QY	1968	TGAATATGTGAATAATGATGTCACAGAGAAAGCCTTCTGTATCTGTGTACAGATATGG	2027
Db	2139	TGAATATGTGAATAATGATGTCACAGAGAAAGCCTTCTGTATCTGTGTGTACAGATATGG	2198
QY	2028	AGATGATGAAGATGATGGGAAACAAAGAAATATCAATAATCTTCTGAGCGCTGCACAC	2087
Db	2199	AGATGATGAAGATGATGGGAAACAAAGAAATATCAATAATCTTCTGAGCGCTGCACAC	2258
QY	2088	AGGATGGGCTTCTTATGTCAATGTTGAATATGCTCTTAAAGGCAACCTCCGAGAAATAC	2147
Db	2259	AGGATGGGCTTCTTATGTCAATGTTGAATATGCTCTTAAAGGCAACCTCCGAGAAATAC	2318
QY	2148	TCGAGGCCGAGGAGCACCCGGAGTGAAGTACTCTATGACATTTAACGCTGTCTGAGG	2207
Db	2319	TCGAGGCCGAGGAGCACCCGGAGTGAAGTACTCTATGACATTTAACGCTGTCTGAGG	2378
QY	2208	AGCAGATGACTTCAAGACTTGTGTCAATGCACTTACACGCTGGCCAGACGATGAGT	2267
Db	2379	AGCAGATGACTTCAAGACTTGTGTCAATGCACTTACACGCTGGCCAGACGATGAGT	2438
QY	2268	ACTTGGCTTCCAAAATGATATTCATCGAGATTATGACGCCAAGAAATGTTTGTGTAACAG	2327

Db	2439	ACTTGCTCCCAAAAAGTATTCATCGAATTTAGACGCCAAGAAATTTTGGTAACAG	2439
Qy	2328	AAAACAATGTGATGAAAATATGACAGCTTTGGACCTGCGCAGAGATATCAACATATAGACT	2387
Db	2499	AAAACAATGTGATGAAAATATGACAGCTTTGGACCTGCGCAGAGATATCAACATATAGACT	2558
Qy	2388	ATTACAAAACCAACCAATGGGCGGCTTCCAGTCAATGTGATGGCTCCAGAACCCCTGT	2447
Db	2559	ATTACAAAACCAACCAATGGGCGGCTTCCAGTCAATGTGATGGCTCCAGAACCCCTGT	2618
Qy	2448	TTGATAGATATACATCATGAGATGATGTCTGGTCTTGGGGGTGTTAATGTGGAGAG	2507
Db	2619	TTGATAGATATACATCATGAGATGATGTCTGGTCTTGGGGGTGTTAATGTGGAGAG	2678
Qy	2508	TCTTCACCTTTAGGGGGCTCGCCCTACCCAGGAGATTCGCCGTGAGAGAACTTTTAACTGC	2567
Db	2679	TCTTCACCTTTAGGGGGCTCGCCCTACCCAGGAGATTCGCCGTGAGAGAACTTTTAACTGC	2738
Qy	2568	TGAAGGAAGGACACAGATGGATTAAGCCAGCCACTGACCAAGAACTGTACATGATGA	2622
Db	2739	TGAAGGAAGGACACAGATGGATTAAGCCAGCCACTGACCAAGAACTGTACATGATGA	2798
Qy	2628	TGAGGGAATGTGGATGATGAGGCCCTCCAGAGACCAAGCTTCAAGAGTTGGATGAAG	2687
Db	2799	TGAGGGAATGTGGATGATGAGGCCCTCCAGAGACCAAGCTTCAAGAGTTGGATGAAG	2858
Qy	2688	ACTTGGATCGAATTTCTCACTCTCAACCAATGAGAAATCTTGAGCCTCAGCCAACTC	2747
Db	2859	ACTTGGATCGAATTTCTCACTCTCAACCAATGAGAAATCTTGAGCCTCAGCCAACTC	2918
Qy	2748	TCGAACAGATATTCACCTTAGTACCTTGACACAGAAATTTCTTCTTCAAGAGATGAT	2807
Db	2919	TCGAACAGATATTCACCTTAGTACCTTGACACAGAAATTTCTTCTTCAAGAGATGAT	2978
Qy	2808	CTGTTTTTTCCTCCAGACCCCAATGCCCTTAGAACCAATGCTTCCATGATCAACATTA	2867
Db	2979	CTGTTTTTTCCTCCAGACCCCAATGCCCTTAGAACCAATGCTTCCATGATCAACATTA	3038
Qy	2868	ACGCGAGTGTAAAAATGAAATGACTGTGTCTGCTGTCTCCCAACAGAGACGACTGG	2927
Db	3039	ACGCGAGTGTAAAAATGAAATGACTGTGTGTCTGCTGTCTCCCAACAGAGACGACTGG	3098
Qy	2928	AACTAGTCACTGAGCAGGAGAGCAATGCCCTCCAGAGCTTGTGTCTCACTTGTAT	2987
Db	3099	AACTAGTCACTGAGCAGGAGAGCAATGCCCTCCAGAGCTTGTGTCTCACTTGTAT	3158
Qy	2988	ATATGCAATCAGAGAGGTAAATTAATTGGAAAAGTATTCAGACATATGTAAAGATTATAC	3047
Db	3159	ATATGCAATCAGAGAGGTAAATTAATTGGAAAAGTATTCAGACATATGTAAAGATTATAC	3218
Qy	3048	AGTGAAGAACTTGTATCTTCCCGCAGAGAGAGAAAGTTTCTTGACAGTGAAGCTGC	3106
Db	3219	AGTGAAGAACTTGTATCTTCCCGCAGAGAGAGAAAGTTTCTTGACAGTGAAGCTGC	3277
RESULT 7			
US-11-019-829-42			
Sequence 42, Application US/11019829			
Publication No. US20050136465A1			
GENERAL INFORMATION:			
APPLICANT: Hoffmann-La Roche Inc.			
TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat			
FILE REFERENCE: 22304			
CURRENT APPLICATION NUMBER: US/11/019,829			
CURRENT FILING DATE: 2004-12-22			
NUMBER OF SEQ ID NOS: 146			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 42			
LENGTH: 4575			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: fibroblast growth factor receptor 2 transcript variant 5			

Query Match	Best Local Similarity	91.7%;	Score 2849.4;	DB 13;	Length 4575;
Matches 3020;	Conservative 0;	Mismatches 71;	Indels 38;	Gaps 9;	
Query	1	CCCCGAGCAAAAGTTTGGTGGAGGCAACG-CAAGCTTGAATCTTTTCTTCTCTCTGTTCC	59		
Db	168	CTCCGAGCAAAAGTTTGGTGGAGGCAACGCGCAAGCTTGAATCTTTTCTTCTCTCTGTTCC	227		
Qy	60	CCAAATCCGAGGAGAGCCCGGAGGAGTCATG---GCGCTCTCCGAGCCTCGGGGTACG	116		
Db	228	CCAAATCCGAGGAGAGCCCGGAGGAGTCATGCGCGCTCTCTCCGAGCCTCGGGGTACG	287		
Qy	117	G-TGAAGCCCGAGAGGCTTGGCGCGCGGAGAGCAACCAAGACCACTTCTTCCGTTTGA	175		
Db	288	GCTAAGCCCGGAGAGGCTTGGCGCGGAGAGCAACCAAGACCACTTCTTCCGTTTGA	347		
Qy	176	GTTGCTCCCGCAACCCCGGAGCTGTGCTTCTTCATCCCGACCCAGCGCGGCG-CCGG	234		
Db	348	GTTGCTCCCGCAACCCCGGAGCTGTGCTTCTTCATCCCGACCCAGCGCGGCGCGCGG	407		
Qy	235	GACAAACAAGTCCCGAGAGAGGAGGAGGCTTCATTAAGTGAATGACGAGAGCAG-AGAGGCG	293		
Db	408	GACAAACAAGTCCCGAGAGAGGAGGAGGCTTCATTAAGTGAATGACGAGAGCAGAGGAGCG	467		
Qy	294	CTCGGTTCTTGAAGCCACCGCA-GCTGAAGGCAATGCGCGTGAATTCATGCGCCGTAGAGA	352		
Db	468	CTCGGTTCTTGAAGCCACCGCAAGCTGAAGGCAATGCGCGTGAATTCATGCGCCGTAGAGA	527		
Qy	353	AGTGTGAGATGGAGATTAAAGTCAATGAGATATGGAAGAGAGACCGGGGATTGTATCC	412		
Db	528	AGTGTGAGATGGAGATTAAAGTCAATGAGATATGGAAGAGAGACCGGGGATTGTATCC	587		
Qy	413	GTAACCAATGTCACATGCGGAGCTTTTCAATGCGCGTGTGCGTGTACCAATGGCAACCTTG	472		
Db	588	GTAACCAATGTCACATGCGGAGCTTTTCAATGCGCGTGTGCGTGTACCAATGGCAACCTTG	647		
Qy	473	TCCCTGAGCCGAGCCCTCTTCAAGTTTATGAGATACCAATTTAAGAGCCAGAAAGCGCA	532		
Db	648	TCCCTGAGCCGAGCCCTCTTCAAGTTTATGAGATACCAATTTAAGAGCCAGAAAGCGCA	707		
Qy	533	CCAAACCAATATCAAAATCTCTCAACAGAGATGACGTGCTGCGCCAGGGAGTCTGCTTA	592		
Db	708	CCAAACCAATATCAAAATCTCTCAACAGAGATGACGTGCTGCGCCAGGGAGTCTGCTTA	767		
Qy	553	GAGGTGCGCTGCTGTTTGAAGAATGCGCGCTGATCAATTTGAATGAATGAAGATGGGTTGAC	652		
Db	768	GAGGTGCGCTGCTGTTTGAAGAATGCGCGCTGATCAATTTGAATGAATGAAGATGGGTTGAC	827		
Qy	653	TTGGGGGCCCAATATAGGACAGTGCTTATTTGGGGAGTACTTGCAGATTTAAAGGCGCCACA	712		
Db	828	TTGGGGGCCCAATATAGGACAGTGCTTATTTGGGGAGTACTTGCAGATTTAAAGGCGCCACA	887		
Qy	713	CCTAGAGACTCCGGCTCTATGCTTGTATCTGCAAGTGAAGCTGTAGAAGTGAACCTTGG	772		
Db	888	CCTAGAGACTCCGGCTCTATGCTTGTATCTGCAAGTGAAGCTGTAGAAGTGAACCTTGG	947		
Qy	773	TACTTCATGTGTAATGTCAAGATGCGCATCTTCATCCCGAGATGATGAAGATGACCCGAT	832		
Db	948	TACTTCATGTGTAATGTCAAGATGCGCATCTTCATCCCGAGATGATGAAGATGACCCGAT	1007		
Qy	833	GATGCGAGAAATTTTGTCAATGAGAACAGTAAACAAGAGAGACCACTATCTGAACCAAC	892		
Db	1008	GATGCGAGAAATTTTGTCAATGAGAACAGTAAACAAGAGAGACCACTATCTGAACCAAC	1067		
Qy	893	ACAGAAAAGATGAGAAAGCGGCTCCATGCTGTGCTGTGCGCCAAACCTGTCAAGTTTGC	952		
Db	1068	ACAGAAAAGATGAGAAAGCGGCTCCATGCTGTGCTGTGCGCCAAACCTGTCAAGTTTGC	1127		
Qy	953	TGCCAGCCGGGGGAGAACCCAAATGCAACATGCGGTGGCTGAAAAACGGAGAGGATTT	1012		

Db	1128	TGCCACGCGGAGGAGACCCATATCCAACTATGGGTGGCTGAAAACGGGAAAGAGTTT	1187
Oy	1013	AAGCAGGAGCATTCGCATTGAGGCTACAGGTAAGAAACGACCTGAGCTCATTTATG	1072
Db	1188	AAGCAGGAGCATTCGCATTGAGGCTACAGGTAAGAAACGACCTGAGCTCATTTATG	1247
Oy	1073	GAAAGTGTGGTCCCATCTGACAGGGAATTAATCTGTGTATGTGGAATGAATACGGG	1132
Db	1248	GAAAGTGTGGTCCCATCTGACAGGGAATTAATCTGTGTGTGTGGAATGAATACGGG	1307
Oy	1133	TCCATCAATCAACGTACCACTGGATGTTGTGGAAGGATGCGCTACCGGCCATCTC	1192
Db	1308	TCCATCAATCAACGTATCACTGGATGTTGTGGAAGGATGCGCTACCGGCCATCTC	1367
Oy	1193	CAAGCCGAGCTGCGGCAAAATGCTCCACAGTGTTCGAGGAGACGTATGATTTGTCTG	1252
Db	1368	CAAGCCGAGCTGCGGCAAAATGCTCCACAGTGTTCGAGGAGACGTATGATTTGTCTG	1427
Oy	1253	AAGTTTACAGTATGATGCCAGCCCCACATCCAGTGATGAACACGCTGGAAGACGGC	1312
Db	1428	AAGTTTACAGTATGATGCCAGCCCCACATCCAGTGATGAACACGCTGGAAGACGGC	1487
Oy	1313	AGTAATATCGGGCCCGAGGGGTGCCCTCACTCAAGTTCTCAGCACTCGGGATTAAT	1372
Db	1488	AGTAATATCGGGCCCGAGGGGTGCCCTCACTCAAGTTCTCAGGGTTCTCAAGCGCGC	1547
Oy	1373	AGTTCAATGTC-----AGATGTCGTGCTCTGTTCAATGTGACCGAGCGC	1417
Db	1548	GGTGTTAAACACCGAGCAAGAGATTAGGTTCTCTATATTCGGAATGTATCTTTGAG	1607
Oy	1418	GATGCTGGGGAATATATATATATAGGTCTCCATTAATATATAGGCGAGCCACAGTCTGC	1477
Db	1608	GACGCTGGGGAATATATACGTCTTGCGGGTATTTCTATTTGGGATATCTTTCACTGCA	1667
Oy	1478	TGGCTCACTGTCTTCCCAAAAACGAAACGGCTCGAAGAGAAAGAGATTACAGCTTC	1537
Db	1668	TGGTTGACAGTCTTCC-----AGCGCTGGAAGAAAGAGATTACAGCTTC	1718
Oy	1538	CCAGACTACCTGAGATAGACATTACTGCAATAGGGGCTCTTTAATGCTGTATGGTG	1597
Db	1719	CCAGACTACCTGAGATAGACATTACTGCAATAGGGGCTCTTTAATGCTGTATGGTG	1778
Oy	1598	GTAAAGTATCTCTGTGCGATGTAAGAACGACCAAGAACCACTTCAGCAGCCAG	1657
Db	1779	GTAAAGTATCTCTGTGCGATGTAAGAACGACCAAGAACCACTTCAGCAGCCAG	1838
Oy	1658	CCGGCTGTGCACAGCTGACCAACGTATCCCTCTGCGGAACAGTATACGTTTCGGCT	1717
Db	1839	CCGGCTGTGCACAGCTGACCAACGTATCCCTCTGCGGAACAG-----GTTTCGGCT	1892
Oy	1718	GAGTCAGTCTCTGCATGAACTCAACACCCCGCTGTGAGGATPAACAACGCTCTCT	1777
Db	1893	GAGTCAGTCTCTGCATGAACTCAACACCCCGCTGTGAGGATPAACAACGCTCTCT	1952
Oy	1778	TCACGCGCAGACACCCCATGCTGCGAGGGGTCTCCGATATGAATTCAGAGACCCA	1837
Db	1953	TCACGCGCAGACACCCCATGCTGCGAGGGGTCTCCGATATGAATTCAGAGACCCA	2012
Oy	1838	AAATGGAGTTTCCAGAGATAGCTGACACTGGGCAGAGCCCTTGAGAAAGTTGCTTT	1897
Db	2013	AAATGGAGTTTCCAGAGATAGCTGACACTGGGCAGAGCCCTTGAGAAAGTTGCTTT	2072
Oy	1898	GGGCAAGTGTCTATGGCCGGAACACATGGGAATTGACAAAGACACCCCAAGAGCGGTC	1957
Db	2073	GGGCAAGTGTCTATGGCCGGAACACATGGGAATTGACAAAGACACCCCAAGAGCGGTC	2132
Oy	1958	ACCGTGGCCGTGAAGTGTGAAAGATATGTCACAGAAAGACCTTCTGATGTGTTG	2017
Db	2133	ACCGTGGCCGTGAAGTGTGAAAGATATGTCACAGAAAGACCTTCTGATGTGTTG	2192
Oy	2018	TCAGATGAGAGATGATGAAGTGAATGTGGGAACAAGAAATATCATTAATCTTCTTGA	2077

Db	2193	TCAGAGATGCGAGATGATGAAAGATGATTTGGGAAACACAAAGATATCAAAATCTTCTTGGAA	2252
Qy	2078	GCCCTGCACACAGATGGGCGCTCTCTATGTGATAGTATGCTCTTAAGGCAACCTC	2137
Db	2253	GCTGTGCACACAGATGGGCGCTCTCTATGTGATAGTATGCTCTTAAGGCAACCTC	2312
Qy	2138	CGAAGATATCTCCGAGGCCCGGAGGCCACCCGGGATGGAGATACCTGATGACATTAACCGT	2197
Db	2313	CGAAGATATCTCCGAGGCCCGGAGGCCACCCGGGATGGAGATACCTGATGACATTAACCGT	2372
Qy	2198	GTTCTCTGAGGAGCAGATGACCTCTCAAGGACTTGGTGTATGACCTTACCGAGCTGGCCAGA	2257
Db	2373	GTTCTCTGAGGAGCAGATGACCTCTCAAGGACTTGGTGTATGACCTTACCGAGCTGGCCAGA	2432
Qy	2258	CGAGATGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGACGCCAGAAATGTT	2317
Db	2493	GGCATGAGATGACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGACGCCAGAAATGTT	2492
Qy	2318	TTGGTAAACAGAAAACAATGTGATGTAATAATAGCACACTTGGACTGGCAGAGATATCAAC	2377
Db	2493	TTGGTAAACAGAAAACAATGTGATGTAATAATAGCACACTTGGACTGGCAGAGATATCAAC	2552
Qy	2378	AATATPAGCTATTAACAATAAGACCAACCAATGGGGGCTTCCAGTCAAGTGGATGGCTCCA	2437
Db	2553	AATATPAGCTATTAACAATAAGACCAACCAATGGGGGCTTCCAGTCAAGTGGATGGCTCCA	2612
Qy	2438	GAAGCCCTGTGTTGATAGATATACACTATCAGAGTATGTCTGTCTCTTCGGGGGTGTTA	2497
Db	2613	GAAGCCCTGTGTTGATAGATATACACTATCAGAGTATGTCTGTCTCTTCGGGGGTGTTA	2672
Qy	2498	ATGTGGAGATCTTCACTTTTAGGGGGGCTCGCGCTTACCAAGGAAATTCCTCGTGGAGAACTT	2557
Db	2673	ATGTGGAGATCTTCACTTTTAGGGGGGCTCGCGCTTACCAAGGAAATTCCTCGTGGAGAACTT	2732
Qy	2558	TTTAAAGCTGTGAAGAGAGACACAGAAATGATTAAGCAGACCACTGCAACCAAGAACTG	2617
Db	2733	TTTAAAGCTGTGAAGAGAGACACAGAAATGATTAAGCAGACCACTGCAACCAAGAACTG	2792
Qy	2618	TACATGATGATGAGGAGCTGTTGGCATGACAGTGCCTTCCAGAGACCAACTTCAAGCAG	2677
Db	2793	TACATGATGATGAGGAGCTGTTGGCATGACAGTGCCTTCCAGAGACCAACTTCAAGCAG	2852
Qy	2678	TTTGTAGAAGACTTGGATCGAAATCTCACTCTCAACCAATGAGAAATATTGGAACCTC	2737
Db	2853	TTTGTAGAAGACTTGGATCGAAATCTCACTCTCAACCAATGAGAAATATTGGAACCTC	2912
Qy	2738	AGCCAACTCTCGAAGCAGTATTCACCTAGTATACCTGTACCAAGAAAGTCTTGTCTTCA	2797
Db	2913	AGCCAACTCTCGAAGCAGTATTCACCTAGTATACCTGTACCAAGAAAGTCTTGTCTTCA	2972
Qy	2798	GGAGATGATTTCTGTTTTTCTCGAAGCCCAATGCTTACGAACCAATGCTTCTCAGTAT	2857
Db	2973	GGAGATGATTTCTGTTTTTCTCGAAGCCCAATGCTTACGAACCAATGCTTCTCAGTAT	3032
Qy	2858	CCACACATPAAACGCGAGTGTAAAAATGAAATGACTGTGTCTGCTGCCCAACACAGA	2917
Db	3033	CCACACATPAAACGCGAGTGTAAAAATGAAATGACTGTGTCTGCTGCCCAACACAGA	3092
Qy	2918	CAGGACTGGGAACCTTAGCTACCTGAGGAGGGAACCAATGCTGCCCAAGCTTGTGTCT	2977
Db	3093	CAGGACTGGGAACCTTAGCTACCTGAGGAGGGAACCAATGCTGCCCAAGCTTGTGTCT	3155
Qy	2978	CCACTTGTATATATGATCAGAGGAGTAAATTAATTGAAAAGTAAATCAGCATATGTGTAA	3037
Db	3153	CCACTTGTATATATGATCAGAGGAGTAAATTAATTGAAAAGTAAATCAGCATATGTGTAA	3212
Qy	3038	AGATTTATPACGTTGAAAATCTTGTATCTTCCCGAGGAGAGAAAGAGTTCTGGACACA	3097
Db	3213	AGATTTATPACGTTGAAAATCTTGTATCTTCCCGAGGAGAGAGAAAGAGTTCTGGACACA	3272
Qy	3098	GTGACACTGC 3106	
Db	3273	GTGACACTGC 3281	

```

RESULT 8
US-09-954-556-25
; Sequence 25, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (612)...(3080)
US-09-954-556-25

Query Match      90.3%; Score 2806.2; DB 3; Length 3080;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2879; Conservative 0; Mismatches 8; Indels 8; Gaps 6;

QY      1 CCCGCGAGCAAGTTGTGTGAGGCAACG-CAGCCTGAGTCCTTCTCTCTCTCC 59
DB      186 CTCGGAGCAAGTTTGTGTGAGGCAACGCAAGCCTGAGTCCTTCTCTCTCTCC 245
QY      60 CCAATTCGAGGCAAGCCCGCGGCGTCAAG---GGCTCTCTCGGAGCCTGGGTAACG 116
DB      246 CCAATTCGAGGCAAGCCCGCGGCGTCAAG---GGCTCTCTCGGAGCCTGGGTAACG 305
QY      117 G-TGAAGCCCGGAGGCTTGGCGCGGCGGCAAGCCCAAGACCACTCTTCTGGTTTGA 175
DB      306 GCTGAGCCCGGAGGCTTGGCGCGGCGGCAAGCCCAAGACCACTCTTCTGGTTTGA 365
QY      176 GTTGTCTCCCGCAAGCCCGGCGTCTGTGCTTCTCTCCATCCGACCCGCGGCGC-CGCG 234
DB      366 GTTGTCTCCCGCAAGCCCGGCGTCTGTGCTTCTCTCCATCCGACCCGCGGCGC-CGCG 425
QY      235 GACAACAAGTGTGCGGAGAGAGGCTTCAATTCAGTGACTGAGAGAGC-GCAGCCG 293
DB      426 GACAACAAGTGTGCGGAGAGAGGCTTCAATTCAGTGACTGAGAGAGC-GCAGCCG 485
QY      294 CTCGGTCTGAGCCCAAGCCGCA-GCTGAGGCAATTGCGGTGATGTCATGCCGTAGAGGA 352
DB      486 CTCGGTCTGAGCCCAAGCCGCAAGCTGAGGCAATTGCGGTGATGTCATGCCGTAGAGGA 545
QY      353 AGTGTGCAAGTGGATTAAAGTTCACATGAGATATGAAAGAGACCGGGGATTGTATAC 412
DB      546 AGTGTGCAAGTGGATTAAAGTTCACATGAGATATGAAAGAGACCGGGGATTGTATAC 605
QY      413 GTAACCATGTGAGCTGGGGGTCTTTCATCTGCTGTGTGTGTGTCACATGCAACCTTG 472
DB      606 GTAACCATGTGAGCTGGGGGTCTTTCATCTGCTGTGTGTGTGTCACATGCAACCTTG 665
QY      473 TCCCTGGCCCGGCGCTCTTCAAGTTAGTTAGGATACCAATTGAGCAGAAAGGCA 532
DB      666 TCCCTGGCCCGGCGCTCTTCAAGTTAGTTAGGATACCAATTGAGCAGAAAGGCA 725
QY      533 CCAACCAATTAACAATCTCTCAACCAAGATGTAGTGTGCGCAGGGGAGTGTGCTA 592
DB      726 CCAACCAATTAACAATCTCTCAACCAAGATGTAGTGTGCGCAGGGGAGTGTGCTA 785
QY      593 GAGGTGCGCTGCTGTGTAAGATGCGCGGTGATGATGTTGAGCTTAAGATGGGTGAC 652
DB      786 GAGGTGCGCTGCTGTGTAAGATGCGCGGTGATGATGTTGAGCTTAAGATGGGTGAC 845
QY      653 TTGGGGCCCAACATAGAGCAGTGTATTATGGGAGTACTTGCAGATTAAGGGCGCAC 712

```

```

DB      846 TTGGGGCCCAACATAGAGCAGTGTATTATGGGAGTACTTGCAGATTAAGGGCGCAC 905
QY      713 CCTAGAGATCCGGGCTCTATGTCTGTACTGCGCAGTGAAGTGAAGACTTGG 772
DB      906 CCTAGAGATCCGGGCTCTATGTCTGTACTGCGCAGTGAAGTGAAGACTTGG 965
QY      773 TACTTCATGTGAATGTCAAGATGCTATCTATCCGGAGTGAATGAAGCAACGAT 832
DB      966 TACTTCATGTGAATGTCAAGATGCTATCTATCCGGAGTGAATGAAGCAACGAT 1025
QY      833 GGTGCGAAGATTTTGTCAGTAGAAACAGTAAACAAGAGAGCACCATACTGACCAAC 892
DB      1026 GGTGCGAAGATTTTGTCAGTAGAAACAGTAAACAAGAGAGCACCATACTGACCAAC 1085
QY      893 ACAGAAAGATGAAAGAGCGCTCCATGCTGTGCTGCGGCAACCTGTCAAGTTTCCG 952
DB      1086 ACAGAAAGATGAAAGAGCGCTCCATGCTGTGCTGCGGCAACCTGTCAAGTTTCCG 1145
QY      953 TGCCCAAGCCGGGGGGAACCAATGCAACATGCGGTGCTGAAAAAGGGAAGATT 1012
DB      1146 TGCCCAAGCCGGGGGGAACCAATGCAACATGCGGTGCTGAAAAAGGGAAGATT 1205
QY      1013 AAGCAGAGCATGCAATTGAGAGCTTAAAGTAAACCAAGCACTGAGCCTCATTTATG 1072
DB      1206 AAGCAGAGCATGCAATTGAGAGCTTAAAGTAAACCAAGCACTGAGCCTCATTTATG 1265
QY      1073 GAAAGTGTGTCCTCATGCAAGGGAATTATACCTGTGTAGTGAATGAATACGGG 1132
DB      1266 GAAAGTGTGTCCTCATGCAAGGGAATTATACCTGTGTGTGGAATGAATACGGG 1325
QY      1133 TCCATCAATCAAGCTACCACTGATGATGTGTGAGAGCCATGCTTCAACGGGCTATCTTC 1192
DB      1326 TCCATCAATCAAGCTACCACTGATGATGTGTGAGAGCCATGCTTCAACGGGCTATCTTC 1385
QY      1193 CAAGCCGAGCTCCGGCAAAATGCTTCAAGTGTGCGAGAGAGAGTAAAGTTTGTCTCG 1252
DB      1386 CAAGCCGAGCTCCGGCAAAATGCTTCAAGTGTGCGAGAGAGAGTAAAGTTTGTCTCG 1445
QY      1253 AAGGTTTACATGATGCTCCAGCCCAATCCAGTGAATCAAGCAGTGAAGAAAGAGCGC 1312
DB      1446 AAGGTTTACATGATGCTCCAGCCCAATCCAGTGAATCAAGCAGTGAAGAAAGAGCGC 1505
QY      1313 AGTAAATACGGGCGCGAGCGGCTGCTTCAAGTGTCTCAAGCTTCAAGCTTGGGATTAAT 1372
DB      1506 AGTAAATACGGGCGCGAGCGGCTGCTTCAAGTGTCTCAAGCTTCAAGCTTGGGATTAAT 1565
QY      1373 AGTTCCAATGCAAGTGTGCTGCTCTGTTCAATGTGACCGAGCGGATGCTTGGGAAATAT 1432
DB      1566 AGTTCCAATGCAAGTGTGCTGCTCTGTTCAATGTGACCGAGCGGATGCTTGGGAAATAT 1625
QY      1433 ATATGTAAAGTCTCAATTAATATAGGAGCGCAACAGTGTGCTGCTGCTCTG 1492
DB      1626 ATATGTAAAGTCTCAATTAATATAGGAGCGCAACAGTGTGCTGCTGCTCTG 1685
QY      1493 CCAAAAACAGCAAGCCCTGGAAGAGAGAAAGAGATTAAGCTTCCCGAGACTTGGAG 1552
DB      1686 CCAAAAACAGCAAGCCCTGGAAGAGAGAAAGAGATTAAGCTTCCCGAGACTTGGAG 1745
QY      1553 ATAGCATTTACTGATAGGGGTCTTCTTAATGCGCTGTATGATGATGATCAATCTCG 1612
DB      1746 ATAGCATTTACTGATAGGGGTCTTCTTAATGCGCTGTATGATGATGATCAATCTCG 1805
QY      1613 TGCCGAATGAAGAACAGCAAGAGAGCAGACTTCAAGCAGCAGCGCTGTGCAAG 1672
DB      1806 TGCCGAATGAAGAACAGCAAGAGAGCAGACTTCAAGCAGCAGCGCTGTGCAAG 1865
QY      1673 CTGACCAACATGATCTCCCTGTGGAGAGACAGGTAACAGTTTGGCTGATCTCAGCTCTCC 1732
DB      1866 CTGACCAACATGATCTCCCTGTGGAGAGACAGGTAACAGTTTGGCTGATCTCAGCTCTCC 1925
QY      1733 ATGAATCTCAACACCCGCTGATGAGATTAACAACCCCTCTCTTCAACGGCAGACACC 1792

```

Db 1926 ATGAATCTCAACACCCCGCTGTGAGGATTAACAACGCTCTTCAACGGCAGACACC 1985
Qy 1793 CCATGCTGGAGGGGCTCTCCGAGTATGAATTCAGAGGACCCAAATGGAGTTTCCA 1852
Db 1986 CCAATGCTGGAGGGGCTCTCCGAGTATGAATTCAGAGGACCCAAATGGAGTTTCCA 2045
Qy 1853 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGAGTTTCTTGGGCAAGTGTATG 1912
Db 2046 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGAGTTTCTTGGGCAAGTGTATG 2105
Qy 1913 GCGGAAGCAGTGGGAATTTGACAAAGACCAAGAGGGGGGCTACCGTGGCCGTGAG 1972
Db 2106 GCGGAACAGTGGGAATTTGACAAAGACCAAGAGGGGGGCTACCGTGGCCGTGAG 2165
Qy 1973 ATGTTGAAAAGATGATGCTGACAGAAAAGACCTTTCTGATCTGTGTGTGAGATGATG 2032
Db 2166 ATGTTGAAAAGATGATGCTGACAGAAAAGACCTTTCTGATCTGTGTGTGAGATGATG 2225
Qy 2033 ATGAAGATGATGGGAAAACAAGAAATATCAATTAATCTTCTTGGAGCCTGACACAGAT 2092
Db 2226 ATGAAGATGATGGGAAAACAAGAAATATCAATTAATCTTCTTGGAGCCTGACACAGAT 2285
Qy 2093 GGGGCTCTATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2152
Db 2286 GGGGCTCTATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2345
Qy 2153 GCCCGAGGAGCCACCCGGGATGAGTACTCTATGACATTTAACGCTGTTCTTGGAGAGAG 2212
Db 2346 GCCCGAGGAGCCACCCGGGATGAGTACTCTATGACATTTAACGCTGTTCTTGGAGAGAG 2405
Qy 2213 ATGACCTTCAAGAGACTTGTGTATGCACTTAACGAGCTGGGCAAGAGGATGATGATG 2465
Db 2406 ATGACCTTCAAGAGACTTGTGTATGCACTTAACGAGCTGGGCAAGAGGATGATGATG 2465
Qy 2273 GCTTCCCAAAATGATTCATCGAGATTTACAGCAGAAATGTTTGGTAAACGAAAC 2332
Db 2466 GCTTCCCAAAATGATTCATCGAGATTTACAGCAGAAATGTTTGGTAAACGAAAC 2525
Qy 2333 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2392
Db 2526 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2585
Qy 2393 AAAAAACCAACCAATGAGGAGGCTTCAGTCAAGTGAAGGCTTCAGAAACCCCTGTTGAT 2452
Db 2586 AAAAAACCAACCAATGAGGAGGCTTCAGTCAAGTGAAGGCTTCAGAAACCCCTGTTGAT 2645
Qy 2453 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGTTTCTTGGGCAAGTGTATG 2512
Db 2646 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGTTTCTTGGGCAAGTGTATG 2705
Qy 2513 ACTTGAAGGAGGCTCGCTTACCCAGAGATTTCCGTTGAGAGAACTTTTAAAGCTGTGAAG 2572
Db 2706 ACTTGAAGGAGGCTCGCTTACCCAGAGATTTCCGTTGAGAGAACTTTTAAAGCTGTGAAG 2765
Qy 2573 GAAAGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
Db 2766 GAAAGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2825
Qy 2633 GACTTGGAGTGAAGTGGGCTTCAGAGACCAAGTTCAGACAGTGGTAAAGACTTG 2692
Db 2826 GACTTGGAGTGAAGTGGGCTTCAGAGACCAAGTTCAGACAGTGGTAAAGACTTG 2885
Qy 2693 GATCAAAATCTCACTCTCAACAACCAATGAGAAATCTTGAAGCTTCAAGCCACTCTCGAA 2752
Db 2886 GATCAAAATCTCACTCTCAACAACCAATGAGAAATCTTGAAGCTTCAAGCCACTCTCGAA 2945
Qy 2753 CAGTATTAAGCTGATTAAGCTTCAACAAGAAATGTTCTTGTCTTCAAGAGATATCTGT 2812
Db 2946 CAGTATTAAGCTGATTAAGCTTCAACAAGAAATGTTCTTGTCTTCAAGAGATATCTGT 3005
Qy 2813 TTTTCTCCGAGACCCATGCTTCAAGAAACGATGCTTCTCAAGATTCACATTAACGGC 2872
Db 3006 TTTTCTCCGAGACCCATGCTTCAAGAAACGATGCTTCTCAAGATTCACATTAACGGC 3065

Qy 2873 AGTGTAAACATGA 2887
Db 3066 AGTGTAAACATGA 3080

RESULT 9
US-09-954-456-293
; Sequence 293, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OR INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OR INVENTION: Sels
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 293
; LENGTH: 4268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-293

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

Qy 149 CCCAAGACCACTTCTGCTTGGAGTTGCTCCCGCAACCCGGGCTGTGCTTTC 208
Db 1 CCCAAGACCACTTCTGCTTGGAGTTGCTCCCGCAACCCGGGCTGTGCTTTC 60

Qy 209 TCCATCCGACCCCAAGCGGAGC-CGGGACAACAAGTTCGGAGAGAGCGTTGCCATTTC 267
Db 61 TCCATCCGACCCCAAGCGGAGC-CGGGACAACAAGTTCGGAGAGAGCGTTGCCATTTC 120

Qy 268 AAGTACTGACAGCAGCAGC-CCAGCGCTCGCTTCTGAGCCCAACCGA-GCTGAAGCA 325
Db 121 AAGTACTGACAGCAGCAGCAGCAGCAGCCTCGCTTCTGAGCCCAACCGAAGCA 180

Qy 326 TTGGCGCTGATCCATGCCCGGTGAGAGAGTGTGAGAGTGGATTAAAGTTCACATGAGA 385
Db 181 TTGGCGCTGATCCATGCCCGGTGAGAGAGTGTGAGAGTGGATTAAAGTTCACATGAGA 240

Qy 386 TATGAAGAAGACCGGGGATTTGTAACGTAACATGTCAGCTGGGCTGTTTCAATCTGC 445
Db 241 TATGAAGAAGACCGGGGATTTGTAACGTAACATGTCAGCTGGGCTGTTTCAATCTGC 300

Qy 446 CTGCTGTGTGTCACCATGGAACCTTGTCTGCTGCGCGGCTCTTCAATTTAGTTAG 505
Db 301 CTGCTGTGTGTCACCATGGAACCTTGTCTGCTGCGCGGCTCTTCAATTTAGTTAG 360

QY 506 GATACCACTTAGAGCAGAGAGGCCAACCAATAATCAATCTCTCAACAGAGT 565
 DB 361 GATACCACTTAGAGCAGAGAGGCCAACCAATAATCAATCTCTCAACAGAGT 420
 QY 566 TACGTGGCTGCGCAGAGAGGTGCTAGAGGTGCGCTGCTGTGAAAGATGCGCGT 625
 DB 421 TACGTGGCTGCGCAGAGAGGTGCTAGAGGTGCGCTGCTGTGAAAGATGCGCGT 480
 QY 626 ATCACTGGAGCTTAAGATGGGTGCACTTGGGGCCCAACAATAGACAGTCTTATGG 685
 DB 481 ATCACTGGAGCTTAAGATGGGTGCACTTGGGGCCCAACAATAGACAGTCTTATGG 540
 QY 686 GAGTACTTGCAGATTAAGGGCGCCACCTAGAGCTCGGCTCTATGCTGTACTGCC 745
 DB 541 GAGTACTTGCAGATTAAGGGCGCCACCTAGAGCTCGGCTCTATGCTGTACTGCC 600
 QY 746 AGTAGAGCTGTAGACAGTAACTTGGTACTTCACTGTGATGTCACAGTCCACTTCA 805
 DB 601 AGTAGAGCTGTAGACAGTAACTTGGTACTTCACTGTGATGTCACAGTCCACTTCA 660
 QY 806 TCCGAGATGATGAGAGTACACCGATGGTCCGAAAGATTTGTGTCAGTGAACAGTAA 865
 DB 661 TCCGAGATGATGAGAGTACACCGATGGTCCGAAAGATTTGTGTCAGTGAACAGTAA 720
 QY 866 AACAGAGAGCACATCTGACCAACAGAGAAAGATGAAAGCGGCTCCATGCTG 925
 DB 721 AACAGAGAGCACATCTGACCAACAGAGAAAGATGAAAGCGGCTCCATGCTG 780
 QY 926 CCTGCGGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGACCCCAATGCGAACATG 985
 DB 781 CCTGCGGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGACCCCAATGCGAACATG 840
 QY 986 CGGTGGCTGAAAAACGGGAAAGATTAAAGAGAGCATGCACTTGAAGGCTTCAAGGTA 1045
 DB 841 CGGTGGCTGAAAAACGGGAAAGATTAAAGAGAGCATGCACTTGAAGGCTTCAAGGTA 900
 QY 1046 CGAAACCGACACTGAGGCTCTTATGAAAGTGGTCCCATCTGCAAGGGAAATTAAT 1105
 DB 901 CGAAACCGACACTGAGGCTCTTATGAAAGTGGTCCCATCTGCAAGGGAAATTAAT 960
 QY 1106 ACCTGTGTAGTGAAGATTAATCGGGTCCATTCATCAGACGTAACCTGTGATGTTG 1165
 DB 961 ACCTGTGTAGTGAAGATTAATCGGGTCCATTCATCAGACGTAACCTGTGATGTTG 1020
 QY 1166 GAGCGATGCTTCAACGGCCCATCTTCAAGCGGACTGCGGCAATGCTTCAACAGT 1225
 DB 1021 GAGCGATGCTTCAACGGCCCATCTTCAAGCGGACTGCGGCAATGCTTCAACAGT 1080
 QY 1226 GTTCGAGAGAGCTAAGTTTGTCTGCAAGTTTAAGTATGCCAGGCCCAATCCAG 1285
 DB 1081 GTTCGAGAGAGCTAAGTTTGTCTGCAAGTTTAAAGTATGCCAGGCCCAATCCAG 1140
 QY 1286 TGGATCAAGCAGTGAAGAAAGAGCGCAGTAAATTAAGGCGCGGCTGCCCTCACTC 1345
 DB 1141 TGGATCAAGCAGTGAAGAAAGAGCGCAGTAAATTAAGGCGCGGCTGCCCTCACTC 1200
 QY 1346 AAGGTTCTCAAGCACTGCGGGATTAATAGTTTCAATGACAGAGTGTGCTGT----- 1400
 DB 1201 AAGGTTCTCAAGCGCGCGGTGTTAACCAACGGAACAAAGATGAGGTTCTCTATAT 1260
 QY 1401 -TCAATGTGACCGAGCGGATGCTGGGGAATATATGTAAAGTCTCCAAATTAATAGG 1459
 DB 1261 CGGAATGTAACTTTAAGACGCTGGGGAATATACGTGCTTGGCGGATATCTTATGG 1320
 QY 1460 CAGGCAACAGTCTGCTGCTGCTCACTGCTGCCAAACAGCAACGCGCTGAGAGAGA 1519
 DB 1321 ATATCTTTTCACTGTGATGTTGACAGTTCTGCG-----ACGCGCTGAGAGAGA 1371
 QY 1520 AAGAGATTAACAGCTTCCCGAGCTTACTGTGAGATAGCACTTTACTGCAATAGGGGTCTTC 1579
 DB 1372 AAGAGATTAACAGCTTCCCGAGCTTACTGTGAGATAGCACTTTACTGCAATAGGGGTCTTC 1431
 QY 1580 TTAATGCGCTGTATGTGTGTATACATCATCTGTGCGGAATGAAGAACAGCAAGAAAG 1639

DB 1432 TTAATGCGCTGTATGTGTGTAAAGTCACTCTGTGCCAATGAAAGACAGCAAGAG 1491
 QY 1640 CCAAGCTTCAAGAGCAACCGGCTGTGCAAAAGTGAACCAACATATCCCTGGGGAGA 1699
 DB 1492 CCAAGCTTCAAGAGCAACCGGCTGTGCAAAAGTGAACCAACATATCCCTGGGGAGA 1551
 QY 1700 CAGGTAAAGTTTGGCTGAGTCAAGCTCTTCATGAATCCCAACACCGGCTGTGAG 1759
 DB 1552 CAGGTAAAGTTTGGCTGAGTCAAGCTCTTCATGAATCCCAACACCGGCTGTGAG 1611
 QY 1760 ATAAACAACGCGCTCTTCAACGCGAACAACCCCATGCTGCGAGGGTCTCCAGTAT 1819
 DB 1612 ATAAACAACGCGCTCTTCAACGCGAACAACCCCATGCTGCGAGGGTCTCCAGTAT 1671
 QY 1820 GAACCTTCAAGAGCAACCAAAATGGAGTTTCCAAAGATTAAGTGAACCTGCGCAAGCC 1879
 DB 1672 GAACCTTCAAGAGCAACCAAAATGGAGTTTCCAAAGATTAAGTGAACCTGCGCAAGCC 1731
 QY 1880 CTGGAGAAAGTTGCTTTGGGCAAGTGGTCAATGGGGAAGCAAGTGGAAATTAACAAGAC 1939
 DB 1732 CTGGAGAAAGTTGCTTTGGGCAAGTGGTCAATGGGGAAGCAAGTGGAAATTAACAAGAC 1791
 QY 1940 AAGCCCAAGAGGCGGTCAACGCTGCGGTGAAGATGTTGAAGATGATGCCAGAGAAA 1999
 DB 1792 AAGCCCAAGAGGCGGTCAACGCTGCGGTGAAGATGTTGAAGATGATGCCAGAGAAA 1851
 QY 2000 GAACCTTCTGATCTGTGTGACAGATGAGATGAAGATTAAGTGGAAACAACAAGAT 2059
 DB 1852 GAACCTTCTGATCTGTGTGACAGATGAGATGAAGATTAAGTGGAAACAACAAGAT 1911
 QY 2060 ATCAATTAATCTTCTGAGGCGTCAACAGATGGGCGCTCTATGTCAATGTTAGTAT 2119
 DB 1912 ATCAATTAATCTTCTGAGGCGTCAACAGATGGGCGCTCTATGTCAATGTTAGTAT 1971
 QY 2120 GCCTTAAAGGCAACCTCCAGATACTCCAGGCCCGGAGCCACCCGGAATGAGTAC 2179
 DB 1972 GCCTTAAAGGCAACCTCCAGATACTCCAGGCCCGGAGCCACCCGGAATGAGTAC 2031
 QY 2180 TCCATTAATTAACCGGTCTCTGAGAGCAAGATGACCTTCAAGACCTTGTGTCAATG 2239
 DB 2032 TCCATTAATTAACCGGTCTCTGAGAGCAAGATGACCTTCAAGACCTTGTGTCAATG 2091
 QY 2240 ACTTACCGGCTGCGGAGAGAGTGGATGCTGGCTCCCAAAATGATTAATCAAGAT 2299
 DB 2092 ACTTACCGGCTGCGGAGAGAGTGGATGCTGGCTCCCAAAATGATTAATCAAGAT 2151
 QY 2300 TTAGCAGCAGAAATGTTTGTGTAACAGAAAACAATGTGATGAAATAGCAGCTTGA 2359
 DB 2152 TTAGCAGCAGAAATGTTTGTGTAACAGAAAACAATGTGATGAAATAGCAGCTTGA 2211
 QY 2360 CTGCGCAAGATATCAACATATTAATTAACAAAAGCAACCAATGGGCGCTTCA 2419
 DB 2212 CTGCGCAAGATATCAACATATTAATTAACAAAAGCAACCAATGGGCGCTTCA 2271
 QY 2420 GTCAAGTGAATGCTTCCAGAAACCGCTTGTGATGATGATTAACCTCAAGTGAATG 2479
 DB 2272 GTCAAGTGAATGCTTCCAGAAACCGCTTGTGATGATGATTAACCTCAAGTGAATG 2331
 QY 2480 TGGTCTTGGGGTGTATATGAGAGATCTTCACTTATGGGGGCTGCGCTTACCAAGG 2539
 DB 2332 TGGTCTTGGGGTGTATATGAGAGATCTTCACTTATGGGGGCTGCGCTTACCAAGG 2391
 QY 2540 ATTCCGATGAGAACTTTTAAGTGTGTAAGAGAGCAACAAATGATTAAGCGAGC 2599
 DB 2392 ATTCCGATGAGAACTTTTAAGTGTGTAAGAGAGCAACAAATGATTAAGCGAGC 2451
 QY 2600 AACTGCAACAAGACTGTATCAATGATGAAGGACTGTGCAATGAGTAAAGCCAGC 2659
 DB 2452 AACTGCAACAAGACTGTATCAATGATGAAGGACTGTGCAATGAGTAAAGCCAGC 2511
 QY 2660 AAGCAACCTTCAAGCAAGTGTGTAAGAGCTTGAATGCAATTCCTCACTCAACCAAT 2719

LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (274) ... (2739)
US-09-954-556-3

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCGAAGACCACTCTTCTGCGTTGGAGTTGCTCCCGCAACCCCGGCTGTGCTTTC 208
DB 1 CCGAAGACCACTCTTCTGCGTTGGAGTTGCTCCCGCAACCCCGGCTGTGCTTTC 60
QY 209 TCCATCCCGACCCCAACCGCGGGC-CGGGGAACAACAGGTGCGGAGGAGCGTTCATTC 267
DB 61 TCCATCCCGACCCCAACCGCGGGGCGGGGAACAACAGGTGCGGAGGAGCGTTCATTC 120
QY 268 AAGTACCTGCAGCAGCAGC-GCAGCGCTCGGTTCTGAGCCCAACCGA-CCTGAAGCA 325
DB 121 AAGTACCTGCAGCAGCAGCAGCAGCGCCTCGGTTCTGAGCCCAACCGAAGGCA 180
QY 326 TTGCGCGTAGTTCATGCTCCGTAGAGGAAGTGTGCAGATGGGATTAAAGTCCATGAGA 385
DB 181 TTGCGCGTAGTTCATGCTCCGTAGAGGAAGTGTGCAGATGGGATTAAAGTCCATGAGA 240
QY 386 TATGGAAGAAGACCGGGGATTGTATCCGTAACCAATGTGAGCTGGGGTGGTTTCATCTGC 445
DB 241 TATGGAAGAAGACCGGGGATTGTATCCGTAACCAATGTGAGCTGGGGTGGTTTCATCTGC 300
QY 446 CTGGCTGTGATCAACATGGCAACTTGTCTCTGCGCCGGCCCTCTCTTCAATTAGTTAG 505
DB 301 CTGGCTGTGATCAACATGGCAACTTGTCTCTGCGCCGGCCCTCTCTTCAATTAGTTAG 360
QY 506 GATACCACTTATAGACCCAGAAGAGCCCAACCAATATCAATATCTTCAACAGAAAGT 565
DB 361 GATACCACTTATAGACCCAGAAGAGCCCAACCAATATCAATATCTTCAACAGAAAGT 420
QY 566 TACGTGCTGCGCCGAGGGAGTGTGCTAGAGGTGCGCTGCTGTAAAGATGCGCGGTG 625
DB 421 TACGTGCTGCGCCGAGGGAGTGTGCTAGAGGTGCGCTGCTGTAAAGATGCGCGGTG 480
QY 626 ATCAGTTGGACTTAAAGATGGGTGTGCACTTGGGCCCCAACAATAGGACAGTGTATTGG 685
DB 481 ATCAGTTGGACTTAAAGATGGGTGTGCACTTGGGCCCCAACAATAGGACAGTGTATTGG 540
QY 686 GAGTACTTGCAGATTAAGGGCCGACACTTAAAGACTCCGGCTCTATGTCTTGTACTGCC 745
DB 541 GAGTACTTGCAGATTAAGGGCCGACACTTAAAGACTCCGGCTCTATGTCTTGTACTGCC 600
QY 746 AGTAGAGCTGTAGACAGTGAACCTTGGTACTTCAATGTGATGTGACAGATGCCATCTCA 805
DB 601 AGTAGAGCTGTAGACAGTGAACCTTGGTACTTCAATGTGATGTGACAGATGCCATCTCA 660
QY 806 TCCGAGATGATAGGATGACACCGATGTGCGGAAGATTTTGTCACTGAGAAACAGTAAC 865
DB 661 TCCGAGATGATAGGATGACACCGATGTGCGGAAGATTTTGTCACTGAGAAACAGTAAC 720
QY 866 AACAGAGAGCACCATATCTGACCAACACAGAAAAGATGAAAAGGGCTTCCATGTCTG 925
DB 721 AACAGAGAGCACCATATCTGACCAACACAGAAAAGATGAAAAGGGCTTCCATGTCTG 780
QY 926 CCTGCGCGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGAACCAATGCAACCAATG 985
DB 781 CCTGCGCGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGAACCAATGCAACCAATG 840
QY 986 CCGTGGCTGAAAAACGGGAAGAGTTTAAGCAGAGACATCGCATTTGAGAGCTTACAAGGTA 1045
DB 841 CCGTGGCTGAAAAACGGGAAGAGTTTAAGCAGAGACATCGCATTTGAGAGCTTACAAGGTA 900
QY 1046 CGAAACCAAGCACTGAGCCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAAATTAT 1105

DB 901 CGAAACCAAGCACTGAGCCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAAATTAT 960
QY 1106 ACTGTGTAGTGAAGAAATGAATACGGGTCCATCAATCACAGTACCACTGATGTTGTG 1165
DB 961 ACTGTGTAGTGAAGAAATGAATACGGGTCCATCAATCACAGTACCACTGATGTTGTG 1020
QY 1166 GAGCGATCGCTCACCGGCCCCATCTTCCAAACCGGAACTGGCGGAAATGCTCCACAGTG 1225
DB 1021 GAGCGATCGCTCACCGGCCCCATCTTCCAAACCGGAACTGGCGGAAATGCTCCACAGTG 1080
QY 1226 GTGCGAGAGACGTAGAGTTTGTCTGCAAGTTTACAGTATGCCAGCCCAATCCAG 1285
DB 1081 GTGCGAGAGACGTAGAGTTTGTCTGCAAGTTTACAGTATGCCAGCCCAATCCAG 1140
QY 1286 TGATCAAGCACGTGAAAAAAGACGCGATTAATCGGGCCGACGGGCTGCTTACTC 1345
DB 1141 TGATCAAGCACGTGAAAAAAGACGCGATTAATCGGGCCGACGGGCTGCTTACTC 1200
QY 1346 AAGGTTCTCAAGCACTGGGGGATTAATAGTTCCAAATGCAAGTGTGGGCTGT----- 1400
DB 1201 AAGGTTCTCAAGCGCGCCGCGGTTTACACACGACAAAGAGATTGAGTTCTTAAATT 1260
QY 1401 -TCAATGTGACCGAGCGGATGTGCGGGAATATATATGTAAAGTCTCAATTATAGG 1459
DB 1261 CGGAATGTACTTTTGAAGACGCTGGGGAATATAGTGTGGGGTAATTCTATTGGG 1320
QY 1460 CAGGCCAACAGTGTGCTGCTGCTCACTGTCTGCGCAAAACAGCAGCGCTGGAAGAA 1519
DB 1321 ATATCTTTCACTCTGATAGTGTGACAGTTCTGCC-----AGCGCTGGAAGAA 1371
QY 1520 AAGGATTTACAGTTTCCCACTACCTGAGATAGCAATTTACTGATAGGGGTCTTC 1579
DB 1372 AAGGATTTACAGTTTCCCACTACCTGAGATAGCAATTTACTGATAGGGGTCTTC 1431
QY 1580 TTAATGCTGTATGTAGTGTAAACAGTATCTGTGCGGAATGAAGAACACGACCAAGAG 1639
DB 1432 TTAATGCTGTATGTAGTGTAAACAGTATCTGTGCGGAATGAAGAACACGACCAAGAG 1491
QY 1640 CCAAGCTTCAAGCAGCCGAGCTGTGTGCAAAAGTGTGACCAAGCTTATCCCTGCGAGA 1699
DB 1492 CCAAGCTTCAAGCAGCCGAGCTGTGTGCAAAAGTGTGACCAAGCTTATCCCTGCGAGA 1551
QY 1700 CAGGTAACAGTTTGGGCTGATCCAGCTCTCCATGAACTTCAACACCCGCTGGTGG 1759
DB 1552 CAGGTAACAGTTTGGGCTGATCCAGCTCTCCATGAACTTCAACACCCGCTGGTGG 1611
QY 1760 ATTAACAACCGCTCTCTTCAACCGGACAGACCCCAATGCTGGCAAGGGTCTCGAGTAT 1819
DB 1612 ATTAACAACCGCTCTCTTCAACCGGACAGACCCCAATGCTGGCAAGGGTCTCGAGTAT 1671
QY 1820 GAACCTTCAAGAGACCCAAAAATGGAGATTTTCCAAAGATTAAGCTGACCTGGGCAAGCC 1879
DB 1672 GAACCTTCAAGAGACCCAAAAATGGAGATTTTCCAAAGATTAAGCTGACCTGGGCAAGCC 1731
QY 1880 CTGGAGAAAGTTGTTGGGCAAGTGTGCTATGGCGAAGAGTGGAAATTGACAAAGAC 1939
DB 1732 CTGGAGAAAGTTGTTGGGCAAGTGTGCTATGGCGAAGAGTGGAAATTGACAAAGAC 1791
QY 1940 AAGCCCAAGAGGCGGTCAACGTGACCTGGAAGATGTTGAAGATGATGCCACAGAGAA 1999
DB 1792 AAGCCCAAGAGGCGGTCAACGTGACCTGGAAGATGTTGAAGATGATGCCACAGAGAA 1851
QY 2000 GACCTTTTGTATCTGTGTCAAGATGGAATGATGAAGATTTGGGAAACACAAGAT 2059
DB 1852 GACCTTTTGTATCTGTGTCAAGATGGAATGATGAAGATTTGGGAAACACAAGAT 1911
QY 2060 ATCATTAATCTTCTTGAAGCTTGCACAGATAGGCGCTCTATGTATGATGATGAT 2119
DB 1912 ATCATTAATCTTCTTGAAGCTTGCACAGATAGGCGCTCTCTATGTATGATGATGAT 1971
QY 2120 GCCTTAAGGCACTCCAGAAATACCTCCAGAGCCCGAAGCCACCCGGATGAGTAC 2179

Db 1972 GCCTTAAGGCAACCTCCAGAAATACCTCCAGGCCCGGAGCCACCCGGAGTAGAGTAC 2031
 Qy 2180 TCCATGACATTAACCGGTGTTCTGAGAGCAGATGACCTTCAAGACCTTGGTGATGC 2239
 Db 2032 TCCATGACATTAACCGGTGTTCTGAGAGCAGATGACCTTCAAGACCTTGGTGATGC 2091
 Qy 2240 ACCTACAGCTGGCCAGAGGAGTAGAGTACTTGGCTTCCAAAATGATTCATCGAGAT 2299
 Db 2092 ACTTACAGCTGGCCAGAGGAGTAGAGTACTTGGCTTCCAAAATGATTCATCGAGAT 2151
 Qy 2300 TTAGACGACGAAATGTTTGTGTAACAGAAAATGATGAAAAATAGACAGCTTTGGA 2359
 Db 2152 TTAGACGACGAAATGTTTGTGTAACAGAAAATGATGAAAAATAGACAGCTTTGGA 2211
 Qy 2360 CTGCGCAGAGATATCAACATATAGACTATTACAAAAGACCAATGGCGGCTTCCA 2419
 Db 2212 CTGCGCAGAGATATCAACATATAGACTATTACAAAAGACCAATGGCGGCTTCCA 2271
 Qy 2420 GTCAAGTGAATGGCTCCAGAGCCCTGTTGATAGATATCACTGATCAGATGATGTC 2479
 Db 2272 GTCAAGTGAATGGCTCCAGAGCCCTGTTGATAGATATCACTGATCAGATGATGTC 2331
 Qy 2480 TGGTCTTGGGGGTGTTAATGTGGAGATCTTCACTTAAAGGGGCTGCGCTTACCGAGG 2539
 Db 2332 TGGTCTTGGGGGTGTTAATGTGGAGATCTTCACTTAAAGGGGCTGCGCTTACCGAGG 2391
 Qy 2540 ATTCCGCTGAGGAACTTTTAAAGCTGCTGAGAGAGACAGAAATGATTAAGCAGCC 2599
 Db 2392 ATTCCGCTGAGGAACTTTTAAAGCTGCTGAGAGAGACAGAAATGATTAAGCAGCC 2451
 Qy 2600 AACTGACCAACGACATGATGATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAG 2659
 Db 2452 AACTGACCAACGACATGATGATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAG 2511
 Qy 2660 AGACCAACGTTCAAGAGCTGTGTAAGACCTTGAATGAAATCTCACTCAACCAAT 2719
 Db 2512 AGACCAACGTTCAAGAGCTGTGTAAGACCTTGAATGAAATCTCACTCAACCAAT 2571
 Qy 2720 GAGGAATACCTGGAACCTGAGCCAACTCTGAAACATGATACCTAGTTACCTGACACA 2779
 Db 2572 GAGGAATACCTGGAACCTGAGCCAACTCTGAAACATGATACCTAGTTACCTGACACA 2631
 Qy 2780 AGAAGTTCTGTTCTTCAAGAGATGATGTTTCTTCCAGACCCAGCTTACGAA 2839
 Db 2632 AGAAGTTCTGTTCTTCAAGAGATGATGTTTCTTCCAGACCCAGCTTACGAA 2691
 Qy 2840 CCATGCTTCTCTAGATATCAACATTAACGAGAGTAAACATGATGACCTGATGC 2899
 Db 2692 CCATGCTTCTCTAGATATCAACATTAACGAGAGTAAACATGATGACCTGATGC 2751
 Qy 2900 GCCTGTCCCAAAACAGGACAGCACTGGAACCTAGCTACACTGAGCAGGAGACATGCC 2959
 Db 2752 GCCTGTCCCAAAACAGGACAGCACTGGAACCTAGCTACACTGAGCAGGAGACATGCC 2811
 Qy 2960 TCCCAAGAGCTTGTGTTCTCACTTGTATATATGATCAAGAGATTAATATGGAAG 3019
 Db 2812 TCCCAAGAGCTTGTGTTCTCACTTGTATATATGATCAAGAGATTAATATGGAAG 2871
 Qy 3020 TAATCAGCATATGTTAAAGATTTATACATTTGAAAACTGTATCTTCCCGAGAGAG 3079
 Db 2872 TAATCAGCATATGTTAAAGATTTATACATTTGAAAACTGTATCTTCCCGAGAGAG 2931
 Qy 3080 AAGAAGTTTCTGAGCAGTGAAGTGC 3106
 Db 2932 AAGAAGTTTCTGAGCAGTGAAGTGC 2958

RESULT 12

US-09-968-007A-461
 ; Sequence 461, Application US/09968007A
 ; Publication No. US20040115625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
 ; FILE OF INVENTION: Gene Sets
 ; FILE REFERENCE: 689290-71
 ; CURRENT APPLICATION NUMBER: US/09/968, 007A
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 172
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 173
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 278
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 294
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 295
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 316
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 1001
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 461
 ; LENGTH: 4268
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-968-007A-461

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

Qy 149 CCCAAGACACCTCTTCTGCGTTGAGTGTCTCCCGCAACCCGCGCTCGTCCCTTC 208
 Db 1 CCCAAGACACCTCTTCTGCGTTGAGTGTCTCCCGCAACCCGCGCTCGTCCCTTC 60
 Qy 209 TCCATCCGACCCAGCGGGGCG-CCGGGACAAACAGTCCGCGAGAGAGCTTCCATTC 267
 Db 61 TCCATCCGACCCAGCGGGGCGCGGGGACAAACAGTCCGCGAGAGAGCTTCCATTC 120
 Qy 268 AAGTACCTGACACAGAC-AGAGGCTCGGGTCTTGAAGCCCAACGCA-GCTGAAGGCA 325
 Db 121 AAGTACCTGACACAGACAGCGGCGCTCGGGTCTTGAAGCCCAACGCAAGGCA 180
 Qy 326 TTGCGGTAGTCCATGCGCCGTAGAGAGAGTGTGAGATGAGATTAACGTCAATGAGA 385
 Db 181 TTGCGGTAGTCCATGCGCCGTAGAGAGAGTGTGAGATGAGATTAACGTCAATGAGA 240
 Qy 386 TATGAAAGAGACCGGGGATTGTACCTGTACATGTCTGAGTGGGTCTTCACTGC 445
 Db 241 TATGAAAGAGACCGGGGATTGTACCTGTACATGTCTGAGTGGGTCTTCACTGC 300
 Qy 446 CTGCTGTGTGTCAACATGGAACCTTGTCCCTGGCCCGGCTCTTCACTTGAATGAG 505
 Db 301 CTGCTGTGTGTCAACATGGAACCTTGTCCCTGGCCCGGCTCTTCACTTGAATGAG 360
 Qy 506 GATPACCATTAAGAGCAGAGAGCCAAACCAATACCAATCTCTCAACAGAGTG 565
 Db 361 GATPACCATTAAGAGCAGAGAGCCAAACCAATACCAATCTCTCAACAGAGTG 420
 Qy 566 TAGTGTGCTGCGCCAGGGGAGTGGTGAAGTGTGCGCTGTGTAAGAGTCCGCGTG 625
 Db 421 TAGTGTGCTGCGCCAGGGGAGTGGTGAAGTGTGCGCTGTGTAAGAGTCCGCGTG 480
 Qy 626 ATCAGTTGACATTAAGATGAGGTGTGCACTTGGGGCCCAACATAGACAGTGTATTTGG 685
 Db 481 ATCAGTTGACATTAAGATGAGGTGTGCACTTGGGGCCCAACATAGACAGTGTATTTGG 540
 Qy 686 GATGCTTGCAGATTAAGAGGCGCCACACTAGAGACTCGGCTCTATGCTTGTACTGC 745
 Db 541 GATGCTTGCAGATTAAGAGGCGCCACACTAGAGACTCGGCTCTATGCTTGTACTGC 600
 Qy 746 AGTAGACTGTAGACAGTGAACCTTGTATCTTCACTGTGATGTCAAGATGCCATCTCA 805
 Db 601 AGTAGACTGTAGACAGTGAACCTTGTATCTTCACTGTGATGTCAAGATGCCATCTCA 660

[illegible]

Db	1732	CTGGGAGAAAGTTCCTTTGGGCAATGGTTCATGGCGGGAAGCAGTGGGAATTTGACAAAGAC	1791
Qy	1940	AAGCCCAAGAGGCGGTCAACGTCGCGGTGAAGAATGTTGAAGAATGATGCAACAGAAAA	1999
Db	1792	AAGCCCAAGAGGCGGTCAACGTCGCGGTGAAGAATGTTGAAGAATGATGCAACAGAAAA	1851
Qy	2000	GACCTTTCGATCTGGTGTCAAGATGAGATGATGAAGATGATGGGAAACACAGAAAT	2059
Db	1852	GACCTTTCGATCTGGTGTCAAGATGAGATGATGAAGATGATGGGAAACACAGAAAT	1911
Qy	2060	ATCATTAATCTTCTTGGAGCTTGCAACAGATGGGGCTCTCTATGTCATATGTTGAGTAT	2119
Db	1912	ATCATTAATCTTCTTGGAGCTTGCAACAGATGGGGCTCTCTATGTCATATGTTGAGTAT	1971
Qy	2120	GCCCTTAAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGAGCCACCCGGAGTGAATAC	2179
Db	1972	GCCCTTAAAGGCAACCTCCGAGAAATACCTCCGAGCCCGAGAGCCACCCGGAGTGAATAC	2031
Qy	2180	TCCATGACATTTAACCGTTCCTGAGAGCAGATGACCTTCAAGACCTTGGTGTCAATGC	2239
Db	2032	TCCATGACATTTAACCGTTCCTGAGAGCAGATGACCTTCAAGACCTTGGTGTCAATGC	2091
Qy	2240	ACCTACAGTGGCCGAGAGGATGAGATCTTGGCTTCCCAAAAATGATTCATCGAGAT	2299
Db	2092	ACCTACAGTGGCCGAGAGGATGAGATCTTGGCTTCCCAAAAATGATTCATCGAGAT	2151
Qy	2300	TTTAGCCGCCGAATATGTTTGGTAAACAGAAAACAATGTGATGAATAATGACACCTTGGGA	2359
Db	2152	TTTAGCCGCCGAATATGTTTGGTAAACAGAAAACAATGTGATGAATAATGACACCTTGGGA	2211
Qy	2360	CTGCGCAGAGATATCAACATATATGACTATTAACAAAAAGCCACCAATGGCGGCTTCCA	2419
Db	2212	CTGCGCAGAGATATCAACATATATGACTATTAACAAAAAGCCACCAATGGCGGCTTCCA	2271
Qy	2420	GTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATAGAGATATACCTCATCAGAGATGTC	2479
Db	2272	GTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATAGAGATATACCTCATCAGAGATGTC	2331
Qy	2480	TGGTCTTGGGGGTGTTAATGTCGAGATCTTCACTTTAGGGGGCTCCGCCCTACCCAGGG	2539
Db	2332	TGGTCTTGGGGGTGTTAATGTCGAGATCTTCACTTTAGGGGGCTCCGCCCTACCCAGGG	2391
Qy	2540	ATTCCCGTGAAGAACCTTTTAAAGTCTGTGAAGAGACACAGAAATGATTAAGCAGCC	2599
Db	2392	ATTCCCGTGAAGAACCTTTTAAAGTCTGTGAAGAGACACAGAAATGATTAAGCAGCC	2451
Qy	2600	AACCTGACCAAGACTGTATCATGATGATGAGGACTGTTGGCATGCACTGCCCTCCAG	2659
Db	2452	AACCTGACCAAGACTGTATCATGATGATGAGGACTGTTGGCATGCACTGCCCTCCAG	2511
Qy	2660	AGACCAAGCTTTCAGACAGCTTGTGTGAAGAATTGGAATCCGAATCTCACTCAACACAAAT	2719
Db	2512	AGACCAAGCTTTCAGACAGCTTGTGTGAAGAATTGGAATCCGAATCTCACTCAACACAAAT	2571
Qy	2720	GAGGAATACTTGGACCTCAGCCCAACTCTCGAAACAGTATTCACCTAGTTACCTTGACA	2779
Db	2572	GAGGAATACTTGGACCTCAGCCCAACTCTCGAAACAGTATTCACCTAGTTACCTTGACA	2631
Qy	2780	AGAAATTCTTGTCTTCAGAGATGATCTGTTTTTCTCCAGACCCCAATGCTTTAGGA	2839
Db	2632	AGAAATTCTTGTCTTCAGAGATGATCTGTTTTTCTCCAGACCCCAATGCTTTAGGA	2691
Qy	2840	CCATGCTCTCTCAGATTCACACATTAACGGAGGTTAAAAACATGATGCTGTCT	2899
Db	2692	CCATGCTCTCTCAGATTCACACATTAACGGAGGTTAAAAACATGATGCTGTCT	2751
Qy	2900	GCTGTGCCCAACAGGACGACCTGGGAAACTAGTATCACTGACAGGAGAACCATGCC	2959
Db	2752	GCTGTGCCCAACAGGACGACCTGGGAAACTAGTATCACTGACAGGAGAACCATGCC	2811
Qy	2960	TCCAGAGCTTGTGTCTCACTTGTATATATGATCAGAGAGTAATATTTGAAAAAG	3019

Db 2812 TCCAGAGCTGTGTGTCTCACTGTATATATATGATCAGAGAGTAATATATGGAAGA 2871
QY 3020 TAATCGCATATGTGTAAAGATTATATACAGTTGAAACCTTATATTTCCCGAGAGAG 3079
Db 2872 TAATCGCATATGTGTAAAGATTATATACAGTTGAAACCTTATATTTCCCGAGAGAG 2931
QY 3080 AAGAAGCTTTCTGAGACAGTGCATGCC 3106
Db 2932 AAGAAGCTTTCTGAGACAGTGCATGCC 2958

RESULT 13
US-10-843-641A-3320
Sequence 3320, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3320
LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-3320

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCCAAGACCACTCTTGTGCTTGAAGTTGCTCCCGGACCCCGGGCTGCTGCTTTC 208
Db 1 CCCAAGACCACTCTTGTGCTTGAAGTTGCTCCCGGACCCCGGGCTGCTGCTTTC 60
QY 209 TCCATCCGACCCAGCGGGGCGCGGGACCAACAGAGTCCGAGAGAGGTTGCCATTC 267
Db 61 TCCATCCGACCCAGCGGGGCGCGGGACCAACAGAGTCCGAGAGAGGTTGCCATTC 120
QY 268 AAGTGAAGTGAAGAGC-GCAGCGCTCGGTTCTGAGCCGCA-GCTGAAGGA 325
Db 121 AAGTGAAGTGAAGAGC-GCAGCGCTCGGTTCTGAGCCGCA-GCTGAAGGA 180
QY 326 TTGCGGTGATGCAATGCGGCTAGAGAAAGTGTGCAATGGGATTAAGTTCATGGA 385
Db 181 TTGCGGTGATGCAATGCGGCTAGAGAAAGTGTGCAATGGGATTAAGTTCATGGA 240
QY 386 TATGAAGAGGACCGGGGATTTGTACCGTAACAGTGTGAGGAGTTCATCTGC 445

Db 241 TATGGAAGAGACCGGGGATTGTATCCGTAACATGTACAGTGGGTGCTTTCATCTGC 300
QY 446 CTGTCGTGTGACCATGAGCAACCTTGTCCGTGGCGGGCCCTCTTCAAGTTAGTGA 505
Db 301 CTGTCGTGTGACCATGAGCAACCTTGTCCGTGGCGGGCCCTCTTCAAGTTAGTGA 360
QY 506 GATACCAATTAGAGCCAGAAAGAGCCAAACCAATATCAAAATCTTCAACAGAAAGT 565
Db 361 GATACCAATTAGAGCCAGAAAGAGCCAAACCAATATCAAAATCTTCAACAGAAAGT 420
QY 566 TACGTGTGTCGCGAGGAGTGTCTAGAGTGTGCTGCTGTTGAAGATGCCCGTG 625
Db 421 TACGTGTGTCGCGAGGAGTGTCTAGAGTGTGCTGCTGTTGAAGATGCCCGTG 480
QY 626 ATCACTTGAAGTAAAGATGGGTGCACTTGGGGGCCCAATAGACAGTGTCTTATGG 685
Db 481 ATCACTTGAAGTAAAGATGGGTGCACTTGGGGGCCCAATAGACAGTGTCTTATGG 540
QY 686 GAGTACTTGACAGATTAAGGGGCGCAACCTAGAGACTCGGCTTATGCTGTGATGCC 745
Db 541 GAGTACTTGACAGATTAAGGGGCGCAACCTAGAGACTCGGCTTATGCTGTGATGCC 600
QY 746 AGTAGAAGTGAAGACAGTGAACCTTGTACTTCAATGTGAATGTCAAGATGCCATCTCA 805
Db 601 AGTAGAAGTGAAGACAGTGAACCTTGTACTTCAATGTGAATGTCAAGATGCCATCTCA 660
QY 806 TTCCGAGATGATGAGATGAACCCGATGTGCGGAAGATTTGTGATGAGAAAGCTAAC 865
Db 661 TTCCGAGATGATGAGATGAACCCGATGTGCGGAAGATTTGTGATGAGAAAGCTAAC 720
QY 866 AACAGAGAGCACCATATGCAACCAAGAAAAGTGAAGAAAGCGGCTCATGCTGTG 925
Db 721 AACAGAGAGCACCATATGCAACCAAGAAAAGTGAAGAAAGCGGCTCATGCTGTG 780
QY 926 CTGCGGCGCAACCTGTCAAGTTGTGCTGCCAGCGGGGGAGAACCAATGCCAATG 985
Db 781 CTGCGGCGCAACCTGTCAAGTTGTGCTGCCAGCGGGGGAGAACCAATGCCAATG 840
QY 986 CGGTGGCTGAAAACGGGAAGAGTTTAAGCAGAGCATCCGATTTGAGGCTTACAAAGTA 1045
Db 841 CGGTGGCTGAAAACGGGAAGAGTTTAAGCAGAGCATCCGATTTGAGGCTTACAAAGTA 900
QY 1046 GGAACCAAGCATGAGGCTCTTATGGAAGTGTGCTCCATCTGCAAGAGGAATAT 1105
Db 901 GGAACCAAGCATGAGGCTCTTATGGAAGTGTGCTCCATCTGCAAGAGGAATAT 960
QY 1106 ACTGTGTATGTGAAGATGAATACGGGTCTCATCAATCAACAGTACCTGTGATGTG 1165
Db 961 ACTGTGTGTGTGAAGATGAATACGGGTCTCATCAATCAACAGTACCTGTGATGTG 1020
QY 1166 GAGGATGCTCTACCGGCTCATCTCCAGCCGAGCTGCGGCAATGCTTCCACAGTG 1225
Db 1021 GAGGATGCTCTACCGGCTCATCTCCAGCCGAGCTGCGGCAATGCTTCCACAGTG 1080
QY 1226 GTGGAAGAGAGCTGAGGTTGTCTGCAAGGTTTACAGTATGCCAGGCCACATCCAG 1285
Db 1081 GTGGAAGAGAGCTGAGGTTGTCTGCAAGGTTTACAGTATGCCAGGCCACATCCAG 1140
QY 1286 TGGATCAAGCACTGTGAAGAAAGACGGAGTAATACGGGCGGACAGGCTGCTTCACTC 1345
Db 1141 TGGATCAAGCACTGTGAAGAAAGACGGAGTAATACGGGCGGACAGGCTGCTTCACTC 1200
QY 1346 AAGTTTCTCAAGCACTCGGGATTAATATGTTTCAATGCAAGAGTGTGCTGTG----- 1400
Db 1201 AAGTTTCTCAAGCGCGCGGTGTTTAAACCAACGGAAGAGATTTGAGGTTCTCATATTT 1260
QY 1401 -TCAATGTGACGAGAGCGGATGCTGGGATATATATGTAAGTCTTCAATTTATAGG 1459
Db 1261 CGGAATGTAACTTTTGAAGAGCTGGGAAATATAGTCTTGGCGGATATTTATTTGG 1320
QY 1460 CAGGCCAACAGATCTGCTGCTCACTGTCTGCCAAACAGCAAGCGCTTGAAGAGAA 1519
Db 1321 ATATCTTTTCACTGTGATGATGTGACAGTTCTGCC-----AGCGCTGGAAGAGAA 1371

1520 AAGAGATTACAGCTTCCCAAGACTACCTGGAGATAGCCATTATCTGATAGGGGCTTTC 1579
Db 1372 AAGAGATTACAGCTTCCCAAGACTACCTGGAGATAGCCATTATCTGATAGGGGCTTTC 1431
Qy 1580 TTAATGCGCTGTATGTTGTTAAAGTCACTCTGTGCGCAATGAAAGAACACAGCAAGAG 1639
Db 1432 TTAATGCGCTGTATGTTGTTAAAGTCACTCTGTGCGCAATGAAAGAACACAGCAAGAG 1491
Qy 1640 CCAAGCTTACAGAGCAGCGCGCTGTGCAAGAGCTGACCAAGCAGTATCCCTGCGAGAG 1699
Db 1492 CCAAGCTTACAGAGCAGCGCGCTGTGCAAGAGCTGACCAAGCAGTATCCCTGCGAGAG 1551
Qy 1700 CAGGTACAGTTTCGGCTGAGTCCAGCTCTCATGAACTCCACACCCCGCTGTGAGG 1759
Db 1552 CAGGTACAGTTTCGGCTGAGTCCAGCTCTCATGAACTCCACACCCCGCTGTGAGG 1611
Qy 1760 ATAAACAACGCGCTCTTTCACACGCGACACACCCCATGCTGGCAGGGGCTCTCCAGAT 1819
Db 1612 ATAAACAACGCGCTCTTTCACACGCGACACACCCCATGCTGGCAGGGGCTCTCCAGAT 1671
Qy 1820 GAATTTCCAGAGAGCAGCAAAATGGAGTTTCCAGAGATAGCTGACCTGGGCAAGGCC 1879
Db 1672 GAATTTCCAGAGAGCAGCAAAATGGAGTTTCCAGAGATAGCTGACCTGGGCAAGGCC 1731
Qy 1880 CTGGAGAGAGGTTGCTTTGGGCAAGTGTCTATGCGGAAAGCAGTGGGAATTGACAAAGAC 1939
Db 1732 CTGGAGAGAGGTTGCTTTGGGCAAGTGTCTATGCGGAAAGCAGTGGGAATTGACAAAGAC 1791
Qy 1940 AAGCCCAAGAGAGCGGCTCAACCGTGGCGGTGAAGATGTTGAAGATGATGCCACAGAGAA 1999
Db 1792 AAGCCCAAGAGAGCGGCTCAACCGTGGCGGTGAAGATGTTGAAGATGATGCCACAGAGAA 1851
Qy 2000 GACCTTTCTGATCTGTGTGACAGATGAGATGATGATGATGATGATGATGATGATGATGAT 2059
Db 1852 GACCTTTCTGATCTGTGTGACAGATGAGATGATGATGATGATGATGATGATGATGATGAT 1911
Qy 2060 ATCATTAATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCTATGATGATGAT 2119
Db 1912 ATCATTAATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCTATGATGATGAT 1971
Qy 2120 GCTCTTAAAGCACTCTCCGAGATCTCTCCGAGCGCCGAGGCTCCCGGAGTGAAGTAC 2179
Db 1972 GCTCTTAAAGCACTCTCCGAGATCTCTCCGAGCGCCGAGGCTCCCGGAGTGAAGTAC 2031
Qy 2180 TCCCTATGATTAACCGTGTCTCTGAGGAGCAGATGACCTTCAAGGACTTGTGTCTATG 2239
Db 2032 TCCCTATGATTAACCGTGTCTCTGAGGAGCAGATGACCTTCAAGGACTTGTGTCTATG 2091
Qy 2240 ACCTACAGAGCTGCGCAGAGATGAGTACTTGGCTTCCCAAAATGATTCATGAGAT 2299
Db 2092 ACCTACAGAGCTGCGCAGAGATGAGTACTTGGCTTCCCAAAATGATTCATGAGAT 2151
Qy 2300 TTAAGCAGCAAAATGTTTGTGAACAAGAAACATGTGATGAAATATACAGACTTTGGA 2359
Db 2152 TTAAGCAGCAAAATGTTTGTGAACAAGAAACATGTGATGAAATATACAGACTTTGGA 2211
Qy 2360 CTGCGCAGAGATTAACAATATAGCTATTAACAAAGACCAACATGGGCGGCTTCCA 2419
Db 2212 CTGCGCAGAGATTAACAATATAGCTATTAACAAAGACCAACATGGGCGGCTTCCA 2271
Qy 2420 GTCAATGATGATGCTCAGAGAGCTGTTGATGATGATGATGATGATGATGATGATGATG 2479
Db 2272 GTCAATGATGATGCTCAGAGAGCTGTTGATGATGATGATGATGATGATGATGATGATG 2331
Qy 2480 TGGTCTTTGGGGGTGTTATGTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCAAGGG 2539
Db 2332 TGGTCTTTGGGGGTGTTATGTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCAAGGG 2391
Qy 2540 ATTCCCGTGAAGAACTTTTAAAGCTGCTGAAGAAAGACAGAGATGATGATGATGATGATG 2599
Db 2392 ATTCCCGTGAAGAACTTTTAAAGCTGCTGAAGAAAGACAGAGATGATGATGATGATGATG 2451

Qy 2600 AACTGACCAACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2659
Db 2452 AACTGACCAACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511
Qy 2660 AGACCAAGCTTCAAGCAGTTGTTGAAGACTTGAAGATGATGATGATGATGATGATGATGAT 2719
Db 2512 AGACCAAGCTTCAAGCAGTTGTTGAAGACTTGAAGATGATGATGATGATGATGATGATGAT 2571
Qy 2720 GAGGAATACTTGAAGCTTCAAGCAGTTGTTGAAGACTTGAAGATGATGATGATGATGATGAT 2779
Db 2572 GAGGAATACTTGAAGCTTCAAGCAGTTGTTGAAGACTTGAAGATGATGATGATGATGATGAT 2631
Qy 2780 AGAAGTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2839
Db 2632 AGAAGTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2691
Qy 2840 CCATGCTTCTCTAGATTCACATTAACGAGTGTAAACATGATGATGATGATGATGATGATGAT 2899
Db 2692 CCATGCTTCTCTAGATTCACATTAACGAGTGTAAACATGATGATGATGATGATGATGATGAT 2751
Qy 2900 GCTGTCTCCCAACAGACAGACTGCGAACTTACTGATCACTGAGCAGGAGACCATGCC 2959
Db 2752 GCTGTCTCCCAACAGACAGACTGCGAACTTACTGATCACTGAGCAGGAGACCATGCC 2811
Qy 2960 TCCAGAGCTTGTGTCTCCACTGTATATATGATGATGATGATGATGATGATGATGATGATGAT 3019
Db 2812 TCCAGAGCTTGTGTCTCCACTGTATATATGATGATGATGATGATGATGATGATGATGATGAT 2871
Qy 3020 TAATCAGATATGTTAAAGATTTATACAGTTGAAAACCTGTATCTTCCAGAGAGAG 3079
Db 2872 TAATCAGATATGTTAAAGATTTATACAGTTGAAAACCTGTATCTTCCAGAGAGAG 2931
Qy 3080 AAGAAGTTTCTGAGACAGTGAAGTGC 3106
Db 2932 AAGAAGTTTCTGAGACAGTGAAGTGC 2958

RESULT 14
US-10-843-641A-4626
Sequence 4626, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843, 641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873, 367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954, 531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954, 456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962, 436
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962, 832
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964, 824
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967, 768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968, 007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969, 347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969, 708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4626
LENGTH: 4268

TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc. feature
LOCATION: (1) .. (4268)
OTHER INFORMATION: n=a,l,g or c
US-10-843-641A-4626

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCCAAGACCACTCTTGTGGTTGAGTTGCTCCCGGACCCCGGGCTGGTCTTC 208
DB 1 CCCAAGACCACTCTTGTGGTTGAGTTGCTCCCGGACCCCGGGCTGGTCTTC 60
QY 209 TCCATCCGACCCACCGCGGGC-CGGGCAACAACAGGTGCGGAGAGGTGCCATT 267
DB 61 TCCATCCGACCCACCGCGGGC-CGGGCAACAACAGGTGCGGAGAGGTGCCATT 120
QY 268 AAGTGACTGACAGACGAC-GCAGCCCTCGGTTCTTGAGCCGCA-CTTGAAGCA 325
DB 121 AAGTGACTGACAGACGACGCGCCCTCGGTTCTTGAGCCGCA-CTTGAAGCA 180
QY 326 TTGCGGCTAGTCCATCCCTAGAGAGAGTGCAGATGGATTAACTGTCATGGAGA 385
DB 181 TTGCGGCTAGTCCATCCCTAGAGAGAGTGCAGATGGATTAACTGTCATGGAGA 240
QY 386 TATGAAGAGACCGGGGATTGGTACGTTACGTTACGATGTCAGTGGGGTCTTCATCTGC 445
DB 241 TATGAAGAGACCGGGGATTGGTACGTTACGTTACGATGTCAGTGGGGTCTTCATCTGC 300
QY 446 CTGGTCTGCTGTCACATGCGAACCTTGTCTCGCCCGGCTCTTCAAGTTAGTTAG 505
DB 301 CTGGTCTGCTGTCACATGCGAACCTTGTCTCGCCCGGCTCTTCAAGTTAGTTAG 360
QY 506 GATACCACTTAAAGCCAGAGAGCCACCAACCAATTAAGTCTTCAACGAGAAAGT 565
DB 361 GATACCACTTAAAGCCAGAGAGCCACCAACCAATTAAGTCTTCAACGAGAAAGT 420
QY 566 TACGTGGCTGCGCCAGGGGAGTGCCTAGAGTGCCTGCTTGAAGAGTCCGCGT 625
DB 421 TACGTGGCTGCGCCAGGGGAGTGCCTAGAGTGCCTGCTTGAAGAGTCCGCGT 480
QY 626 ATCAGTTGACCTAAGAGATGGGCTGCACTTGGGGCCCAACATAGACAGTCTTATTTGG 685
DB 481 ATCAGTTGACCTAAGAGATGGGCTGCACTTGGGGCCCAACATAGACAGTCTTATTTGG 540
QY 686 GAGTACTTGGAGTTAAAGGGCCGCAACCTAAGACCTCCGGCTTATGTTTACTGTC 745
DB 541 GAGTACTTGGAGTTAAAGGGCCGCAACCTAAGACCTCCGGCTTATGTTTACTGTC 600
QY 746 AATGAGACTGTAGACAGTGAACCTTGGTACTTATGATGTAATGTCACAGATGCACTCA 805
DB 601 AATGAGACTGTAGACAGTGAACCTTGGTACTTATGATGTAATGTCACAGATGCACTCA 660
QY 806 TCCGAGATGATGAGATGACACCGATGTCGGAAGATTTGTCACTGTAAGACAGTAAC 865
DB 661 TCCGAGATGATGAGATGACACCGATGTCGGAAGATTTGTCACTGTAAGACAGTAAC 720
QY 866 AACAAAGAGACATTAATCTGGAACCAACAGAAAGATGAAAGGGCTCCCATGCTG 925
DB 721 AACAAAGAGACATTAATCTGGAACCAACAGAAAGATGAAAGGGCTCCCATGCTG 780
QY 926 CTTGCGGCAACCTGTCAAGTTTGTGCTGCGACCGGGGGAACCAATGCAACATG 985
DB 781 CTTGCGGCAACCTGTCAAGTTTGTGCTGCGACCGGGGGAACCAATGCAACATG 840
QY 986 CCGTGGCTGAAGAAACGGGAAGAGTTTAACGACAGAGATGCACTTGAAGCTTCAAGTA 1045
DB 841 CCGTGGCTGAAGAAACGGGAAGAGTTTAACGACAGAGATGCACTTGAAGCTTCAAGTA 900
QY 1046 CGAAACGACGCTGAGGCTTATTAAGAAAGTGTGCTCCATCTGACAAAGGAATTAAT 1105

DB 901 CGAAACGACGCTGAGCTCATTAATGAAAGTGTGCTCCATCTGACAAAGGAATTAAT 960
QY 1106 AACTGTGATGAGAGAAATGAATACGGGTCCATCATCAACGTACACCTGATGTTGG 1165
DB 961 AACTGTGATGAGAGAAATGAATACGGGTCCATCATCAACGTACACCTGATGTTGG 1020
QY 1166 GAGCATGCGCTCACCGGCCCATCTCTCAAGCCGAGCTGCGGCAATGCTTCAACATG 1225
DB 1021 GAGCATGCGCTCACCGGCCCATCTCTCAAGCCGAGCTGCGGCAATGCTTCAACATG 1080
QY 1226 GTGAGAGAGAGTGAAGTTTGTGCAAGTTTACATGATGCCAAGCCCAATCCAG 1285
DB 1081 GTGAGAGAGAGTGAAGTTTGTGCAAGTTTACATGATGCCAAGCCCAATCCAG 1140
QY 1286 TGGATCAAGACAGTGAAGAAACGGCAATTAACGGGCCGAGCGGCTGCTTACCTC 1345
DB 1141 TGGATCAAGACAGTGAAGAAACGGCAATTAACGGGCCGAGCGGCTGCTTACCTC 1200
QY 1346 AAGTTCTCAAGCACTCGGGGATTAATAGTTCCAAAGCAGAGTCTGCTGT----- 1400
DB 1201 AAGTTCTCAAGCCGCGGCTTAAACACAGCAAGAGATGAGTTCTTATAT 1260
QY 1401 -TCAATGTAACCGAGCGGATGCTGGGAAATATATATGTAAGTCTCAATTATAGG 1459
DB 1261 CGGAATGTAACCTTTGAGGACGCTGGGGAATATAGTGTGCGGGTAACTTATG 1320
QY 1460 CAGGCCAACAGTCTGCTGCTCACTGTCTTCCAAACAGCAAGCGCTGGAAGAA 1519
DB 1321 ATATCTTCACTCTGACATGTTGACAGTTCTGC-----AGCGCTGGAAGAA 1371
QY 1520 AAGGAGATTAGAGCTTCCCAAGCTAACCTGAGATAGCACTTATCTGATAGGGCTTC 1579
DB 1372 AAGGAGATTAGAGCTTCCCAAGCTAACCTGAGATAGCACTTATCTGATAGGGCTTC 1431
QY 1580 TTATTCGCTGTATGATGTTAAACATCACTCTGTCGGAATGAAGAACGACAAAG 1639
DB 1432 TTATTCGCTGTATGATGTTAAACATCACTCTGTCGGAATGAAGAACGACAAAG 1491
QY 1640 CCAAGCTTACAGACCGACCGGCTGTGCAAGCTGACCAACGATTCCTCCGCGA 1699
DB 1492 CCAAGCTTACAGACCGACCGGCTGTGCAAGCTGACCAACGATTCCTCCGCGA 1551
QY 1700 CAGGTAAAGTTCGGCTGAGTCAAGCTCTCAAGAACTTCAACACCCGCTGAGAG 1759
DB 1552 CAGGTAAAGTTCGGCTGAGTCAAGCTCTCAAGAACTTCAACACCCGCTGAGAG 1611
QY 1760 ATTAACAACGCTCTTCAACGCGACACCCCATGCTGCAAGGGCTTCCAGTAT 1819
DB 1612 ATTAACAACGCTCTTCAACGCGACACCCCATGCTGCAAGGGCTTCCAGTAT 1671
QY 1820 GAACCTTCAAGAGACCCAAATAGGAGTTTCCAAAGATTAAGCTGACATGCGCAAGCC 1879
DB 1672 GAACCTTCAAGAGACCCAAATAGGAGTTTCCAAAGATTAAGCTGACATGCGCAAGCC 1731
QY 1880 CTGGAGAAAGTTGCTTGGGCAAGTGCATGGGGAAGCAGTGGGAATTTGACAAAGAC 1939
DB 1732 CTGGAGAAAGTTGCTTGGGCAAGTGCATGGGGAAGCAGTGGGAATTTGACAAAGAC 1791
QY 1940 AAGCCCAAGAGAGCGGTCAACGTGACCTGAAGATTTGAAGATGATCCACAGAA 1999
DB 1792 AAGCCCAAGAGAGCGGTCAACGTGACCTGAAGATTTGAAGATGATCCACAGAA 1851
QY 2000 GACCTTCTGATCTGCTCAAGATGAGATGATGAATATTTGGAAACAAAGAT 2059
DB 1852 GACCTTCTGATCTGCTCAAGATGAGATGATGAATATTTGGAAACAAAGAT 1911
QY 2060 ATCAATAATCTTGTGAGGCTGCAACAGATGGGCTCTATATGCTATAGTAT 2119
DB 1912 ATCAATAATCTTGTGAGGCTGCAACAGATGGGCTCTATATGCTATAGTAT 1971
QY 2120 GCCTTAAGGCAACTCCGAGATTAATCTCGAGCCCGAGGCAACCCGGAATGAGTAC 2179

Db 1972 GCTCTAAAGCACTCCGAGATACCTCCGAGCCCGAGGCCACCCGGATGAGTAC 2031
Oy 2180 TCCTATGACATTAACCGTGTCTGAGGAGAGATGACCTTCAAGACCTTGATGATG 2239
Db 2032 TCCTATGACATTAACCGTGTCTGAGGAGAGATGACCTTCAAGACCTTGATGATG 2091
Oy 2240 ACTTACGAGTGGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 2239
Db 2092 ACTTACGAGTGGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 2151
Oy 2300 TTAGAGGAG 2359
Db 2152 TTAGAGGAG 2211
Oy 2360 CTCGCGAGAGATATCAATATATATATATATATATATATATATATATATATAT 2419
Db 2212 CTCGCGAGAGATATCAATATATATATATATATATATATATATATATATAT 2271
Oy 2420 GTCAAGTGAATGCTCCAGAGCCCTGTTGATGATGATGATGATGATGATGATG 2479
Db 2272 GTCAAGTGAATGCTCCAGAGCCCTGTTGATGATGATGATGATGATGATGATG 2331
Oy 2480 TGTGCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2539
Db 2332 TGTGCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2391
Oy 2540 ATTCCGAG 2599
Db 2392 ATTCCGAG 2451
Oy 2600 AACTGACCAAG 2659
Db 2452 AACTGACCAAG 2511
Oy 2660 AGACCAAGTGAAG 2719
Db 2512 AGACCAAGTGAAG 2571
Oy 2720 GAGGATATCTGAG 2779
Db 2572 GAGGATATCTGAG 2631
Oy 2780 AGAGGATCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2839
Db 2632 AGAGGATCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
Oy 2840 CCATGCTCTCTGAG 2899
Db 2692 CCATGCTCTCTGAG 2751
Oy 2900 GCTGCTCCCAAG 2959
Db 2752 GCTGCTCCCAAG 2811
Oy 2960 TCCGAGAGCTGTTGCTCCATCTGATATATATATATATATATATATATATAT 3019
Db 2812 TCCGAGAGCTGTTGCTCCATCTGATATATATATATATATATATATATATAT 2871
Oy 3020 TATATGAG 3079
Db 2872 TATATGAG 2931
Oy 3080 AAGAGAGTCTGAG 3106
Db 2932 AAGAGAGTCTGAG 2958

RESULT 15
US-10-843-641A-6931
; Sequence 6931, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.

;; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;; FILE REFERENCE: 689290-189
;; CURRENT FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: US/09/873,367
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US/09/954,531
;; PRIOR FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: US/09/954,456
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US/09/962,436
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US/09/962,832
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US/09/964,824
;; PRIOR FILING DATE: 2001-09-27
;; PRIOR APPLICATION NUMBER: US/09/967,768
;; PRIOR FILING DATE: 2001-09-28
;; PRIOR APPLICATION NUMBER: US/09/968,007
;; PRIOR FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US/09/969,347
;; PRIOR FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US/09/969,708
;; PRIOR FILING DATE: 2001-10-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 8447
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 6931
;; LENGTH: 4268
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)..(4268)
;; OTHER INFORMATION: n=a,t,c,g or c
US-10-843-641A-6931

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;
Oy 149 CCCAAGGACCACTCTGCTGAGTGTCTCCCGCAACCCCGGCTGCTCTTC 208
Db 1 CCCAAGGACCACTCTGCTGAGTGTCTCCCGCAACCCCGGCTGCTCTTC 60
Oy 209 TCCATCCGACCAAGCGGAGC-CGGGAGACAACAAGTGGGAGAGAGAGAGAGAG 267
Db 61 TCCATCCGACCAAGCGGAGC-CGGGAGACAACAAGTGGGAGAGAGAGAGAGAG 120
Oy 268 AAGTACCTGACAGAGAGC-GAGGCGCTCGGTTCTGAGCCCAACCGA-GCTGAAGCA 325
Db 121 AAGTACCTGACAGAGAGC-GAGGCGCTCGGTTCTGAGCCCAACCGA-GCTGAAGCA 180
Oy 326 TTGGCGGTATGTCAGTCCCGTGAAGAGAGTGGAGATTAACGTCCACATGAGAGA 385
Db 181 TTGGCGGTATGTCAGTCCCGTGAAGAGAGTGGAGATTAACGTCCACATGAGAGA 240
Oy 386 TATGAAGAAGAGACCGGAGATGTTACCGTAAACATGATCAAGTGGAGTCTTCAATCTGC 445
Db 241 TATGAAGAAGAGACCGGAGATGTTACCGTAAACATGATCAAGTGGAGTCTTCAATCTGC 300
Oy 446 CTGCTGCTGATCAATGAGCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
Db 301 CTGCTGCTGATCAATGAGCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 506 GATACCACTTGAAG 565
Db 361 GATACCACTTGAAG 420
Oy 566 TACGTGCTGCGCAGAGAGAGTGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 625
Db 421 TACGTGCTGCGCAGAGAGAGTGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 626 ATCACTTGAAGCTAAGATGGGGTGCATTTGGGGCCCAACATATGACAGTGTCTTAATGGG 685
 DB 481 ATCACTTGAAGCTAAGATGGGGTGCATTTGGGGCCCAACATATGACAGTGTCTTAATGGG 540
 QY 686 GAGTACTTGAAGATTAAGGGGCGCACACTAGAGACTCCGGCTCTATGCTGTGATGCG 745
 DB 541 GAGTACTTGAAGATTAAGGGGCGCACACTAGAGACTCCGGCTCTATGCTGTGATGCG 600
 QY 746 AGTAGAGCTGTAGACAGTGAACCTTGTATCTTCAATGTGAATGTCAACAGTCCATCTCA 805
 DB 601 ACTTAGAGCTGTAGACAGTGAACCTTGTATCTTCAATGTGAATGTCAACAGTCCATCTCA 660
 QY 806 TCCGAGATGATGAGATGACACCGATGTGTGGGAAAGATTTTGTCACTGTAGAACAGTAA 865
 DB 661 TCCGAGATGATGAGATGACACCGATGTGTGGGAAAGATTTTGTCACTGTAGAACAGTAA 720
 QY 866 AACAGAGAGCACATATCTGAGACCAACAGAAAAGATGAAAAGCGGCTCCATGCTGTG 925
 DB 721 AACAGAGAGCACATATCTGAGACCAACAGAAAAGATGAAAAGCGGCTCCATGCTGTG 780
 QY 926 CCTGGCGGCACACATGTCAAGTTTCGCTGCCAGCCGGGGGAAACCAATGCGAACATG 985
 DB 781 CCTGGCGGCACACATGTCAAGTTTCGCTGCCAGCCGGGGGAAACCAATGCGAACATG 840
 QY 986 CCGTGTCTGAATAACGGGAAAGATTTAAGCAGAGACATCGCATTTGAGAGCTTAACAAGTA 1045
 DB 841 CCGTGTCTGAATAACGGGAAAGATTTAAGCAGAGACATCGCATTTGAGAGCTTAACAAGTA 900
 QY 1046 CGAAACACAGACATGAGCCTCATTTATGAAAAGTGTGTCCCATCTGACAAAGGGAATTAAT 1105
 DB 901 CGAAACACAGACATGAGCCTCATTTATGAAAAGTGTGTCCCATCTGACAAAGGGAATTAAT 960
 QY 1106 ACCTGTGTGTGAGAGATGAATAACGGGTCATCATACAGATGACAGTCCATGATGTTGTG 1165
 DB 961 ACCTGTGTGTGAGAGATGAATAACGGGTCATCATACAGATGACAGTCCATGATGTTGTG 1020
 QY 1166 GAGCGATGCTCTCAACGGCCCATCTCTCAAGCCGAGCTGCGCAAAATGCTCTCAACAGT 1225
 DB 1021 GAGCGATGCTCTCAACGGCCCATCTCTCAAGCCGAGCTGCGCAAAATGCTCTCAACAGT 1080
 QY 1226 GTCCGAGGAGAGATGATTTGTCTGCAAGTTTACAGATGAGCCAGGCCCAACATCCAG 1285
 DB 1081 GTCCGAGGAGAGATGATTTGTCTGCAAGTTTACAGATGAGCCAGGCCCAACATCCAG 1140
 QY 1286 TGGATCAACAGCTGTGAAAAGACAGCAGTAAATACGGGCCGACAGCGGCTGCTTACCTC 1345
 DB 1141 TGGATCAACAGCTGTGAAAAGACAGCAGTAAATACGGGCCGACAGCGGCTGCTTACCTC 1200
 QY 1346 AAGGTTCTCAAGACATCGGGGATTAATAGTCCATATGCAAGATGCTGCTGT----- 1400
 DB 1201 AAGGTTCTCAAGACATCGGGGATTAATAGTCCATATGCAAGATGCTGCTGT----- 1260
 QY 1401 -TCAATGTAACGAGGCGAGATGCTGGGGAATATATATGTAAGTCTCCAAATATATAGG 1459
 DB 1261 CCGAATGTACTTTTAAAGACGCTGGGGAATATATGTAAGTCTCCAAATATATAGG 1320
 QY 1460 CAGGCAACAGCTGCTGCTGCTCACTGTCTGCAAAAACAGCAACGCTGTGAGAGAA 1519
 DB 1321 AATATCTTTCACTGTGATGTGATGACAGTCTGCT-----ACGCTGTGAGAGAA 1371
 QY 1520 AAGGAGATTAACGCTTCCCAAGATACCTGTGAGATGAGCAATTTTACTGTGATGGGCTTTC 1579
 DB 1372 AAGGAGATTAACGCTTCCCAAGATACCTGTGAGATGAGCAATTTTACTGTGATGGGCTTTC 1431
 QY 1580 TTAATGCGCTGATGTGTGTAACATCATCTGTGTGCGAATGAAGAAACGACCAAGAG 1639
 DB 1432 TTAATGCGCTGATGTGTGTAACATCATCTGTGTGCGAATGAAGAAACGACCAAGAG 1491
 QY 1640 CCAGACTTGAAGCAGCCGCGCTGTGCAACAGCTGACCAAAAGTATCCCTGCGAGAG 1699
 DB 1492 CCAGACTTGAAGCAGCCGCGCTGTGCAACAGCTGACCAAAAGTATCCCTGCGAGAG 1551

QY 1700 CAGGTAAAGTTCGCGTGAAGTCCAGCTCTCCATGAATCCCAACACCCCGCTGTGAGG 1759
 DB 1552 CAGGTAAAGTTCGCGTGAAGTCCAGCTCTCCATGAATCCCAACACCCCGCTGTGAGG 1611
 QY 1760 AATAACAACGCTCTCTTCAACCGCAGACACCCCATGCTGTGAGGAGGCTCTCCAGAT 1819
 DB 1612 AATAACAACGCTCTCTTCAACCGCAGACACCCCATGCTGTGAGGAGGCTCTCCAGAT 1671
 QY 1820 GACTTCCAGAGAACCCCAAAATGGAGTTTCCAGAGATTAAGCTGACATGCGGCAAGGCC 1879
 DB 1672 GAACTTCCAGAGAACCCCAAAATGGAGTTTCCAGAGATTAAGCTGACATGCGGCAAGGCC 1731
 QY 1880 CTGGAGAGAGGTTGCTTGTGGCAAGTGTCAATGCGGAGAGAGTGGAAATTAACAAGAC 1939
 DB 1732 CTGGAGAGAGGTTGCTTGTGGCAAGTGTCAATGCGGAGAGAGTGGAAATTAACAAGAC 1791
 QY 1940 AAGCCCAAGAGGCGGTCAACGCTGCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1999
 DB 1792 AAGCCCAAGAGGCGGTCAACGCTGCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1851
 QY 2000 GACTTCTGTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGGAAACACAAAGAT 2059
 DB 1852 GACTTCTGTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGGAAACACAAAGAT 1911
 QY 2060 ATCATTAATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCAATGATGAT 2119
 DB 1912 ATCATTAATCTTCTTGAAGCTGACACAGATGAGGCTCTCTATGTCAATGATGAT 1971
 QY 2120 GCTCTTAAAGGCACTTCAGAAATACCTCCGAGCCGAGAGCCACCCGGAGTGAATAC 2179
 DB 1972 GCTCTTAAAGGCACTTCAGAAATACCTCCGAGCCGAGAGCCACCCGGAGTGAATAC 2031
 QY 2180 TCTTATGACATTAACCGTGTCTGTGAGAGAGATGACCTTCAAGAGCTTGTGTCAATG 2239
 DB 2032 TCTTATGACATTAACCGTGTCTGTGAGAGAGATGACCTTCAAGAGCTTGTGTCAATG 2091
 QY 2240 ACTTACAGCTGTGCGACAGATGAGTACTGTGCTTCCCAAAATGATTTATCATGAGAT 2299
 DB 2092 ACTTACAGCTGTGCGACAGATGAGTACTGTGCTTCCCAAAATGATTTATCATGAGAT 2151
 QY 2300 TTAGCAGCAGAAATGTTTTGTGTAACAGAAAACAAATGTATGAATAATGACAGCTTTG 2359
 DB 2152 TTAGCAGCAGAAATGTTTTGTGTAACAGAAAACAAATGTATGAATAATGACAGCTTTG 2211
 QY 2360 CTGCGCAGAGATATCAACATATATGACATTTTCAAAAAAGACCAACAAATGGGGCTTCA 2419
 DB 2212 CTGCGCAGAGATATCAACATATATGACATTTTCAAAAAAGACCAACAAATGGGGCTTCA 2271
 QY 2420 GTCAAGTGAATGCTCCAGAAAGCCGTGTGTAAGATATACATCATCAGATGATGTC 2479
 DB 2272 GTCAAGTGAATGCTCCAGAAAGCCGTGTGTAAGATATACATCATCAGATGATGTC 2331
 QY 2480 TGGTCTTCCGCGGTGTATATGTGAGATCTTCACTTTAAGGGGCTGCGCTTACCCAGG 2539
 DB 2332 TGGTCTTCCGCGGTGTATATGTGAGATCTTCACTTTAAGGGGCTGCGCTTACCCAGG 2391
 QY 2540 ATTCCCGTGAAGAACTTTTAAAGCTGTGAAGAGAGACACAGATGATTAAGCAAGCC 2599
 DB 2392 ATTCCCGTGAAGAACTTTTAAAGCTGTGAAGAGAGACACAGATGATTAAGCAAGCC 2451
 QY 2600 AACTGACCAACGACTGTACATGATGATGAAGGACTGTTGGCATGAGTGCCTCCAG 2659
 DB 2452 AACTGACCAACGACTGTACATGATGATGAAGGACTGTTGGCATGAGTGCCTCCAG 2511
 QY 2660 AAGACCAAGTTCAACAGTGTGATGAAGCTTGAATGCAATTTCTCATCAACCAAT 2719
 DB 2512 AAGACCAAGTTCAACAGTGTGATGAAGCTTGAATGCAATTTCTCATCAACCAAT 2571
 QY 2720 GAGGAATCTTGAAGCTTCAAGCACTCTGCAAGAGATTTCACTTAAGTTACCTTGAACA 2779
 DB 2572 GAGGAATCTTGAAGCTTCAAGCACTCTGCAAGAGATTTCACTTAAGTTACCTTGAACA 2631
 QY 2780 AAGAGTCTTGTCTTCAAGAGATGATTTCTGTTTTCTCCAGACCCCATGCTTACGAA 2839

```
Db      2632 AGAAGTTCTTGTCTTCAGGAGATGATTTCTTTTCTCCAGACCCCATGCTTACGAA 2691
Qy      2840 CCATGCCCTTCCCTCAGTATCCACATATAACGAGTGTAAACATGATGACTGTGCT 2899
Db      2692 CCAATGCCCTTCCCTCAGTATCCACATATAACGAGTGTAAACATGATGACTGTGCT 2751
Qy      2900 GCCTGTCCCAACAGACAGCACTGGGAACTTAGCTAAGCTGAGCAGGAGACCATGCC 2959
Db      2752 GCCTGTCCCAACAGACAGCACTGGGAACTTAGCTAAGCTGAGCAGGAGACCATGCC 2811
Qy      2960 TCCGAGAGCTGTGTCTCCCACTGTATATATGATCAGAGAGTAAATATGGAAAG 3019
Db      2812 TCCGAGAGCTGTGTGTCTCCCACTGTATATATGATCAGAGAGTAAATATGGAAAG 2871
Qy      3020 TAATCAGCATATGTGTAAAGATTATACAGTTGAAAACCTGTAAATCTTCCCAGAGGAG 3079
Db      2872 TAATCAGCATATGTGTAAAGATTATACAGTTGAAAACCTGTAAATCTTCCCAGAGGAG 2931
Qy      3080 AAGAAGGTTTCTGAGAGAGTGACTGC 3106
Db      2932 AAGAAGGTTTCTGAGAGAGTGACTGC 2958
```

Search completed: October 2, 2006, 18:59:47
Job time : 3260 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:59:37 ; Search time 1091 Seconds
(without alignments)
5253.440 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaaatgtgtg.....ttctcgagcagtgactgc 3106

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: 4741290

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database :

Published Applications NA New.*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCR_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3025.4	97.4	4612	6	US-10-669-920-566 Sequence 566, App
2	3025.4	97.4	5003	6	US-10-669-920-572 Sequence 572, App
3	2967.4	95.5	4485	6	US-10-669-920-614 Sequence 614, App
4	2890.2	93.1	4609	6	US-10-669-920-576 Sequence 576, App
5	2890.2	93.1	5000	6	US-10-669-920-564 Sequence 564, App
6	2882.2	92.8	4990	6	US-10-669-920-634 Sequence 634, App
7	2867.8	92.3	4607	6	US-10-669-920-608 Sequence 608, App
8	2867.8	92.3	4398	6	US-10-669-920-628 Sequence 628, App
9	2824.2	90.9	4472	6	US-10-669-920-590 Sequence 590, App
10	2780.2	89.5	5080	6	US-10-669-920-598 Sequence 598, App
11	2765.8	89.0	4697	6	US-10-669-920-582 Sequence 582, App
12	2765.8	89.0	5088	6	US-10-669-920-588 Sequence 588, App
13	2641.4	85.0	3241	6	US-10-669-920-602 Sequence 602, App
14	2641.4	85.0	3632	6	US-10-669-920-626 Sequence 626, App
15	2506.2	80.7	3328	6	US-10-669-920-570 Sequence 570, App
16	2506.2	80.7	3629	6	US-10-669-920-620 Sequence 620, App
17	2506	80.7	3216	8	US-11-266-748A-30641 Sequence 30641, A
18	2425	78.1	4218	6	US-10-669-920-588 Sequence 588, App
19	2417	77.8	4208	6	US-10-669-920-606 Sequence 606, App
20	2347.8	75.6	4342	6	US-10-669-920-610 Sequence 610, App
21	2347.8	75.6	4733	6	US-10-669-920-604 Sequence 604, App
22	2327.4	74.9	4257	6	US-10-669-920-616 Sequence 616, App
23	2327.4	74.9	4648	6	US-10-669-920-594 Sequence 594, App

24	2327	74.9	4267	6	US-10-669-920-612 Sequence 612, App
25	2327	74.9	4658	6	US-10-669-920-624 Sequence 624, App
26	2319	74.7	4257	6	US-10-669-920-578 Sequence 578, App
27	2319	74.7	4648	6	US-10-669-920-586 Sequence 586, App
28	2269.4	73.1	4130	6	US-10-669-920-630 Sequence 630, App
29	2269	73.1	4140	6	US-10-669-920-622 Sequence 622, App
30	2261	72.8	4130	6	US-10-669-920-568 Sequence 568, App
31	2092.4	67.4	2657	6	US-10-669-920-592 Sequence 592, App
32	2092.4	67.4	3048	6	US-10-669-920-584 Sequence 584, App
33	2015	64.9	2124	7	US-11-365-989-135 Sequence 135, App
34	1898.2	61.1	3104	6	US-10-669-920-581 Sequence 581, App
35	1441.6	46.4	2219	6	US-10-669-920-574 Sequence 574, App
36	1441.6	46.4	1828	6	US-10-669-920-596 Sequence 596, App
37	1110.8	35.8	3809	8	US-11-266-748A-354004 Sequence 354004, A
38	1110.8	35.8	3809	8	US-11-266-748A-384732 Sequence 384732, A
39	1110.8	35.8	3809	8	US-11-266-748A-437383 Sequence 437383, A
40	1102.6	35.5	2011	6	US-10-669-920-580 Sequence 580, App
41	1102.6	35.5	2402	6	US-10-669-920-632 Sequence 632, App
42	1078.2	34.7	1882	8	US-11-266-748A-185251 Sequence 185251, A
43	1068	34.4	3722	6	US-10-669-920-432 Sequence 432, App
44	1054.4	33.9	3573	6	US-10-669-920-423 Sequence 423, App
45	1045.8	33.7	3203	6	US-10-669-920-425 Sequence 425, App

ALIGNMENTS

```

RESULT 1
US-10-669-920-566
; Sequence 566, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-566

Query Match      97.4%; Score 3025.4; DB 6; Length 4612;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

QY      1  CCGGAGCAAGCTTGTGAGGAGCAAG-CAAGCTGAGTCTTCTCTGCTTC 59
DB      187 CCGGAGCAAGCTTGTGAGGAGCAAGCAAGCTGAGTCTTCTCTGCTTC 246
QY      60 CCAATTCGAGGAGCCCGCGGCGTCAATG---GCGCTCTCGCAGCTGGGATACG 116
DB      247 CCAATTCGAGGAGCCCGCGGCGTCAATGCGCGCTCTCGCAGCTGGGATACG 306

```

OY	117	GTGAAGCCCGGGAGGCTTGGCGCCGGGAGAGACCCMAAGACACTCTTCTTCGCTTGGAG	176
Db	307	GTGAAGCCCGGGAGGCTTGGCGCCGGGAGAGACCCMAAGACACTCTTCTTCGCTTGGAG	366
OY	177	TTGCTCCCGGCAACCCCGGGGCTCGTGCCTTCTCATCTCCGACCCAGCGGGGCG	235
Db	367	TTGCTCCCGGCAACCCCGGGGCTCGTGCCTTCTCATCTCCGACCCAGCGGGGCGGGG	426
OY	236	ACAAACAAGGTCGCGGAGGACGTTGCCATTCAAGTGACTGCAGACAGACG-GCAGCGCC	294
Db	427	ACAAACAAGGTCGCGGAGGACGTTGCCATTCAAGTGACTGCAGACAGCGGACAGCGCC	486
OY	295	TCGGTTCCTTGAGCCCAACCGCA-GCCTGAAGGACATTGGCGGTATGTCATGCCCCGTAGAGAA	353
Db	487	TCGGTTCCTTGAGCCCAACCGCAAGGCTGAAGGACATTGGCGGTATGTCATGCCCCGTAGAGAA	546
OY	354	GTGTGACAGATGGATTTAACTGTCCAATGAGATATGGAAGAGACCGGGGATTGGTACG	413
Db	547	GTGTGACAGATGGATTTAACTGTCCAATGAGATATGGAAGAGACCGGGGATTGGTACG	606
OY	414	TTAACATAGGTCAAGCTGGGGGTGTTTCACTGCTCGTGTGTGTGTACCATGGCAACTTGT	473
Db	607	TTAACATAGGTCAAGCTGGGGGTGTTTCACTGCTCGTGTGTGTGTACCATGGCAACTTGT	666
OY	474	CCCTGGCCCGGCCCCCTTCAGTTTATGTTGAGATACCACTTAGAGCCAGAGAGCCAC	533
Db	667	CCCTGGCCCGGCCCCCTTCAGTTTATGTTGAGATACCACTTAGAGCCAGAGAGCCAC	726
OY	534	CAACCAATATCCAAATCTTCTCAACCAAGTGTATGTGGCTGCGCCAGAGGAGTCTGTAG	593
Db	727	CAACCAATATCCAAATCTTCTCAACCAAGTGTATGTGGCTGCGCCAGAGGAGTCTGTAG	786
OY	594	AGGTGCGGCGCTGTTGAAGAATGTCGCGCGGTGATCAGTTGACATAAGGATGGGTGCACT	653
Db	787	AGGTGCGGCGCTGTTGAAGAATGTCGCGCGGTGATCAGTTGACATAAGGATGGGTGCACT	846
OY	654	TGGGGCCCAACAAATGAGCAAGTGCTTATTTGGGGAGTACTTGCAGATTAAGGGCGCAAC	713
Db	847	TGGGGCCCAACAAATGAGCAAGTGCTTATTTGGGGAGTACTTGCAGATTAAGGGCGCAAC	906
OY	714	CTAAGACATTCGGGCTCTATGCTGTACTGTGCAGATGAGACGTGTAGACAGTBAACCTTGGT	773
Db	907	CTAAGACATTCGGGCTCTATGCTGTACTGTGCAGATGAGACGTGTAGACAGTBAACCTTGGT	966
OY	774	ACTTCATGCTGAATGTCAACAATGCCATCTCATCCGAGATGATGAGATGACCCGATG	833
Db	967	ACTTCATGCTGAATGTCAACAATGCCATCTCATCCGAGATGATGAGATGACCCGATG	1026
OY	834	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAGAAGACACATACCTGAGACCAACA	893
Db	1027	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAAGAAGACACATACCTGAGACCAACA	1086
OY	894	CAGAAAAGATGGAAGAAAGCGGCTCAATGCTGTGCTCGCGGACCAACTGTCAAGTTTCGCT	953
Db	1087	CAGAAAAGATGGAAGAAAGCGGCTCAATGCTGTGCTCGCGGACCAACTGTCAAGTTTCGCT	1146
OY	954	GCCACGCCGGGGGGAACCCCAATGCCAACCATGCGGTGCTGTAAAAACGGGAAGAGTTTA	1013
Db	1147	GCCACGCCGGGGGGAACCCCAATGCCAACCATGCGGTGCTGTAAAAACGGGAAGAGTTTA	1206
OY	1014	AGCAGAGAGATGCAATGGAGGCTTCAAGGTACAGAAACAGACACTGGAGCCTCATTTATGG	1073
Db	1207	AGCAGAGAGATGCAATGGAGGCTTCAAGGTACAGAAACAGACACTGGAGCCTCATTTATGG	1266
OY	1074	AAAGTGTGTTCCCATCTGCAAGAGGAATTTATACCTGTGTATGTGAGATGATATCGGGT	1133
Db	1267	AAAGTGTGTTCCCATCTGCAAGAGGAATTTATACCTGTGTGTGAGATGATATCGGGT	1326
OY	1134	CCATCAATACACGTAACCACTGGAATGTTGTGAGACGATATGCGCTCAACGGGCCCATCTTCC	1199
Db	1327	CCATCAATACACGTAACCACTGGAATGTTGTGAGACGATATGCGCTCAACGGGCCCATCTTCC	1386

QY	1194	AAGCGGAGCTGCCGGAATAGCTCTCAACAGTGGTCGAGGAGACGTAGAGTTGTCTGCA	1253
Db	1387	AAGCGGAGCTGCCGGAATAGCTCTCAACAGTGGTCGAGGAGACGTAGAGTTGTCTGCA	1446
QY	1254	AGGTTTACAGTGAAGGCCCAAGCCCCACATCCAGTGGATCAAGCAGCTGGAAAAAGAACGGCA	1313
Db	1447	AGGTTTACAGTGAAGGCCCAAGCCCCACATCCAGTGGATCAAGCAGCTGGAAAAAGAACGGCA	1506
QY	1314	GTAATATCGGGCCCGAGCGGGCTGCCCTTACCTCAAGTTCTTCAAGCACTCGGGATAAATA	1373
Db	1507	GTAATATCGGGCCCGAGCGGGCTGCCCTTACCTCAAGTTCTTCAAGCACTCGGGATAAATA	1566
QY	1374	GTTCCAAATGCAGAAAGTGTGGCTCTGTTCAAATGTGACCGAGGCGGATGCTGGGAATATA	1433
Db	1567	GTTCCAAATGCAGAAAGTGTGGCTCTGTTCAAATGTGACCGAGGCGGATGCTGGGAATATA	1626
QY	1434	TATGTAAAGTCTCCAAATATATATAGGGAGGCGAACAGTCGGCTGTCACTGTCTCTGC	1493
Db	1627	TATGTAAAGTCTCCAAATATATATAGGGAGGCGAACAGTCGGCTGTCACTGTCTCTGC	1686
QY	1494	CAAAACAGCAAGCCCTGGAAGAGAAAAAGAGATTACAGCTTCCCAAGACTTACCTGAGAG	1553
Db	1687	CAAAACAGCAAGCCCTGGAAGAGAAAAAGAGATTACAGCTTCCCAAGACTTACCTGAGAG	1746
QY	1554	TAGCCATTACTGCAATAGGGGTCTTCTTAATCGCTGTATGTGTGTAAACATCATCTCTGT	1613
Db	1747	TAGCCATTACTGCAATAGGGGTCTTCTTAATCGCTGTATGTGTGTAAACATCATCTCTGT	1806
QY	1614	GCCCAATGAACAACAGCACGACCAAGAAAGCGACCTTACAGAGCACGCGGCTGTGACAAAG	1673
Db	1807	GCCCAATGAACAACAGCACGACCAAGAAAGCGACCTTACAGAGCACGCGGCTGTGACAAAG	1866
QY	1674	TGACCAAACTATCCCCCTGCGGAGACAGGTATAC----AGTTTGAGGTAGTCCAGCTCC	1729
Db	1867	TGACCAAACTATCCCCCTGCGGAGACAGGTATACAAAGAAATTTGGCTGAGTCCAGCTCC	1926
QY	1730	TCCATGAATCTCOAACACCCCGCTGGTGAAGATTAACAACGCTCTCTTCAAAGGCAAGC	1789
Db	1927	TCCATGAATCTCOAACACCCCGCTGGTGAAGATTAACAACGCTCTCTTCAAAGGCAAGC	1986
QY	1790	AACCCCAATGCTGGGAGGGGTCTCCGAGTATGAATCTTCAGAGAGACCCAAAATGGGAATTT	1849
Db	1987	AACCCCAATGCTGGGAGGGGTCTCCGAGTATGAATCTTCAGAGAGACCCAAAATGGGAATTT	2046
QY	1850	CCAAGAGATTAAGCTGACACTGAGGCAAGCCCTGGGAGAGAGTTGCTTTGGCAAGTGTCTC	1909
Db	2047	CCAAGAGATTAAGCTGACACTGAGGCAAGCCCTGGGAGAGAGTTGCTTTGGCAAGTGTCTC	2106
QY	1910	ATGGCGAAGCAGTGGGAATTTGACAAAGACAAGCCCAAGAGGGGTGATCCGTGGCCGTG	1965
Db	2107	ATGGCGAAGCAGTGGGAATTTGACAAAGACAAGCCCAAGAGGGGTGATCCGTGGCCGTG	2166
QY	1970	AAAGATGTTGAAGAATGATATGCCACAGAGAAACAACCTTCTGATCTGGTGTCAAGATGGAG	2022
Db	2167	AAAGATGTTGAAGAATGATATGCCACAGAGAAACAACCTTCTGATCTGGTGTCAAGATGGAG	2222
QY	2030	ATGATGAAGATGAATTGGGAAAAACAAGAAATATCATAAATCTTCTTGGAGCCTGCAACAG	2083
Db	2227	ATGATGAAGATGAATTGGGAAAAACAAGAAATATCATAAATCTTCTTGGAGCCTGCAACAG	2288
QY	2090	GATGGGAGCTCTCTATGTATCATATGTTAGTATGCTCTTAAAGGCACCTCCGAAATATCTCTC	2145
Db	2287	GATGGGAGCTCTCTATGTATCATATGTTAGTATGCTCTTAAAGGCACCTCCGAAATATCTCTC	2346
QY	2150	CGAGGCCCGGAGGCCACCCCGGATGGAGATATCCCTATATGCAATTAAACCGTGTCTGAGGAG	2209
Db	2347	CGAGGCCCGGAGGCCACCCCGGATGGAGATATCCCTATATGCAATTAAACCGTGTCTGAGGAG	2406
QY	2210	CAGATGACCTTCAAAGACTTGGTGTCAAGCACTTACAGCTGAGCGGACGAGATGAGATAC	2265
Db	2407	CAGATGACCTTCAAAGACTTGGTGTCAAGCACTTACAGCTGAGCGGACGAGATGAGATAC	2466
QY	2270	TTGGCTTCCCAAAATGATATTCATGAGATTTAGCAGCGCAAGAAATGTTTGGTAAACAGAA	2322

Db	2467	TTGGCTTCCAAAATGTATTCATGAGATTTCAGACCGCAAAAGTTTGGTAACAGAA	2522
Qy	2330	AACAATGTATGATAAATATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATPAGACTAT	2385
Db	2527	AACAATGTATGATAAATATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATPAGACTAT	2588
Qy	2390	TACAAAAAGCACCAATGAGGCGCTTCCAGTCAGTAGTGATGSGCTCCAGAGCCCTGTTT	2443
Db	2587	TACAAAAAGCACCAATGAGGCGCTTCCAGTCAGTAGTGATGSGCTCCAGAGCCCTGTTT	2644
Qy	2450	GATGAGATATACCTCATCAGAGTATGTCGTGCTTCGGGGGTGTATGNGGGAGATC	2509
Db	2647	GATGAGATATACCTCATCAGAGTATGTCGTGCTTCGGGGGTGTATGNGGGAGATC	2700
Qy	2510	TTCACTTTAGGGGGGCTCGCCCTACACAGGAGATTCCTGGTGAAGAACTTTTTAAGCTGCTG	2561
Db	2707	TTCACTTTAGGGGGGCTCGCCCTACACAGGAGATTCCTGGTGAAGAACTTTTTAAGGCTGCTG	2766
Qy	2570	AAGGAAGGACACAGATGAGTAAAGCCAGCCAACTGACCAAGAACTGTACATGATGATG	2622
Db	2767	AAGGAAGGACACAGATGAGTAAAGCCAGCCAACTGACCAAGAACTGTACATGATGATG	2822
Qy	2630	AGGAGCTGTGGCATGCAATGCGCTTCCAGAGAACCAAGTTCAACAGTGTGTAAAGAC	2688
Db	2827	AGGAGCTGTGGCATGCAATGCGCTTCCAGAGAACCAAGTTCAACAGTGTGTAAAGAC	2888
Qy	2690	TTGGATCGAATTCCTCACTCTCAACAACAATGAGAAATCTTGAAGCTCAGCCAACTCTC	2743
Db	2887	TTGGATCGAATTCCTCACTCTCAACAACAATGAGAAATCTTGAAGCTCAGCCAACTCTC	2943
Qy	2750	GAAACGATTCACCTAGATTACCTGTACACAGAGTTCTTGTCTTCAGAGATGATTTCT	2800
Db	2947	GAAACGATTCACCTAGATTACCTGTACACAGAGTTCTTGTCTTCAGAGATGATTTCT	3000
Qy	2810	GTTTTTTTCTCCAGACCCCATGCGCTTAAGAAACAATGCTTCTCAGATACACAAATAAC	2866
Db	3007	GTTTTTTTCTCCAGACCCCATGCGCTTAAGAAACAATGCTTCTCAGATACACAAATAAC	3066
Qy	2870	GGCAGTGTAAAAACATGATGACTGTGTCGCTGTCGCCAACAACAGACAGCACTGGGAA	2922
Db	3067	GGCAGTGTAAAAACATGATGACTGTGTCGCTGTCGCCAACAACAGACAGCACTGGGAA	3122
Qy	2930	CCTAGCTACACTGACAGGAGACCAATGCTTCAGAGCTGTGTCTCCACTTGTATAT	2988
Db	3127	CCTAGCTACACTGACAGGAGACCAATGCTTCAGAGCTGTGTCTCCACTTGTATAT	3188
Qy	2990	ATGATCAGAGAGTAAATATTTGAAAAATGATACATATGTGTAAAGATTTATACAG	3043
Db	3187	ATGATCAGAGAGTAAATATTTGAAAAATGATACATATGTGTAAAGATTTATACAG	3243
Qy	3050	TTGAAACTTGTAATCTTCCCAAGAGGAGAAAGGTTCTGGAGCAGTGCATGC	3106
Db	3247	TTGAAACTTGTAATCTTCCCAAGAGGAGAAAGGTTCTGGAGCAGTGCATGC	3303
RESULT 2			
US-10-669-920-572			
: Sequence 572, Application US/10669920			
: Publication No. US20060194265A1			
: GENERAL INFORMATION:			
: APPLICANT: Moritz, David W.			
: APPLICANT: Malandro, Marc S.			
: TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER			
: FILE REFERENCE: 20366-066001			
: CURRENT APPLICATION NUMBER: US/10/669,920			
: CURRENT FILING DATE: 2003-09-23			
: PRIOR APPLICATION NUMBER: US 10/004,113			
: PRIOR FILING DATE: 2001-10-23			
: PRIOR APPLICATION NUMBER: US 10/052,482			
: PRIOR FILING DATE: 2001-11-08			
: PRIOR APPLICATION NUMBER: US 09/997,722			
: PRIOR FILING DATE: 2001-11-30			

	Query Match	97.4%	Score 3025.4	DB 6	Length 5003	
	Best Local Similarity	99.5%	Pred. No. 0			
	Matches 3100	Conservative	0	Mismatches	6	Indels 11
						Gaps 6
QY	1	CCCGGAGCAAGTTGATGAGGCAACG-CAGGCTGAGTCTTTCTTCTCTGTTCC	59			
DB	578	CTCCGAGCAAGTTGTGTGAGGCAACGCAAGCTGAGTCTTTCTTCTCTGTTCC	637			
QY	60	CCAAATTCGAGGAGGACCCCGGGGCTGATG--GGCTCTCTCCGAGGCTGGGGTACGC	116			
DB	638	CCAAATTCGAGGAGGACCCCGGGGCTGATG--GGCTCTCTCCGAGGCTGGGGTACGC	697			
QY	117	GTAAGGCCGGGGAAGGCTTGGGCGCGGGAGAGACCCAGAGACCACTTCTGCTTGGAG	176			
DB	698	GTAAGGCCGGGGAAGGCTTGGGCGCGGGAGAGACCCAGAGACCACTTCTGCTTGGAG	757			
QY	177	TTGCTCCCGGCAACCCCGGGCTCGTCTTCTTCATTCGACCCGAGCCGCGGAGC-CGAGG	235			
DB	758	TTGCTCCCGGCAACCCCGGGCTCGTCTTCTTCATTCGACCCGAGCCGCGGAGC-CGAGG	817			
QY	236	ACAACACAGGTGCGGAGAGAGCGTTGCCATTCAAGTAATGACAGACAGC-CGAGG	294			
DB	818	ACAACACAGGTGCGGAGAGAGCGTTGCCATTCAAGTAATGACAGACAGC-CGAGG	877			
QY	295	TTCGTTTCTGAGCCCAACCGCA-GGTGAAGGATTTGGCGGTAGTCATGCCCCGTAGAGAA	353			
DB	878	TTCGTTTCTGAGCCCAACCGCAAGGTGAAGGATTTGGCGGTAGTCATGCCCCGTAGAGAA	937			
QY	354	GTAAGGAGATGGAATTAACGTCACATGAGAGATTAAGAGAGACCCGGGATTTGTACCG	413			
DB	938	GTAAGGAGATGGAATTAACGTCACATGAGAGATTAAGAGAGACCCGGGATTTGTACCG	997			
QY	414	TAAACATGTCAGCTGGGGGTGTTTCATCTGCTGTGCTGTGTCACCATGCAACTTGT	473			
DB	998	TAAACATGTCAGCTGGGGGTGTTTCATCTGCTGTGCTGTGTCACCATGCAACTTGT	1057			
QY	474	CCCTGGCCCGGCTCTCTTCAAGTTAGTTAGATACCACTTATAGACCCAGAAAGCCAC	533			
DB	1058	CCCTGGCCCGGCTCTCTTCAAGTTAGTTAGATACCACTTATAGACCCAGAAAGCCAC	1117			
QY	534	CAACCAATATCAAAATCTCTCAACACAGAGGTGACGTGCTGCCCAAGGAGGTGCTAG	593			
DB	1118	CAACCAATATCAAAATCTCTCAACACAGAGGTGACGTGCTGCCCAAGGAGGTGCTAG	1177			
QY	594	AGGTGCGGTGCTTTGAAAGATGCGCGGTGATCAAGTTGACATTAAGGATGGGTGACT	653			
DB	1178	AGGTGCGGTGCTTTGAAAGATGCGCGGTGATCAAGTTGACATTAAGGATGGGTGACT	1237			
QY	654	TGGGGCCCAAAATAGACAGTGTATATTTGGGAGGTACTTGCAATTAAGGCGCCACAC	713			
DB	1238	TGGGGCCCAAAATAGACAGTGTATATTTGGGAGGTACTTGCAATTAAGGCGCCACAC	1297			
QY	714	CTAAGAGATCCGGGCTCTATGCTTGTACTGCAATAGACATGTAGACAGTGAACCTTGGT	773			
DB	1298	CTAAGAGATCCGGGCTCTATGCTTGTACTGCAATAGACATGTAGACAGTGAACCTTGGT	1357			

OY	774	ACTTCATGCTGAATGTCA	CAGATG	CCATCTCA	TCCGAGATGATGATGAGATGACACCGAGT	893		
Db	1358	ACTTCATGCTGAATGTCA	CAGATG	CCATCTCA	TCCGAGATGATGATGAGATGACACCGAGT	1417		
OY	834	GTGCGGAAGA	TTTTGT	CTAGTGA	AACGTAAACAACAAGAGGACCACTACTGACACACA	893		
Db	1418	GTGCGGAAGA	TTTTGT	CTAGTGA	AACGTAAACAACAAGAGGACCACTACTGACACACA	1477		
OY	894	CAGAAAAGATGAAA	AAGCGCTCA	TGCTGTG	CTGCGGCCACACCTGTCAAGTTTCGT	953		
Db	1478	CAGAAAAGATGAAA	AAGCGCTCA	TGCTGTG	CTGCGGCCACACCTGTCAAGTTTCGT	1537		
OY	954	GCCCAAGCCGGGGGGA	ACCCTA	TGCCCA	ACCAATGCGGTGGCTGAAAAAAGGGGAAGAGTTTA	1013		
Db	1538	GCCCAAGCCGGGGGGA	ACCCTA	TGCCCA	ACCAATGCGGTGGCTGAAAAAAGGGGAAGAGTTTA	1597		
OY	1014	AGCAGAGACAT	TGCAATTG	AGAGGCTTA	CAAGATGACAAAACAGCACTGAGGCTCAATTATG	1073		
Db	1588	AGCAGAGACAT	TGCAATTG	AGAGGCTTA	CAAGATGACAAAACAGCACTGAGGCTCAATTATG	1657		
OY	1074	AAAGTGTGTC	CCCATCTG	ACAAGGAA	TTATACCTGTGTGATGAGAAATGATACGGGT	1133		
Db	1658	AAAGTGTGTC	CCCATCTG	ACAAGGAA	TTATACCTGTGTGATGAGAAATGATACGGGT	1717		
OY	1134	CCATCAATCA	CACGTA	CCCACTG	TAATGTTTGAGAGCAATGCGCTCACCGGCCCATCTCC	1193		
Db	1718	CCATCAATCA	CACGTA	CCCACTG	TAATGTTTGAGAGCAATGCGCTCACCGGCCCATCTCC	1777		
OY	1194	AAGCGGAG	CTGCGCGGCA	ATGCGCTCA	CAGTGTGCGAGAGAGATGAGTTTGTCTGA	1253		
Db	1778	AAGCGGAG	CTGCGCGGCA	ATGCGCTCA	CAGTGTGCGAGAGAGATGAGTTTGTCTGA	1837		
OY	1254	AGGTTTAC	AGTGA	TGTC	CCCAAGCCCAATCCAGTGTGATCAGCACTGTGAAAAAGACGCA	1313		
Db	1838	AGGTTTAC	AGTGA	TGTC	CCCAAGCCCAATCCAGTGTGATCAGCACTGTGAAAAAGACGCA	1897		
OY	1314	GTAATA	TCGGGCGGCA	CGGGGCTG	CCCTTA	CTCAAGGTTCTCAAGCACTCGGGGATTAATA	1373	
Db	1898	GTAATA	TCGGGCGGCA	CGGGGCTG	CCCTTA	CTCAAGGTTCTCAAGCACTCGGGGATTAATA	1957	
OY	1374	GTTCCAA	TGCAAGATG	CTGCTCT	CTGTTCAATGTGACCGAGCGGATGCTGGGGAATATA	1433		
Db	1958	GTTCCAA	TGCAAGATG	CTGCTCT	CTGTTCAATGTGACCGAGCGGATGCTGGGGAATATA	2017		
OY	1434	TATGTAA	GGTCT	CCAA	TATATATAGGGCAGGCCAACCA	GTGCTGCTCACTGTCTGCG	1493	
Db	2018	TATGTAA	GGTCT	CCAA	TATATATAGGGCAGGCCAACCA	GTGCTGCTCACTGTCTGCG	2077	
OY	1494	CAAAACAG	CAACCGCTG	GAABAGAAAGGAG	TTACAGCTTCC	CACATCACTACCTGGAGA	1553	
Db	2078	CAAAACAG	CAACCGCTG	GAABAGAAAGGAG	TTACAGCTTCC	CACATCACTACCTGGAGA	2137	
OY	1554	TAGCA	TTTATCTG	CAATAG	GGGTCTTCTTA	TGCGCTGTATGGTGTAA	CAGTCACTCGT	1613
Db	2138	TAGCA	TTTATCTG	CAATAG	GGGTCTTCTTA	TGCGCTGTATGGTGTAA	CAGTCACTCGT	2197
OY	1614	GCGAATGA	GAACA	CGACCA	AGAAAGCAGACTT	CAGACGCCAGCGGCTGTGCA	CAAGC	1673
Db	2198	GCGAATGA	GAACA	CGACCA	AGAAAGCAGACTT	CAGACGCCAGCGGCTGTGCA	CAAGC	2257
OY	1674	TGA	CCAAAGTAT	TCCCGCTG	CGGAGACAGGTAA	C---AGTTGGGCTGAGTCCAGCTCC	1729	
Db	2258	TGA	CCAAAGTAT	TCCCGCTG	CGGAGACAGGTAA	C---AGTTGGGCTGAGTCCAGCTCC	2317	
OY	1730	TCATATGA	CTCCA	CAACCCCGCTG	GTGAGATTAACA	CAACGCGCTCTCTTCAACGGACAC	1789	
Db	2318	TCATATGA	CTCCA	CAACCCCGCTG	GTGAGATTAACA	CAACGCGCTCTCTTCAACGGACAC	2377	
OY	1790	ACCCCATG	CTGG	CAGGGGTCT	TCCAGTATGA	ATTCCAGAGAACCCAAATGGGAGTTT	1849	
Db	2378	ACCCCATG	CTGG	CAGGGGTCT	TCCAGTATGA	ATTCCAGAGAACCCAAATGGGAGTTT	2437	

QY	1850	CCAAAGATTAAGCTGCA	CACTGGGCAACCCCTGGGAAAGGTTGCTTGGGCAAGTGTG	1909			
Db	2438	CCAAAGATTAAGCTGCA	CACTGGGCAACCCCTGGGAAAGGTTGCTTGGGCAAGTGTG	2497			
QY	1910	ATGGCGAAGACGTGGGA	TTGACAAAGA	CAAGCCCAAGGAGCGGTCA	CGTGGCGTG	1969	
Db	2498	ATGGCGAAGACGTGGGA	TTGACAAAGA	CAAGCCCAAGGAGCGGTCA	CGTGGCGTG	2557	
QY	1970	AAAGTGTGAAGAATGAT	CCACAGAGAAAGACCTTTCTGATCTGGTGTCA	GAGATGGAG	2029		
Db	2558	AAAGTGTGAAGAATGAT	CCACAGAGAAAGACCTTTCTGATCTGGTGTCA	GAGATGGAG	2617		
QY	2030	ATGATGAAGAATGAT	TTGGGAAACA	CAAGAAATTCATTAATCTTCTTGAAGCTGCA	CAG	2089	
Db	2618	ATGATGAAGAATGAT	TTGGGAAACA	CAAGAAATTCATTAATCTTCTTGAAGCTGCA	CAG	2677	
QY	2090	GATGGGCGCTCTAT	GTGATAGTTGAGATGCTCTAAAGGCA	CTCCGAAATACCTC	2149		
Db	2678	GATGGGCGCTCTCTAT	GTGATAGTTGAGATGCTCTAAAGGCA	CTCCGAAATACCTC	2737		
QY	2150	CGAGCCCGGAGGCA	CCCGGAGTGAAGTACTCTATGA	CATTAA	CCGTGTTCTTGAAGG	2209	
Db	2738	CGAGCCCGGAGGCA	CCCGGAGTGAAGTACTCTATGA	CATTAA	CCGTGTTCTTGAAGG	2797	
QY	2210	CAGATGACCTTCA	BAGACTTGGTGTCA	TGCACCTACAGCTGGGCA	ACGGA	TGGAAGTAC	2269
Db	2798	CAGATGACCTTCA	BAGACTTGGTGTCA	TGCACCTACAGCTGGGCA	ACGGA	TGGAAGTAC	2857
QY	2270	TTGGCTTCCAAAAT	GTATTCATGAGATTTAGACG	CAAGAAATGTTTGGTAA	CAGAA	2329	
Db	2858	TTGGCTTCCAAAAT	GTATTCATGAGATTTAGACG	CAAGAAATGTTTGGTAA	CAGAA	2917	
QY	2330	AACAATGTGATGATAA	ATATAGCAGACTTTTGGACTGCGCAGAGATATCA	CAATATATAGACTAT	2389		
Db	2918	AACAATGTGATGATAA	ATATAGCAGACTTTTGGACTGCGCAGAGATATCA	CAATATATAGACTAT	2977		
QY	2390	TACAAAAAAGACA	CAATAGGGGCTTCCAGTCA	ATGGAATGGCTCCGAAAGCCCTGTT	2449		
Db	2978	TACAAAAAAGACA	CAATAGGGGCTTCCAGTCA	ATGGAATGGCTCCGAAAGCCCTGTT	3037		
QY	2450	GATAGAGTATAC	CTCATCAGAGTATGTCTGGTCTTCCGGGAGTGTAA	TATGTGGAGATC	2509		
Db	3038	GATAGAGTATATAC	CTCATCAGAGTATGTCTGGTCTTCCGGGAGTGTAA	TATGTGGAGATC	3097		
QY	2510	TTCACTTTAGGGG	GTCTGCCCCACAGGAAATCCGTGAGAGAA	CTTTTTAAGCTGTG	2568		
Db	3098	TTCACTTTAGGGG	GTCTGCCCCACAGGAAATCCGTGAGAGAA	CTTTTTAAGCTGTG	3157		
QY	2570	AAGGAAAGACAC	AAGATGATTAAGCGAGCCACATGCA	CCAA	CGA	CTGTACATGATGATG	2622
Db	3158	AAGGAAAGACAC	AAGATGATTAAGCGAGCCACATGCA	CCAA	CGA	CTGTACATGATGATG	3217
QY	2630	AAGGACTGTGGCA	TGCAAGTGCCCTCCAGAGACA	CGTTCAAGCAGTTGGTAA	GAAC	2688	
Db	3218	AAGGACTGTGGCA	TGCAAGTGCCCTCCAGAGACA	CGTTCAAGCAGTTGGTAA	GAAC	3277	
QY	2690	TTGGATCGAATTC	CTCACTCAACCAATGGAATATCTTGA	CCTGAGCAACCTGTG	2745		
Db	3278	TTGGATCGAATTC	CTCACTCAACCAATGGAATATCTTGA	CCTGAGCAACCTGTG	3333		
QY	2750	GAA	CAGTATTCACCTTAGTACCTCTGA	CACAGAAAGTTCTTGTCTTCA	GAGATGATCT	2803	
Db	3338	GAA	CAGTATTCACCTTAGTACCTCTGA	CACAGAAAGTTCTTGTCTTCA	GAGATGATCT	3397	
QY	2810	GTTTTTCTTC	CGAGCCCGGCTTACGAACATGCTTCTCA	GTATTCACACATTAAC	2865		
Db	3398	GTTTTTCTTC	CGAGCCCGGCTTACGAACATGCTTCTCA	GTATTCACACATTAAC	3455		
QY	2870	GCGAGTGTAAAA	CAATGATGACTGTGTGCTGTGCCAA	ACAGACAGACTGGGAA	2922		
Db	3458	GCGAGTGTAAAA	CAATGATGACTGTGTGCTGTGCCAA	ACAGACAGACTGGGAA	3511		
QY	2930	CTTAGCTTAC	CTGAGCAGGAGACCATGCTCTCCAGAGCTTGTGTCTTCA	CTTGTATAT	2988		

1434 TATGTAAAGTCTCCAAATTATATAGGGCAGGCGCAACCACTGTGCTGTCTCACTGTCTGC 1493
1434 TATGTAAAGTCTCCAAATTATATAGGGCAGGCGCAACCACTGTGCTGTCTCACTGTCTGC 1493
2018 TATGTAAAGTCTCCAAATTATATAGGGCAGGCGCAACCACTGTGCTGTCTCACTGTCTGC 2077
1494 CAAAACAGCAGCGCTGTGGAAGAAAGAGATTACAGCTTCCCAACATCACTGTGGA 1553
2078 CAAAACAGCAGCGCTGTGGAAGAAAGAGATTACAGCTTCCCAACATCACTGTGGA 2137
1554 TAGCCATTATCTGATAGGGGCTCTTAAATGCTGTATGTGTGTAAACATCACTGTG 1613
2138 TAGCCATTATCTGATAGGGGCTCTTAAATGCTGTATGTGTGTAAACATCACTGTG 2197
1614 GCCGAATGAAGAAACGACCAAGAACCAAGCTTCAAGCCAGCGCTGTGCAAGC 1673
2198 GCCGAATGAAGAAACGACCAAGAACCAAGCTTCAAGCCAGCGCTGTGCAAGC 2257
1674 TGACCAAACTATATCCCTGTGCGGAGACAGGTAC---AGTTTGGCTGAGTCCAGCTGC 1729
2258 TGACCAAACTATATCCCTGTGCGGAGACAGGTACAGAAAGTTTGGCTGAGTCCAGCTGC 2317
1730 TCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCTCTCTTCAACGCGCAGAC 1789
2318 TCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCTCTCTTCAACGCGCAGAC 2377
1790 ACCCCATGCTGTGCGAGGGGCTCTCGAGTATGAATCTTCAAGAGACCCAAATGGAGTTT 1849
2378 ACCCCATGCTGTGCGAGGGGCTCTCGAGTATGAATCTTCAAGAGACCCAAATGGAGTTT 2437
1850 CCAAGATTAAGCTGACACTGTGGCAAGCCCTGGGAGAAAGTTGTCTTTGGGCAAGTGTG 1909
2438 CCAAGATTAAGCTGACACTGTGGCAAGCCCTGGGAGAAAGTTGTCTTTGGGCAAGTGTG 2497
1910 ATGCGGAAAGCAGTGTGGAATTGACAAAGCAAGCCCAAGAGGCGGTCAACGCTGGCGT 1969
2498 ATGCGGAAAGCAGTGTGGAATTGACAAAGCAAGCCCAAGAGGCGGTCAACGCTGGCGT 2557
1970 AAGATGTTGAAAAGATGATGCCACAGAGAAAGCCTTTCTGATCTGTGTCAAGATGAG 2029
2558 AAGATGTTGAAAAGATGATGCCACAGAGAAAGCCTTTCTGATCTGTGTCAAGATGAG 2617
2020 ATGATGAAGATGATGGAAGAAACAAGAAATATCATTAATCTTCTGAGCCGTGACAG 2089
2618 ATGATGAAGATGATGGAAGAAACAAGAAATATCATTAATCTTCTGAGCCGTGACAG 2677
2090 GATGGGCTCTCTATGTCATAGTGTGATGCTCTTAAAGGCAACCTCGAAGATACCTC 2149
2678 GATGGGCTCTCTATGTCATAGTGTGATGCTCTTAAAGGCAACCTCGAAGATACCTC 2737
2150 CGAGCCCGGAGGCGACCCGGGATGAGATCTCTTATGACATTAACCGTGTCTGAGAG 2209
2738 CGAGCCCGGAGGCGACCCGGGATGAGATCTCTTATGACATTAACCGTGTCTGAGAG 2797
2210 CAGATGACCTTAAAGACTTGTGTGTCATGCACTTCCAGCTGCGCAGCGATGAGTAC 2269
2798 CAGATGACCTTAAAGACTTGTGTGTCATGCACTTCCAGCTGCGCAGCGATGAGTAC 2857
2270 TTGGCTTCCCAAAAATGATATCATGAGATTTAGCAGCCAGAAATGTTTGTGTAACAGA 2329
2858 TTGGCTTCCCAAAAATGATATCATGAGATTTAGCAGCCAGAAATGTTTGTGTAACAGA 2917
2330 AACAAATGTATGATAAATATGACAGCTTTGAGCTGCGCAGAGATATCAACATATAGACTAT 2389
2918 AACAAATGTATGATAAATATGACAGCTTTGAGCTGCGCAGAGATATCAACATATAGACTAT 2977
2390 TACAAAAGAACCAAGATGGGGGCTTCCAGTCAAGTGAATGGCTCCAGAACCCCTGTT 2449
2978 TACAAAAGAACCAAGATGGGGGCTTCCAGTCAAGTGAATGGCTCCAGAACCCCTGTT 3037
2450 GATAGAGTATACACTATCAGAGTGTCTGTGCTTGGGGTGTAAATGTGTGAGATC 2509
3038 GATAGAGTATACACTATCAGAGTGTCTGTGCTTGGGGTGTAAATGTGTGAGATC 3097

QY 2510 TTCACTTAGGGGGCTGCGCCCTTACCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGCTG 2569
DB 3098 TTCACTTAGGGGGCTGCGCCCTTACCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGCTG 3157
QY 2570 AAGGAGAGACAGAAATGATGATTAAGCCAGCCCACTGACCAAGAACTGTATCATGATATG 2629
DB 3158 AAGGAGAGACAGAAATGATGATTAAGCCAGCCCACTGACCAAGAACTGTATCATGATATG 3217
QY 2630 AGGAGCTGTTGGCAGTGCATGCTCTCCAGAGACCAACTTTCAAGCAGTTGTGTGAAGAC 2689
DB 3218 AGGAGCTGTTGGCAGTGCATGCTCTCCAGAGACCAAGTTTCAAGCAGTTGTGTGAAGAC 3277
QY 2690 TTGATGGAATTTCACTCTCAACCAATGAGGAATCTTGACCTCAGCCAACTCTC 2749
DB 3278 TTGATGGAATTTCACTCTCAACCAATGAGGAATCTTGACCTCAGCCAACTCTC 3337
QY 2750 GAACAGTATTCACCTAGTTACCTGACACAAAGATTTCTGTCTTCAAGAGATGATCT 2809
DB 3338 GAACAGTATTCACCTAGTTACCTGACACAAAGATTTCTGTCTTCAAGAGATGATCT 3397
QY 2810 GTTTTTTCTCAAGCCCAATGCTTTAGAACCATGCTTCTCTCAATATCCACATATAC 2869
DB 3398 GTTTTTTCTCAAGCCCAATGCTTTAGAACCATGCTTCTCTCAATATCCACATATAC 3457
QY 2870 GGCAGTGTAAACATGATGACTGTGTGCTGCTGCTCCCAACAGACAGCACTGGGAA 2929
DB 3458 GGCAGTGTAAACATGATGACTGTGTGCTGCTGCTCCCAACAGACAGCACTGGGAA 3517
QY 2930 CTTAGCTTACCTGACGAGGAGACCATGCTTCCAGAGCTTGTCTTCCACTGTATAT 2989
DB 3518 CTTAGCTTACCTGACGAGGAGACCATGCTTCCAGAGCTTGTCTTCCACTGTATAT 3577
QY 2990 ATGATCAGAGAGATTAATTTGGAAGAAATGATACATATGTGTAAAGTTTATACA 3048
DB 3578 ATGATCAGAGAGATTAATTTGGAAGAAATGATACATATGTGTAAAGTTTATACA 3636

RESULT 4

US-10-669-920-576

; Sequence 576, Application US/10669920

; Publication No. US20060194265A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Malandro, Marc S.

; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

; FILE REFERENCE: 20366-066001

; CURRENT FILING DATE: US/10/669, 920

; PRIOR FILING DATE: 2003-09-23

; PRIOR APPLICATION NUMBER: US 10/004,113

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: US 10/052,482

; PRIOR FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: US 09/997,722

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: US 10/034,650

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: US 10/085,117

; PRIOR FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: US 10/087,192

; PRIOR FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 10/322,281

; PRIOR FILING DATE: 2002-12-17

; PRIOR APPLICATION NUMBER: US 10/322,696

; PRIOR FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 1441

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 576

; LENGTH: 4609

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-669-920-576

Query Match

93.1%; Score 2890.2; DB 6; Length 4609;

Best Local Similarity 97.2%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;

```

OY 1 CCCGAGAGCAAGTTTGTGTGAGGCAACG-CAAGCTGAGTCTTTTCTCTCTGTTCC 59
Db 187 CTGGGAGCAAGTTTGTGTGAGGCAACGCAAGCTGAGTCTTTTCTCTCTGTTCC 246
OY 60 CCAATTCGAGGGGCAAGCCCGGGGCTCATG--GGCTCTCCGAGGCTTGGGTAAGC 116
Db 247 CCAAAATCCAGGGGCAAGCCCGGGGCTCATGCGCGGCTCTCCGAGGCTTGGGTAAGC 306
OY 117 GGAAGAGCCGGGAGGCTTGGGCGCGGCGAAGACCAAGAGACCACTTTCGATTGAG 176
Db 307 GGAAGAGCCGGGAGGCTTGGGCGCGGCGAAGACCAAGAGACCACTTTCGATTGAG 366
OY 177 TTGCTCCCCGCAACCCCGGGCTGTGCTTTCTTCATCCGACCAACGCGGGGCG-CGGG 235
Db 367 TTGCTCCCCCAACCCCGGGCTGTGCTTTCTTCATCCGACCAACGCGGGGCGCGGG 426
OY 236 ACAACACAGGTGCGGAGAGGCTTGGCTTCATGATGATGACGACGACG-GCAGCGCC 294
Db 427 ACAACACAGGTGCGGAGAGGCTTGGCTTCATGATGATGACGACGACGCGCGCGC 486
OY 295 TGGGTTCCGAGACCCCAACGCGCA--GCTGAAGCAATTGGCGGTAGTCCATGCGCGTGAAGAA 353
Db 487 TGGGTTCCGAGACCCCAACGCGCAAGCTGAAGCAATTGGCGGTAGTCCATGCGCGTGAAGAA 546
OY 354 GTGTGAGATGAGGATTTAACTGCAACATGAGATATGAGAGAGACCGGGGATTTGTAACG 413
Db 547 GTGTGAGATGAGGATTTAACTGCAACATGAGATATGAGAGAGACCGGGGATTTGTAACG 606
OY 414 TAAACATGATGATGAGGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Db 607 TAAACATGATGATGAGGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
OY 474 CCTGGCCCGGCGCTCTCTCACTTGTAGTGAAGATACCACTTGAAGCCAGAAAGCCAC 533
Db 667 CCTGGCCCGGCGCTCTCTCACTTGTAGTGAAGATACCACTTGAAGCCAGAAAGCCAC 726
OY 534 CAACCAATATCAAAATCTCTCAACAGAGTATAGTGTGCGGCGAGGAGTGTGCTAG 593
Db 727 CAACCAATATCAAAATCTCTCAACAGAGTATAGTGTGCGGCGAGGAGTGTGCTAG 786
OY 594 AGGTGCGCTGCTGTTGAAAGATGCGCGGTGATCACTTGAAGTATGAGGATGAGTGTGCT 653
Db 787 AGGTGCGCTGCTGTTGAAAGATGCGCGGTGATCACTTGAAGTATGAGGATGAGTGTGCT 846
OY 654 TGGGGCCCAACATATGAGAGAGTCTTATGAGGAGTACTTGCAGATTAAGGGGCGCACAC 713
Db 847 TGGGGCCCAACATATGAGAGAGTCTTATGAGGAGTACTTGCAGATTAAGGGGCGCACAC 906
OY 714 CTAGAGACTCCGGCTCTATGCTGTATCTGCGAGTGAAGCTGTGAAGCTTGTGT 773
Db 907 CTAGAGACTCCGGCTCTATGCTGTATCTGCGAGTGAAGCTGTGAAGCTTGTGT 966
OY 774 ACTTCATGTGATATGTCACAGATGCAATTCATCCGAGATGATGAGATGACACCGATG 833
Db 967 ACTTCATGTGATATGTCACAGATGCAATTCATCCGAGATGATGAGATGACACCGATG 1026
OY 834 GTGCGGCAAAATTTTGTCACTGAGAGACAGTAAACAAGAGAGACCAATCTGGACCAACA 893
Db 1027 GTGCGGCAAAATTTTGTCACTGAGAGACAGTAAACAAGAGAGACCAATCTGGACCAACA 1086
OY 894 CAGAAAGATGAGAAAGCGGCTCATGCTGTGCTGCGGCAACACTGTCAAGTTTCGCT 953
Db 1087 CAGAAAGATGAGAAAGCGGCTCATGCTGTGCTGCGGCAACACTGTCAAGTTTCGCT 1146
OY 954 GCCCAGCCCGGGGGAACCCATGCCAAACATGCGGTGCTGAAAGAAACGGGAGAGAGTTTA 1013
Db 1147 GCCCAGCCCGGGGGAACCCATGCCAAACATGCGGTGCTGAAAGAAACGGGAGAGAGTTTA 1206
OY 1014 AGAGAGAGATGCAATTTGAGGCTTACAGAGTACGAAACGAGCACTGAGAGCTCATATAG 1073

```

```

Db 1207 AGAGAGAGATGCAATTTGAGGCTTACAGATACGAAACCAAGCATGAGGCTCATATAG 1266
OY 1074 AAAGTGTGCTCCATCTTGAACAAGGGAATTTATCTGTGTGAGATGAATACGGGT 1133
Db 1267 AAAGTGTGCTCCATCTTGAACAAGGGAATTTATCTGTGTGAGATGAATACGGGT 1326
OY 1134 CCATCAATCAACAGTACCACTGATGTTGTGAGACGATGCGCTCAACGGGCTCATCTCC 1193
Db 1327 CCATCAATCAACAGTACCACTGATGTTGTGAGACGATGCGCTCAACGGGCTCATCTCC 1386
OY 1194 AAGCGGACCTGCGGCAATGCTTCCACATGCTGAGAGAGACGTAAAGTTTGTCTGCA 1253
Db 1387 AAGCGGACCTGCGGCAATGCTTCCACATGCTGAGAGAGACGTAAAGTTTGTCTGCA 1446
OY 1254 AGTTTAAAGATATGCTCCAGGCTCCATCCAGTGTGATCAAGACGTGAAAGAAACGGCA 1313
Db 1447 AGTTTAAAGATATGCTCCAGGCTCCATCCAGTGTGATCAAGACGTGAAAGAAACGGCA 1506
OY 1314 GTPAATACGGGCGCGAGCGGCTGACCTTCAAGTTCTCAAGCACTCGGGGATTAATA 1373
Db 1507 GTPAATACGGGCGCGAGCGGCTGACCTTCAAGTTCTCAAGGCTCGGGGATTAATA 1566
OY 1374 GTTCCATGCAAGATGCTGCTGTG-----TCATGTGACCGAGCGGATGCTGGG 1427
Db 1567 CCAAGCAAAAGATGAGGTTCTTATTCGAAATGTAACCTTTGAGACGCTGGGG 1626
OY 1428 AATATATATGTAAGTCTTCAATTTATAGGCAAGCCCAACAGTCTGCTGCTCACTG 1487
Db 1627 AATATATGCTGCTGCGGGTATTTCTATTTGGATATCTTTTCACTGTGATGTTGACAG 1686
OY 1488 TCCTGCCAAACAGCAAGCGCTGGAAGAGAAAGAAATTAACGCTTCCAGCACTAC 1547
Db 1687 TTCCTCC-----AGCGCTGGAAGAGAAAGAAATTAACGCTTCCAGCACTAC 1737
OY 1548 TGAAGATACCAATTTACTGATAGGAGTCTTCTTATGCTGTATGCTGTAACTAGTCA 1607
Db 1738 TGAAGATACCAATTTACTGATAGGAGTCTTCTTATGCTGTATGCTGTAACTAGTCA 1797
OY 1608 TCTGTGCGGAATGAGAACACAGAACCAAGAGCCGAGCTTTCAGGCGGCTGTGC 1667
Db 1798 TCTGTGCGGAATGAGAACACAGAACCAAGAGCCGAGCTTTCAGGCGGCTGTGC 1857
OY 1668 ACAAGCTGACCAAGATATCCCTGCGGAGACAGATTAAC-----AGTTTGGCTGAGTCC 1723
Db 1858 ACAAGCTGACCAAGATATCCCTGCGGAGACAGATTAACAGAAATTTCCGCTAGTCC 1917
OY 1724 AGCTCTCCATGATCTCAACAACCCCGCTGTGAGATTAACAACGCTCTCTTCAACG 1783
Db 1918 AGCTCTCCATGATCTCAACAACCCCGCTGTGAGATTAACAACGCTCTCTTCAACG 1977
OY 1784 GCAACAACCCCATGCTGCGAGGGTCTCCAGATATGAATCTTCCAGAGACCCCAAAATGG 1843
Db 1978 GCAACAACCCCATGCTGCGAGGGTCTCCAGATATGAATCTTCCAGAGACCCCAAAATGG 2037
OY 1844 GAGTTTCAAGAGATTAAGCTGACATGCGGCAAGCCCTGCGAGAAAGTTGCTTGGGCAA 1903
Db 2038 GAGTTTCAAGAGATTAAGCTGACATGCGGCAAGCCCTGCGAGAAAGTTGCTTGGGCAA 2097
OY 1904 GTGTATGATGCGGAGAGAGTGGAAATTAACAAGCAAGCCCAAGAGGCGGTACCGTG 1963
Db 2098 GTGTATGATGCGGAGAGAGTGGAAATTAACAAGCAAGCCCAAGAGGCGGTACCGTG 2157
OY 1964 GCCGTGAAGATGTTGAAGATATGTCACAGAGAAAGACTTTTGTGATGCTGTCAGAG 2023
Db 2158 GCCGTGAAGATGTTGAAGATATGTCACAGAGAAAGACTTTTGTGATGCTGTCAGAG 2217
OY 2024 ATGAGATGATGAAGATGTTGGAAGAAACAAGAAATATCAATCTTCTGAGAGCTGCG 2083
Db 2218 ATGAGATGATGAAGATGTTGGAAGAAACAAGAAATATCAATCTTCTGAGAGCTGCG 2277
OY 2084 ACAAGATAGGCTCTCTATGTCATATGTAAGTATGCTTAAAGCAACCTCGAGAA 2143
Db 2278 ACAAGATAGGCTCTCTATGTCATATGTAAGTATGCTTAAAGCAACCTCGAGAA 2337

```

2144 TACCTCCAGCCCGAGGCGACCCCGGAGTGAAGTACTCTTAAGACATTACCGTGTCT 2203
2338 TACCTCCAGCCCGAGGCGACCCCGGAGTGAAGTACTCTTAAGACATTACCGTGTCT 2397
2204 GAGGAGGAGTGAAGTCTTCAAGGACTTGTGTCAATGACCTTCAAGCTGCGGAGCGAGT 2263
2398 GAGGAGGAGTGAAGTCTTCAAGGACTTGTGTCAATGACCTTCAAGCTGCGGAGCGAGT 2457
2264 GAGTCTTGGCTCCCAAAAATGATATTCATGAGATTAGCAGCAGAAATGTTTGTGTA 2323
2458 GAGTCTTGGCTCCCAAAAATGATATTCATGAGATTAGCAGCAGAAATGTTTGTGTA 2517
2324 ACAGAAAAATGATGATGAATAATAGCAGCTTGGACTGCGGAGATATCAACATATTA 2383
2518 ACAGAAAAATGATGATGAATAATAGCAGCTTGGACTGCGGAGATATCAACATATTA 2577
2384 GACTTATTAACAAAAACCAACCAATGGGCGCTTCCAGTCAAGTGAATGGCTCCAGAAAGC 2443
2578 GACTTATTAACAAAAACCAACCAATGGGCGCTTCCAGTCAAGTGAATGGCTCCAGAAAGC 2637
2444 CTGTTGATAGAGTATACATCATGAGTGTCTGGTCTTGGGGGTGTTAATGTGG 2503
2638 CTGTTGATAGAGTATACATCATGAGTGTCTGGTCTTGGGGGTGTTAATGTGG 2697
2504 GAGATCTTCACTTAAAGGGGCTGCGCTTACCAAGGAGATTCCTGAGAGAACTTTTAAG 2563
2698 GAGATCTTCACTTAAAGGGGCTGCGCTTACCAAGGAGATTCCTGAGAGAACTTTTAAG 2757
2564 CTGCTGAAGGAAAGGACACAGAAATGATTAAGCCAGCACTGACCAAGAACTGATACATG 2623
2758 CTGCTGAAGGAAAGGACACAGAAATGATTAAGCCAGCACTGACCAAGAACTGATACATG 2817
2624 ATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAGAGACCAACCTTCAAGCAGTTGTA 2683
2818 ATGATGAGGAGCTGTTGGCATGACAGTCCCTCCAGAGACCAACCTTCAAGCAGTTGTA 2877
2684 GAAAGCTTGGATGCAATTTCTCATCTCTCACAAACCAATGAGAAATCTGGACCTCAGCCAA 2743
2878 GAAAGCTTGGATGCAATTTCTCATCTCTCACAAACCAATGAGAAATCTGGACCTCAGCCAA 2937
2744 CCTCTGAAGCAATTTCACTGATTAACCTGACCAAGAAATGTTGTTCTTCAAGAGAT 2803
2938 CCTCTGAAGCAATTTCACTGATTAACCTGACCAAGAAATGTTGTTCTTCAAGAGAT 2997
2804 GATTCTGTTTTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTTCAATCCACAC 2863
2998 GATTCTGTTTTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTTCAATCCACAC 3057
2864 ATAAACGGAGTGTAAACATGAATGACTGTGTCTGCTGTCTCCCAACAGAGACGAC 2923
3058 ATAAACGGAGTGTAAACATGAATGACTGTGTCTGCTGTCTCCCAACAGAGACGAC 3117
2924 TGGGAACCTAGCTACCTGAAGAGGAGACATGCTCTCCAGAGCTTGTGTCTCCACT 2983
3118 TGGGAACCTAGCTACCTGAAGAGGAGACATGCTCTCCAGAGCTTGTGTCTCCACT 3177
2984 GATATATGATCAAGAGAGTAAATATGAAAAATGATATGATATGTAAGATT 3043
3178 GATATATGATCAAGAGAGTAAATATGAAAAATGATATGATATGTAAGATT 3237
3044 ATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGGTTTCTGAGCAGTGAAC 3103
3238 ATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGGTTTCTGAGCAGTGAAC 3297
3104 TGC 3106
3298 TGC 3300

RESULT 5
US-10-669-920-564
; Sequence 564, Application US/10669920

Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 5000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-564

Query Match 93.1%; Score 2890.2; DB 6; Length 5000;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;
1 CCGCGAGCAAGTTGGTGGAGGCAAG-CAGCCTGAGTCTTCTCTCTCTGTTCC 59
578 CTCGGAGCAAGTTGGTGGAGGCAAGCAGCCTGAGTCTTCTCTCTCTGTTCC 637
60 CCAATCCGAGGAGGAGCCCGGCGGCTGATG---GCGCTCTCCGAGCCTGGGATACGC 116
638 CCAATCCGAGGAGGAGCCCGGCGGCTGATG---GCGCTCTCCGAGCCTGGGATACGC 697
117 GTAAAGCCCGGAGGCTTGGCGCGGAGGAGACCAAGACCACTTCTGCTTGGAG 176
698 GTAAAGCCCGGAGGCTTGGCGCGGAGGAGACCAAGACCACTTCTGCTTGGAG 757
177 TTGCTCCCGGAGCCCGGCGGCTGCTGCTTCTCATCCGAGCCAGCGGGAGC-CGGAG 235
758 TTGCTCCCGGAGCCCGGCGGCTGCTGCTTCTCATCCGAGCCAGCGGGAGC-CGGAG 817
236 ACAACACAGTTCGCGAGGAGCGTTGCCATTCAAGTGAATGACAGAGCAGC-GCAGCGCC 294
818 ACAACACAGTTCGCGAGGAGCGTTGCCATTCAAGTGAATGACAGAGCAGCAGCGCC 877
295 TCGGTTCTGAGCCCACTGCA-GCTGAAGGCAATGGCGGTGTCTCATATCCGTAGAGAA 353
878 TCGGTTCTGAGCCCACTGCAAGGAGGCAATGGCGGTGTCTCATATCCGTAGAGAA 937
354 GTGTGCAATGGAATTAACGTCAACATGAGATATGAAAGAGACCGGGGATGGTACCG 413
938 GTGTGCAATGGAATTAACGTCAACATGAGATATGAAAGAGACCGGGGATGGTACCG 997
414 TAACATGATGAGTGGGGTGTGTTCACTGCTGTGTGTGTGTGATCCATGACCACTTGT 473
998 TAACATGATGAGTGGGGTGTGTTCACTGCTGTGTGTGTGTGTGATCCATGACCACTTGT 1057
474 CCTGGCCCGGCGCTCTCTCAAGTTAGTGAATATCAACATTAAGCAGAAAGCCAC 533
1058 CCTGGCCCGGCGCTCTCTCAAGTTAGTGAATATCAACATTAAGCAGAAAGCCAC 1117
534 CAACCAATACCAATCTCTCAACCAAGATGATGCTGCGGCAAGGAGTCTGTAG 593

QY	2744	CCCTCCGAACGTAATTCACCTAGTAAACCTCGACACAGAAGTCTGTGCTTCAGAGAT	2803
Db	3329	CCCTCCGAACGTAATTCACCTAGTAAACCTCGACACAGAAGTCTGTGCTTCAGAGAT	3388
QY	2804	GATTCTGTGTTTTCTCCAGACCCCATGCGCTTACGAAACCATGCTTCCACGATATCCAC	2863
Db	3389	GATTCTGTGTTTTCTCCAGACCCCATGCGCTTACGAAACCATGCTTCCACGATATCCAC	3448
QY	2864	ATAAACCGCAGTGTAAAAACATGAATGACTGTGTGCTGTGCCCTGCCCAACACGACAGC	2923
Db	3449	ATAAACCGCAGTGTAAAAACATGAATGACTGTGTGCTGTGCCCTGCCCAACACGACAGC	3508
QY	2924	TGGGAACTTACTCTACATCGACACAGGGAACCATGCTCCCGAGCTTGTGCTCCACTT	2983
Db	3509	TGGGAACTTACTCTACATCGACACAGGGAACCATGCTCCCGAGCTTGTGCTCCACTT	3568
QY	2984	GTAATATATGATTCAGAGAGAGTAAATAATTTGAAAAGTATACGATATGTGTAAAGATT	3043
Db	3569	GTAATATATGATTCAGAGAGAGTAAATAATTTGAAAAGTATACGATATGTGTAAAGATT	3628
QY	3044	ATACAGTTGAAAACTTGTAATCTTCCCGACGAGGAGAAAGGTTCTTGACGACATGCAC	3103
Db	3629	ATACAGTTGAAAACTTGTAATCTTCCCGACGAGGAGAAAGGTTCTTGACGACATGCAC	3688
QY	3104	TGC 3106	
Db	3689	TGC 3691	

```

RESULT 6
US-10-669-920-634
; Sequence 634, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 634
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-634

```

Query Match	Similarity	Score	2882.2	DB 6	Length	4990	
Best Local	Similarity	97.1%	Pred.	No. of			
Matches	3028	Conservative	0	Mismatches	63	Indels	28
						Gaps	8

Qy	1	CCCGCAGCAAAATTGTTGGTAGGCAACG	CAAGCTGTAGTCTTCTTCTCTGTTCC	59
Db	578	CTCGCAGCAAAATTGTTGGTAGGCAACG	CAAGCTGTAGTCTTCTTCTCTCTGTTCC	637

QY	60	CCAAATCCGAGGGGACGCCCGCGGGCCCTCAGT---	GGGCTCTCCGACGCTCGGGGTACGC	116
Db	638	CCAAATCCGAGGGGACGCCCGCGGGCCCTCAGT---	GGGCTCTCCGACGCTCGGGGTACGC	697
QY	1117	GTGAAGCCCGGGAGAGCTTGGCGCGCGGGAGAACCC	CAAGACACACTCTTCTGCGTTTGGAG	116
Db	698	GTGAAGCCCGGGAGAGCTTGGCGCGCGGGAGAACCC	CAAGACACACTCTTCTGCGTTTGGAG	757
QY	1177	TTGCTCCCGGCAACCCCGGGCTGGTGGCTTTCT	CCATCCGACCCACGCGGGGC--CGGG	235
Db	758	TTGCTCCCGGCAACCCCGGGCTGGTGGCTTTCT	CCATCCGACCCACGCGGGGC--CGGG	817
QY	236	ACAAACAGAGTCTCGGGAGAGACCTTGGCATTTCA	AGTAATGACAGACAGC--GCAAGGCC	294
Db	818	ACAAACAGAGTCTCGGGAGAGACCTTGGCATTTCA	AGTAATGACAGACAGC--GCAAGGCC	877
QY	295	TOGGTTCCTGAGCCCAACCGCA--GCTGAAGGCA	TTGCGCGTATGCTCATGCCCTGAGAGAA	353
Db	878	TOGGTTCCTGAGCCCAACCGCA--GCTGAAGGCA	TTGCGCGTATGCTCATGCCCTGAGAGAA	937
QY	354	GTGTGCAAGTGGGATTTAACTCCATGAGATAT	TGAAAGAGACCGGGGATTGGTACCG	413
Db	938	GTGTGCAAGTGGGATTTAACTCCATGAGATAT	TGAAAGAGACCGGGGATTGGTACCG	997
QY	414	TAACCATGGTCAAGCTGGGGTCTGTTTCATCTG	CGCTGGTCTGGTGTACCAATGGCAACTTGT	473
Db	998	TAACCATGGTCAAGCTGGGGTCTGTTTCATCTG	CGCTGGTCTGGTGTACCAATGGCAACTTGT	1057
QY	474	CCCTGGGCCCGGCCCTCTTCAGTTTATGTTAG	ATACCACTTATGAGCCAAAGACAC	533
Db	1058	CCCTGGGCCCGGCCCTCTTCAGTTTATGTTAG	ATACCACTTATGAGCCAAAGACAC	1117
QY	534	CAACCAATATACCAATCTCTCAACCCAGAGT	GTACGTGGCTGCGCCAGGGGATGCTTAG	593
Db	1118	CAACCAATATACCAATCTCTCAACCCAGAGT	GTACGTGGCTGCGCCAGGGGATGCTTAG	1177
QY	594	AGGTGCGCTGCTGTTGAAGAATGCGCGCGTG	ATCATGTTGACATTAAGATGGGGTGCAT	653
Db	1178	AGGTGCGCTGCTGTTGAAGAATGCGCGCGTG	ATCATGTTGACATTAAGATGGGGTGCAT	1237
QY	654	TGGGGCCCAATATGAGCAGTGGCTTATTTGG	GGGAGTACTTTCAGATTAAGGGCGCACAC	713
Db	1238	TGGGGCCCAATATGAGCAGTGGCTTATTTGG	GGGAGTACTTTCAGATTAAGGGCGCACAC	1297
QY	714	CTAGAGACTCCGGGCTCTATGCTTGTATCTG	CCAGTAGAGACTGTAGACAGTAACTTGGT	773
Db	1298	CTAGAGACTCCGGGCTCTATGCTTGTATCTG	CCAGTAGAGACTGTAGACAGTAACTTGGT	1357
QY	774	ACTTCATGGTGAATGTCAACAATGCCATCTCA	TCCGGATGATGATGAATGACACCCATG	833
Db	1358	ACTTCATGGTGAATGTCAACAATGCCATCTCA	TCCGGATGATGATGAATGACACCCATG	1417
QY	834	GTGCGGAAAGTTTTTGTCACTGAGAACATTA	CAACAAGAGACACATCTGACCAACA	893
Db	1418	GTGCGGAAAGTTTTTGTCACTGAGAACATTA	CAACAAGAGACACATCTGACCAACA	1477
QY	894	CAGAAAAGATGGAAGAAGCGGCTCACTGCTG	TCGCGGCAACACTGTCAAGTTTCGCT	953
Db	1478	CAGAAAAGATGGAAGAAGCGGCTCACTGCTG	TCGCGGCAACACTGTCAAGTTTCGCT	1537
QY	954	GCCCAAGCCGGGGGAAACCCATGCCAACCAT	GCGGTGGCTGTAAAAACGGGAAGAGTTTA	1011
Db	1538	GCCCAAGCCGGGGGAAACCCATGCCAACCAT	GCGGTGGCTGTAAAAACGGGAAGAGTTTA	1597
QY	1014	AGCAGAGATGTGCATTTGAGGCTACAAAGGT	ACAAACAGACCTGAGAGCCCTCATTTAGG	1072
Db	1598	AGCAGAGATGTGCATTTGAGGCTACAAAGGT	ACAAACAGACCTGAGAGCCCTCATTTAGG	1657
QY	1074	AAAGGTGGTCCCATCTGACAAAGGAAATTAT	ACCTGTTAGTGGAGATGAATACGGGT	1133
Db	1658	AAAGGTGGTCCCATCTGACAAAGGAAATTAT	ACCTGTTAGTGGAGATGAATACGGGT	1717
QY	1134	CCATCAATACACATACCACTCGAATGTTGTG	AGACGATGCGCTCACCGGCCCATCTTCC	1197

DB 1718 CCATCAATCAACGTAACCTGGAATGTTGTGAGAGGATCGCTCAACCGGCAATCTCTC 1777
QY 1194 AAGCCGAGCTGCGCGCAAAATGCTCCACAGTGTGCGAGAGACGTAGAATTGTCTGCA 1253
DB 1778 AAGCCGAGCTGCGCGCAAAATGCTCCACAGTGTGCGAGAGACGTAGAATTGTCTGCA 1837
QY 1254 AGGTTTACAGTATGCGCCAGCCCAATCAAGTATCAAGCACTGCGGAAAGAGGCA 1313
DB 1838 AGGTTTACAGTATGCGCCAGCCCAATCAAGTATCAAGCACTGCGGAAAGAGGCA 1897
QY 1314 GTAATATACGCGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGCACTGCGGAAATATA 1373
DB 1898 GTAAATACGCGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGCGCGCGGTTAAACA 1957
QY 1374 GTTCCAGTCAAGATGCTGCTGTGT-----TCAATGTGACCGAGCGGATGCTGCGG 1427
DB 1958 CCAAGGCAAAAGATGAGGTTCTCTAATATTCGAAATGTAACCTTTTGAAGAGCGTGGG 2017
QY 1428 AATATATATGTAAGTCTCAATATATATAGGCGCAACAGTCTGCTGCTCACTG 1487
DB 2018 AATATATGCTGCTGCGGTAATCTAATGGAATATCTTTCACTGCAATGTTGACAG 2077
QY 1488 TCTGTCAAAACAGCAAGCGCTGGAAGAAAGAAAGATTAAGGCTTCCCGACATACC 1547
DB 2078 TTCTGCTC-----AGCGCTGGAAGAAAGAAAGATTAAGGCTTCCCGACATACC 2128
QY 1548 TGAAGATAGCATTTTATCTGATAGGAGTCTTCTTAAATGCTGATATGTTAAACATGA 1607
DB 2129 TGAAGATAGCATTTTATCTGATAGGAGTCTTCTTAAATGCTGATATGTTAAACATGA 2188
QY 1608 TCTGTTGCGGATGAAAGACAGCAAGAGCCAGACTTCAGACGCGCGGCTGTGCG 1667
DB 2189 TCTGTTGCGGATGAAAGACAGCAAGAGCCAGACTTCAGACGCGCGGCTGTGCG 2248
QY 1668 ACAAGCTGACCAAAAGCTATCCCTGCGGAGACAGGTTAAAGTTGCGCTGAGTCCAGCT 1727
DB 2249 ACAAGCTGACCAAAAGCTATCCCTGCGGAGACG-----GTTTGGCTGAGTCCAGCT 2302
QY 1728 CCTCATGATCTTCACACCCCGCTGATGAGATTAACAACGCTCTCTTCAACGCGCAG 1787
DB 2303 CCTCATGATCTTCACACCCCGCTGATGAGATTAACAACGCTCTCTTCAACGCGCAG 2362
QY 1788 ACAACCCCATGCTGCGAGGAGTCTCCGAGTATGAATTCAGAGGACCCAAAATGGAAGT 1847
DB 2363 ACAACCCCATGCTGCGAGGAGTCTCCGAGTATGAATTCAGAGGACCCAAAATGGAAGT 2422
QY 1848 TTCCAGAGATTAAGCTGACATGCGGAGACCCCTGCGGAGAGGTTGCTTGGCAAGTGG 1907
DB 2423 TTCCAGAGATTAAGCTGACATGCGGAGACCCCTGCGGAGAGGTTGCTTGGCAAGTGG 2482
QY 1908 TCATGCGGAGAGAGTGGGATTAAGCAAAAGACAGGCGGCTCAACGTTGGCGG 1967
DB 2483 TCATGCGGAGAGAGTGGGATTAAGCAAAAGACAGGCGGCTCAACGTTGGCGG 2542
QY 1968 TGAAGATGTTGAAAGATGATGCAAGAGAAAGCTTTCTGATCTGCTGTCTGAGATGG 2027
DB 2543 TGAAGATGTTGAAAGATGATGCAAGAGAAAGCTTTCTGATCTGCTGTCTGAGATGG 2602
QY 2028 AGATGATGAAGATTTGGGAAACAAAGATATCAATTAATCTTTGGAGCTGACAC 2087
DB 2603 AGATGATGAAGATTTGGGAAACAAAGATATCAATTAATCTTTGGAGCTGACAC 2662
QY 2088 AGGATGAGCTCTCTATGTCATAGTATGATGCTCTTAAGGCAACTCCGAGAAATACC 2147
DB 2663 AGGATGAGCTCTCTATGTCATAGTATGATGCTCTTAAGGCAACTCCGAGAAATACC 2722
QY 2148 TCCGAGCCGAGAGCCACCCGCGATGAGTATCTCTATGACATTAACGTTTCTGAGG 2207
DB 2723 TCCGAGCCGAGAGCCACCCGCGATGAGTATCTCTATGACATTAACGTTTCTGAGG 2782
QY 2208 AGCAGATGACCTTCAAGATCTGATGATGCACTTACAGCTGCGCAGCGAGTGAAGT 2267

DB 2783 AGCAGATGACCTTCAAGGACTTGTGTATGACCTTACAGCTGCGCAGAGGCAATGAGT 2842
QY 2266 ACTTGGCTTCCCAAAATGATTCATTCGAGATTTAGAGCCAGAAATGTTTGGTAAAG 2327
DB 2843 ACTTGGCTTCCCAAAATGATTCATTCGAGATTTAGAGCCAGAAATGTTTGGTAAAG 2902
QY 2328 AAAACAGTGTATGAAATATGAGACTTGTGACTGCGCAGAGATTAACAATATAGACT 2387
DB 2903 AAAACAGTGTATGAAATATGAGACTTGTGACTGCGCAGAGATTAACAATATAGACT 2962
QY 2388 ATTAACAAAAGACCAACAAATGCGGCTTCAAGTCAATGATGCTCAAGAACCTCTGT 2447
DB 2963 ATTAACAAAAGACCAACAAATGCGGCTTCAAGTCAATGATGCTCAAGAACCTCTGT 3022
QY 2448 TTGATGATATATCACTCATGAGTATGCTGTGCTTCCGCGGTTTAAATGTTGAGAA 2507
DB 3023 TTGATGATATATCACTCATGAGTATGCTGTGCTTCCGCGGTTTAAATGTTGAGAA 3082
QY 2508 TCTTCACTTATAGGAGGCTGCGCTTACCCAGGATTCGCGTGAAGAACTTTTAAAGCTGC 2567
DB 3083 TCTTCACTTATAGGAGGCTGCGCTTACCCAGGATTCGCGTGAAGAACTTTTAAAGCTGC 3142
QY 2568 TGAAGAGAGGACACAGATGATTAAGCCAGCCAACTGCAACGAATCTGTACATGATGA 2627
DB 3143 TGAAGAGAGGACACAGATGATTAAGCCAGCCAACTGCAACGAATCTGTACATGATGA 3202
QY 2628 TGAAGAGCTGTTGCGATGAGTCCCTCCAGAGACCAAGTTCAAGCAGTTGTGTGAAG 2687
DB 3203 TGAAGAGCTGTTGCGATGAGTCCCTCCAGAGACCAAGTTCAAGCAGTTGTGTGAAG 3262
QY 2688 ACTTGGATGAAATTCATCTCTCAACCAATGAGAAATATTTGAGCTCAAGCAACTGC 2747
DB 3263 ACTTGGATGAAATTCATCTCTCAACCAATGAGAAATATTTGAGCTCAAGCAACTGC 3322
QY 2748 TGAACAGATATTCACCTAGTTTACCTGACACAGAAATCTTGTCTTCAAGATGAT 2807
DB 3323 TGAACAGATATTCACCTAGTTTACCTGACACAGAAATCTTGTCTTCAAGATGAT 3382
QY 2808 CTGTTTTTCTCAAGCCCATGCTTACAGAACATGCTTCTCAGTATCCACATTA 2867
DB 3383 CTGTTTTTCTCAAGCCCATGCTTACAGAACATGCTTCTCAGTATCCACATTA 3442
QY 2868 AGCGAGTGTAAACATGATGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2927
DB 3443 AGCGAGTGTAAACATGATGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3502
QY 2928 AACCTAGCTACCTGAGCAGGAGACCAATGCTTCCAGAGCTTGTGTCTCACTGTAT 2987
DB 3503 AACCTAGCTACCTGAGCAGGAGACCAATGCTTCCAGAGCTTGTGTCTCACTGTAT 3562
QY 2988 ATATGATCAAGAGATTAATTAATGAAAGATTAATCAGCATATGTTAAAGATTATAC 3047
DB 3563 ATATGATCAAGAGATTAATTAATGAAAGATTAATCAGCATATGTTAAAGATTATAC 3622
QY 3048 AGTTGAAAATCTGTATCTTCCCAAGAGAGAAAGAGTTTCTGAGCAGTGAATGCG 3106
DB 3623 AGTTGAAAATCTGTATCTTCCCAAGAGAGAAAGAGTTTCTGAGCAGTGAATGCG 3681

RESULT 7
US-10-669-920-608
; Sequence 608, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482

```

; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 4607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-608

```

Query Match	92.3%;	Score 2667.8;	DB 6;	Length 4607;	
Best Local Similarity	96.7%;	Pred. No. 0;			
Matches 3024;	Conservative	0;	Mismatches 67;	Indels 36;	Gaps 8
QY	1	CCCGGAGCAAGTTTGGTGAGGAGCAACG - CAAGCTCTAGTCTTCTCTCTCTGTTCC	59		
DB	187	CTCGGAGCAAGTTTGGTGAGGCAACGCCAAGCTAGTCTTCTCTCTCTGTTCC	246		
QY	60	CCAAATCCGAGGGCAGGCCCGGGGGCTCATG--GCGCTCTTCCGACGCTTGGGTACGC	116		
DB	247	CCAAATCCGAGGGCAGGCCCGGGGGCTCATGCGCGGCTCTTCCGACGCTTGGGTACGC	306		
QY	117	GTTGAAGCCCGGAGAGCTTGGCGCCCGCGCAAGACCAAGGACCACTTCTGTGTTTGAG	176		
DB	307	GTTGAAGCCCGGAGAGCTTGGCGCCCGCGCAAGACCAAGGACCACTTCTGTGTTTGAG	366		
QY	177	TTCGCTCCCGCAACCCCGGGCTGTCGCTTTCATCCGACCGACGCGGGGC -CGGG	235		
DB	367	TTCGCTCCCGCAACCCCGGGCTGTCGCTTTCATCCGACCGACGCGGGGGCGGGG	426		
QY	236	ACAACACAGGTGCGGAGAGCGTTGCAATTCAAGTGACTGACAGCAGC -GCAGCGC	294		
DB	427	ACAACACAGGTGCGGAGAGCGTTGCAATTCAAGTGACTGACAGCAGCAGCGCGCC	486		
QY	295	TTCGTTCTCGAACCCCAACCGCA -GCTGAAGGCAATTGGCGGTAAGTCATGCGCGTAAGGAA	353		
DB	487	TTCGTTCTCGAACCCCAACCGGCTGAAGGCAATTGGCGGTAAGTCATGCGCGTAAGGAA	546		
QY	354	GTTGTCAGATGGGATTTAAGTCCACATYAGAGATATGGAAGAGGACCGGGGATTTGTAACG	413		
DB	547	GTTGTCAGATGGGATTTAAGTCCACATGAGATATGGAAGAGGACCGGGGATTTGTAACG	606		
QY	414	TAAACATGATCAGCTGGGGTCTGTTTCATCTGCTGTCGTGGTCAACATGGCAACTTGT	473		
DB	607	TAAACATGATCAGCTGGGGTCTGTTTCATCTGCTGTCGTGGTCAACATGGCAACTTGT	666		
QY	474	CCCTGGCCCGGCGCTCTTCACTTATGTTAGGATACACATTAAGGCCAAGAAAGCCAC	533		
DB	667	CCCTGGCCCGGCGCTCTTCACTTATGTTAGGATACACATTAAGGCCAAGAAAGCCAC	726		
QY	534	CAACCAATATCCAAATCTCTCAACCAAGAGTGAACGTGGCGCCAGGGGAGTCTGTA	593		
DB	727	CAACCAATATCCAAATCTCTCAACCAAGAGTGAACGTGGCGCCAGGGGAGTCTGTA	786		
QY	594	AGGTGGCTGCTGTTGAAGATGCCGCCGTATCAGTTGACTAAGATGGGGTCACT	653		
DB	787	AGGTGGCTGCTGTTGAAGATGCCGCCGTATCAGTTGACTAAGATGGGGTCACT	846		
QY	654	TGGGGCCCAACATAGACAGTGTCTTATTTGGGAGATCTTGACGATTAAGGGGCCACAC	713		
DB	847	TGGGGCCCAACATAGACAGTGTCTTATTTGGGAGATCTTGACGATTAAGGGGCCACAC	906		

QY	714	CTAAGAACTCGGCGCTCTAAGCTTGTATCTGCAAGTGAAGCACTGTAAGCAAGGAAACTTGGT	773
Db	907	CTAAGAACTCGGCGCTCTAAGCTTGTATCTGCAAGTGAAGCACTGTAAGCAAGGAACTTGGT	966
QY	774	ACTTCAGGTGAATGTCAAGATGCAATGCTCATCTCCGAGATGATGAGATGACACCGATG	833
Db	967	ACTTCATGTATATGTCAAGATGCAATGCTCATCTCATCCGAGATGATGAGATGACACCGATG	1026
QY	834	GTGCGAAGATTTTGTGATGAGAAACGTAAACAAGAGAGCACTACTGACCAACA	893
Db	1027	GTGCGAAGATTTTGTGATGAGAAACGTAAACAAGAGAGCACTACTGACCAACA	1086
QY	894	CAGAAAGATGGAAGAAAGCGGCTCCATCTGTGGCCTGTGGGCCAACATGTCAAGTTTGCT	953
Db	1087	CAGAAAGATGGAAGAAAGCGGCTCCATCTGTGGCCTGTGGGCCAACATGTCAAGTTTGCT	1146
QY	954	GCCGAGCGGGGGGAAACCAATGCAACATGCGGTGGCTGAAAAACGGAGAGGATTTA	1013
Db	1147	GCCGAGCGGGGGGAAACCAATGCAACATGCGGTGGCTGAAAAACGGAGAGGATTTA	1206
QY	1014	AGCAGAGCAATCGCATTTGAGAGCTTACAAGGTACGAAACACGACTGAGCCTCATTAATG	1073
Db	1207	AGCAGAGCAATCGCATTTGAGAGCTTACAAGGTACGAAACACGACTGAGCCTCATTAATG	1266
QY	1074	AAAGTGTGTCCTCATCTGACAAAGGAAATTAATCTGTATGTGAGAAATGAATACGGGT	1133
Db	1267	AAAGTGTGTCCTCATCTGACAAAGGAAATTAATCTGTATGTGAGAAATGAATACGGGT	1326
QY	1134	CCATTAATCACACGATACCACTGTGATGTTGTGAGCGATCGCTCACCGGCCCATCTCTCC	1193
Db	1327	CCATTAATCACACGATACCACTGTGATGTTGTGAGCGATCGCTCACCGGCCCATCTCTCC	1386
QY	1194	AAGCCGAGCTGCGCGCAAAATGCTTCCAAGTGTGCGAGAGACGTAGAGTTGTCTGCA	1253
Db	1387	AAGCCGAGCTGCGCGCAAAATGCTTCCAAGTGTGCGAGAGACGTAGAGTTGTCTGCA	1446
QY	1254	AGGTTTACATGTATGCCCAAGCCCAATCTCAATGTGATTCAGCATGTGAAAAAGAACGGCA	1313
Db	1447	AGGTTTACATGTATGCCCAAGCCCAATCTCAATGTGATTCAGCATGTGAAAAAGAACGGCA	1506
QY	1314	GTAATTAAGGGGCGGAGCGGGCTGACCTCAAGTGTCTCAAGCATCTCGGGAGTAAATA	1373
Db	1507	GTAATTAAGGGGCGGAGCGGGCTGACCTCAAGTGTCTCAAGTGTCTCGGGAGTAAATA	1566
QY	1374	GTTCCAAATGCA-----GAAATGCTGGCTCTGTTCAATGTGACCGAGCGGA	1419
Db	1567	TGTTAAACACACGAGCAAAAGATTGAAGTTCTCTAATTCGATGTAACTTTTGAGAA	1626
QY	1420	TGCTGGGGAATATATATGTAAAGTCTCAATTAATATAGGGCAAGCCAACTGTGCTGTG	1479
Db	1627	CGCTGGGGAATATATATGTCTGTGGCGGATTAATTAATGGGATATCTTTTCACTGTGATG	1686
QY	1480	GCTCACTGTCCTGCCAAAACAGCAAGCGGCTGGAAGAAAGAGATTAACGCTGCC	1539
Db	1687	GTTGACAGTTCTGGCC-----AGGCGCTGGAAGAAAGAGATTAACGCTGCC	1737
QY	1540	AGACATACCTGAGATAGGCATTTACTGATATAGGGGTCTTCTTAAATCGCTGATGTGTGT	1599
Db	1738	AGACATACCTGAGATAGGCATTTACTGATATAGGGGTCTTCTTAAATCGCTGATGTGTGT	1797
QY	1600	AAACAGTCATCTGTGCGGAATGAAGAACAGAACCAAGAACCCAGACTTCAGACGCAAGCC	1659
Db	1798	AAACAGTCATCTGTGCGGAATGAAGAACAGAACCAAGAACCCAGACTTCAGACGCAAGCC	1857
QY	1660	GCGTGTGCAAGCTGACCAACGTAATCCCTGTGGAGACAGGTAAACAGTTTGGGCTGA	1719
Db	1858	GCGTGTGCAAGCTGACCAACGTAATCCCTGTGGAGACAG-----GTTTGGGCTGA	1911
QY	1720	GTCCAGGCTCTGCATGAATCTCAACACCCGCTGTGTGAGATTAACAACCCCTCTCTTC	1779
Db	1912	GTCCAGGCTCTGCATGAATCTCAACACCCGCTGTGTGAGATTAACAACCCCTCTCTTC	1971
QY	1780	AACGGCAACAACCCCAATGCTGGACGGGGTCTCGAGTATGAATCTTCAGAGAACCCAA	1839

```

Db      1972 AACGCGACACCCCACTGCGCAGGCGCTCCAGATGAACTCCAGAGAACCCAA 2031
Qy      1840 ATGGAGATTCCAAAGATAGCTGACATCGGCGAACCCCTGGAGAAAGTTGCTTGG 1899
Db      2032 ATGGAGATTCCAAAGATAGCTGACATCGGCGAACCCCTGGAGAAAGTTGCTTGG 2091
Qy      1900 GCAGTGTCTATGCGCGAGACAGTGGAAATTGACAAAGAACAGCCCAAGAGCGGTGAC 1959
Db      2092 GCAAGTGTCTATGCGCGAGACAGTGGAAATTGACAAAGAACAGCCCAAGAGCGGTGAC 2151
Qy      1960 CGTGGCCGTGAAGATGTTGAAGATATGCCACAGAGAAAGACCTTTGATCTGGTGTG 2019
Db      2152 CGTGGCCGTGAAGATGTTGAAGATATGCCACAGAGAAAGACCTTTGATCTGGTGTG 2211
Qy      2020 AGAGATGAGATGATGAGATGATGAGAAACAAGAAATATCATTAATCTTGGAGC 2079
Db      2212 AGAGATGAGATGATGAGATGATGAGAAACAAGAAATATCATTAATCTTGGAGC 2271
Qy      2080 CTGCAACAGATGGGCTCTATATGTCATATGATGATGCTCTTAAGGCAACCTCG 2139
Db      2272 CTGCAACAGATGGGCTCTATATGTCATATGATGATGCTCTTAAGGCAACCTCG 2331
Qy      2140 AGAATACCTCCGAGCCCGAGGCCACCCGAGATGAGTACTCTATGATTAACCGTGT 2199
Db      2332 AGAATACCTCCGAGCCCGAGGCCACCCGAGATGAGTACTCTATGATTAACCGTGT 2391
Qy      2200 TCCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2259
Db      2392 TCCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2451
Qy      2260 GATGAGATCTTGGCTTCCCAAAATATGATGATGATGATGATGATGATGATGATG 2319
Db      2452 CATGGGATCTTGGCTTCCCAAAATATGATGATGATGATGATGATGATGATGATG 2511
Qy      2320 GGTAAACAGAAACAATGTGATGATGATGATGATGATGATGATGATGATGATGATG 2379
Db      2512 GGTAAACAGAAACAATGTGATGATGATGATGATGATGATGATGATGATGATGATG 2571
Qy      2380 TATAGATATTAACAAAGACCAACATGGCGGCTTCCAGTCAATGATGATGATGATG 2439
Db      2572 TATAGATATTAACAAAGACCAACATGGCGGCTTCCAGTCAATGATGATGATGATG 2631
Qy      2440 AGCCCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2499
Db      2632 AGCCCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2691
Qy      2500 GTGGGAGATCTTCACTTGGGGGCTGCGCCTTACCAAGGATCCCGTGGAGGAACTTT 2559
Db      2692 GTGGGAGATCTTCACTTGGGGGCTGCGCCTTACCAAGGATCCCGTGGAGGAACTTT 2751
Qy      2560 TAACTGCTGAAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATG 2619
Db      2752 TAACTGCTGAAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATG 2811
Qy      2620 CATGATGATGAGGAGCTGTTGGCATGATGATGATGATGATGATGATGATGATGATG 2679
Db      2812 CATGATGATGAGGAGCTGTTGGCATGATGATGATGATGATGATGATGATGATGATG 2871
Qy      2680 GGTAGAGAGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2739
Db      2872 GGTAGAGAGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2931
Qy      2740 CCAACTCTCGAACAGATTAACCTAGTAACTCTGACACAGAAAGTTCTTCTGAG 2799
Db      2932 CCAACTCTCGAACAGATTAACCTAGTAACTCTGACACAGAAAGTTCTTCTGAG 2991
Qy      2800 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2859
Db      2992 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3051
Qy      2860 ACACATTAACGAGATGTTAAACATGATGATGATGATGATGATGATGATGATGATG 2919

```

```

Db      3052 ACACATTAACGAGATGTTAAACATGATGATGATGATGATGATGATGATGATG 3111
Qy      2920 GCACCTGGAGACCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 2979
Db      3112 GCACCTGGAGACCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 3171
Qy      2980 ACTGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3039
Db      3172 ACTGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3231
Qy      3040 ATTATACAGTTGAACCTGTAATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3099
Db      3232 ATTATACAGTTGAACCTGTAATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3291
Qy      3100 GGACTGC 3106
Db      3292 GGACTGC 3298

RESULT 8
US-10-669-920-628
; Sequence 628, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT FILING DATE: US/10/669,920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 4998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-628

Query Match      92.3%; Score 2667.8; DB 6; Length 4998;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 3024; Conservative 0; Mismatches 67; Indels 36; Gaps 8;

```


OY	236	ACAAACAAGGTGCGGGAGGAGCGTTGCCATTCAAGTGACTGACAGACAC- GCAAGGCC	294
Db	818	ACAAACAAGGTGCGGGAGGAGCGTTGCCATTCAAGTGACTGACAGACACGCGAGCGCC	877
OY	295	TGGGTCTTGAGGCCAACCGCA- GCTGAAGGCAATTGCGGTAGTCAAGCCCTGTAAGAA	353
Db	878	TGGGTCTTGAGGCCAACCGCAAGGCTGAAGGCAATTGCCGTAGTCAAGCCCTGTAAGAA	937
OY	354	GTGTGAGATGGATTAAAGTCCACATGAGATATGGAAGGACCGGGATTGTACCG	413
Db	938	GTGTGAGATGGATTAAAGTCCACATGAGATATGGAAGGACCGGGATTGTGTACCG	997
OY	414	TAAACAATGTCAGCTGGGGGTGTTTCATCTGCGGTGATGATCAACATGGCAACTTGT	473
Db	998	TAACATGATGATGCTGGGGGTGTTTCATCTGCGGTGATGATCAACATGGCAACTTGT	1057
OY	474	CCCTGGCCCGGCCCTCTTCTAGTTTATGTAAGATACCACTTAGAGCCAGAGAGCCAC	533
Db	1058	CCCTGGCCCGGCCCTCTTCTAGTTTATGTAAGATACCACTTAGAGCCAGAGAGCCAC	1117
OY	534	CAACCAATATCCAAATCTCTCAACCAAGATGACGTGCGCCAGGGAGTGCCTAG	593
Db	1118	CAACCAATATCCAAATCTCTCAACCAAGATGACGTGCGCCAGGGAGTGCCTAG	1177
OY	594	AGGTGCGCTGCTGTTGAAAGATGCGCGCTGATCATGTTGACTAAGGATGGGTGCACT	653
Db	1178	AGGTGCGCTGCTGTTGAAAGATGCGCGCTGATCATGTTGACTAAGGATGGGTGCACT	1237
OY	654	TGGGCCCCAACATATGAGACAGTGTCTTATTTGGGAGTACTTGCAATATAAAGGCCCCAC	713
Db	1238	TGGGCCCCAACATATGAGACAGTGTCTTATTTGGGAGTACTTGCAATATAAAGGCCCCAC	1297
OY	714	CTAAGACATCCCGGCGCTATATGCTTATCTGACAGTAAAGCACTGTAACATTTGGT	773
Db	1298	CTAAGACATCCCGGCGCTTATATGCTTATCTGACAGTAAAGCACTGTAACATTTGGT	1357
OY	774	ACTTCATGGTGAATGTCACAGATGCAATCTCATCCGAGATGATGAGATGACACCATG	833
Db	1358	ACTTCATGGTGAATGTCACAGATGCAATCTCATCCGAGATGATGAGATGACACCATG	1417
OY	834	GTGCGGAAGATTTTTCAGTGAAGACATGTAACAACAAGAGCACATATCTGACCAACA	893
Db	1418	GTGCGGAAGATTTTTCAGTGAAGACATGTAACAACAAGAGCACATATCTGACCAACA	1477
OY	894	CAGAAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTGGCT	953
Db	1478	CAGAAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTGGCT	1537
OY	954	GCCCAAGCCGGGGGGAACCTAATGCCAACATGCGGTGGCTGAAAAACGGGAAGAGTTTA	1013
Db	1538	GCCCAAGCCGGGGGGAACCTAATGCCAACATGCGGTGGCTGAAAAACGGGAAGAGTTTA	1597
OY	1014	AGCAGAGAGCATGCAATTGGAAGGCTCAAGAGTACGAACACAGCACTGAGGCTCATTTATG	1073
Db	1598	AGCAGAGAGCATGCAATTGGAAGGCTCAAGAGTACGAACACAGCACTGAGGCTCATTTATG	1657
OY	1074	AAAGTGTGTCCCATCTGACAAAGGAATTTATCTGTGTAGTGAATGAATACGGGT	1133
Db	1658	AAAGTGTGTCCCATCTGACAAAGGAATTTATCTGTGTAGTGAATGAATACGGGT	1717
OY	1134	CCATCAATCAACATGTAACCTGGAATGTTGTGAAGATGCGCTCAACGGGCCATCTTCC	1193
Db	1718	CCATCAATCAACATGTAACCTGGAATGTTGTGAAGATGCGCTCAACGGGCCATCTTCC	1777
OY	1194	AAAGCCGACCTGCGCGCAATGCTCCACAGTGTGAGAGACGTAAGTTTGTCTGCA	1253
Db	1778	AAAGCCGACCTGCGCGCAATGCTCCACAGTGTGAGAGACGTAAGTTTGTCTGCA	1837
OY	1254	AGGTTTACAGTATGCCACGCCCACTCACTCACTAGTGATCAAGCACTGTGAAAAAGACGCA	1313
Db	1838	AGGTTTACAGTATGCCACGCCCACTCACTCACTAGTGATCAAGCACTGTGAAAAAGACGCA	1897

QY	1314	GTAATAATCGGGCCCGACGGGCTGCCTTAACCTCAAGGTTCTTCAGCACTCGGGGATTAATA	1373
DB	1898	GTAATAATCGGGCCCGACGGGCTGCCTTAACCTCAAGGTTCTTCAGGTCGAGGCGCGG	1957
QY	1374	GTTCCAATGCA-----GAAAGTGGGCTCTGTTCAAATGTGAACGAGCGGA	1419
DB	1958	TGTTAACACACGCGACAAAGAGATTGAGGTTCTCTAATTCCGAAATGAATCTTTTAGGA	2017
QY	1420	TGCTGGGGAATATATATGTAAAGTCTCCAAATTATATGAGGCAAGGCCAACAGTCTGCTG	1479
DB	2018	CGCTGGGGGAATATATGATGCTGGGGGTAATTTATTTAGGATATCTTTCACTCTGCATG	2077
QY	1480	GCTCACTGCTCTGCCAAAAACAGCAAGCGCTGTGAAGGAAAAAGAGATTACAGTTCCCC	1539
DB	2078	GTTHACAGTTCTGCCC-----AGGCGCTGGAAGGAAAAAGAGATTACAGTTCTCCC	2128
QY	1540	AGACTACCTGGAGATAGCATTTACTGTCAATAGGAGGCTCTTCTTAATCCCTGATAGTGST	1599
DB	2129	AGACTACCTGGAGATAGCATTTACTGTCAATAGGAGGCTCTTCTTAATCCCTGATAGTGST	2188
QY	1600	AACAGTCACTCTGTGCGGAATGAAGAACAGACCAAGAAAGCCAGACTTACAGCAGCCAGCC	1659
DB	2189	AACAGTCACTCTGTGCGGAATGAAGAACAGACCAAGAAAGCCAGACTTACAGCAGCCAGCC	2248
QY	1660	GCGTGTGCAAGGTCACCAAAAGCTATCTCCCTGCGGACAGGTTAACAGTTTGGCTGA	1719
DB	2249	GCGTGTGCAAGGTCACCAAAAGCTATCTCCCTGCGGACAGGTTAACAGTTTGGCTGA	2302
QY	1720	GTCCAGCTCTCCCAATGAATCTCAACACCCCGCTGGTAGGATTAACAACAGCCCTCTCTC	1779
DB	2303	GTCCAGCTCTCCCAATGAATCTCAACACCCCGCTGGTAGGATTAACAACAGCCCTCTCTC	2362
QY	1780	AACGCGACACACCCCATGCTGGCAGGGGGTCTCCGAGTATGAATTCACAGAGACCCAAA	1839
DB	2353	AACGCGACACACCCCATGCTGGCAGGGGGTCTCCGAGTATGAATTCACAGAGACCCAAA	2422
QY	1840	ATGGGAGTTTCCAGAGATTAAGCTGACCTGGGCAAGCCCTTGGGAGAAAGTCTCTTGG	1899
DB	2423	ATGGGAGTTTCCAGAGATTAAGCTGACCTGGGCAAGCCCTTGGGAGAAAGTCTCTTGG	2482
QY	1900	GCAAGTGTCAATGCGGGAAGAGATGGGGAATTGACAAAGACAAAGGCCAAAGAGGCGGTAC	1959
DB	2483	GCAAGTGTCAATGCGGGAAGAGATGGGGAATTGACAAAGACAAAGGCCAAAGAGGCGGTAC	2542
QY	1960	CGTGGCCGTGAAGAGTGTGAAGATGATGCCACAGAGAAACCTTTCTGTCTGTGTC	2019
DB	2543	CGTGGCCGTGAAGAGTGTGTGAAGATGATGCCACAGAGAAACCTTTCTGTCTGTGTC	2602
QY	2020	AGAGATGAGATGATGAAGATGATTTGGGAAACAAGAAATTCATTAATCTTTCTTGAGC	2079
DB	2603	AGAGATGAGATGATGAAGATGATTTGGGAAACAAGAAATTCATTAATCTTTCTTGAGC	2662
QY	2080	CTGCAACAAGATTTGGGCTCTCTAATGTCAATGTTGAGATGCTTAAAGGCAACCTCG	2139
DB	2663	CTGCAACAAGATTTGGGCTCTCTAATGTCAATGTTGAGATGCTTAAAGGCAACCTCG	2722
QY	2140	AGAAATACCTCCGAGGCCGAGGCGCACCCGGAGTGAATCTCTATGACATTAACCGTGT	2199
DB	2723	AGAAATACCTCCGAGGCCGAGGCGCACCCGGAGTGAATCTCTATGACATTAACCGTGT	2782
QY	2200	TCCTTAGAGACAGATGACCTTCAAGGACTTGGTGTCAATGCTACCTACAGCTGGCCAGACG	2255
DB	2783	TCCTTAGAGACAGATGACCTTCAAGGACTTGGTGTCAATGCTACCTACAGCTGGCCAGACG	2842
QY	2260	GATGAGATCTTGGCTTCCCAAAAATGATTCATGGAATTTAGAGGCAAGAAATGTTT	2319
DB	2843	GATGAGATCTTGGCTTCCCAAAAATGATTCATGGAATTTAGAGGCAAGAAATGTTT	2902
QY	2320	GGAACAAGAAAACAATGTGATGAATAATAGACATTTGGAATGCGCAAGATATCAACA	2379
DB	2903	GGAACAAGAAAACAATGTGATGAATAATAGACATTTGGAATGCGCAAGATATCAACA	2962
QY	2380	TAATAGCTAATTAACAAGAACCAACCAATGAGCGGCTTCAAGTCAAGTGAATGCTCAGA	2433

```

Db      2963 TATAGACTATTACAAAAGACCAACCAATGGGCGGCTTCAGTCAAGTATGCTCCACA 3022
Qy      2440 AGCCCTGTTGATAGATATACATCATCAGATGATGTCTGCTCCG369TGTAAAT 2499
Db      3023 AGCCCTGTTGATAGATATACATCATCAGATGATGTCTGCTCCG369TGTAAAT 3082
Qy      2500 GTGGAGATCTTCACTTAGGGGGCTCGCCCTACCCAGGAAATTCCTGTGAGAACTTTT 2559
Db      3083 GTGGAGATCTTCACTTAGGGGGCTCGCCCTACCCAGGAAATTCCTGTGAGAACTTTT 3142
Qy      2560 TAACTGCTGAGAGAGACACAGATGATTAAGCCAGCACTGACCAACCACTGTA 2619
Db      3143 TAACTGCTGAGAGAGACACAGATGATTAAGCCAGCACTGACCAACCACTGTA 3202
Qy      2620 CATGATGATAGAGGACTGTTGGCAGTCAGTCGCTCCAGAGACCAAGTTCAGAGATT 2679
Db      3203 CATGATGATAGAGGACTGTTGGCAGTCAGTCGCTCCAGAGACCAAGTTCAGAGATT 3262
Qy      2680 GGTAGAAACTTGTGATGAAATTTCTCACTTCAACAACCAATGAGAAATCTTGGACCTCAG 2739
Db      3263 GGTAGAAACTTGTGATGAAATTTCTCACTTCAACAACCAATGAGAAATCTTGGACCTCAG 3322
Qy      2740 CCAACCTCTGAAACAGATTCACTAGTGAACCTGACACAAGAGTTCTTGTTCAGG 2799
Db      3323 CCAACCTCTGAAACAGATTCACTAGTGAACCTGACACAAGAGTTCTTGTTCAGG 3382
Qy      2800 AGATGATCTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTCTTCAAGTATCC 2859
Db      3383 AGATGATCTGTTTTTCTCCAGACCCCATGCTTACGAACATGCTCTTCAAGTATCC 3442
Qy      2860 ACACATTAACGGCAGTGTAAACATGATGATCTGTCTGCTGTCCCAACAGAGACA 2919
Db      3443 ACACATTAACGGCAGTGTAAACATGATGATCTGTCTGCTGTCCCAACAGAGACA 3502
Qy      2920 GCACTGGAACTAGCTACACTGAGCAGGAGACCAATGCTCCAGAGCTTGTGTCTCC 2979
Db      3503 GCACTGGAACTAGCTACACTGAGCAGGAGACCAATGCTCCAGAGCTTGTGTCTCC 3562
Qy      2980 ACTTGTATATATGATCAGAGAGTAATAATTTGAAAGTAATCAGCATATGTGTAAAG 3039
Db      3563 ACTTGTATATATGATCAGAGAGTAATAATTTGAAAGTAATCAGCATATGTGTAAAG 3622
Qy      3040 ATTATATCAGTTGAAAATCTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGAGAT 3099
Db      3623 ATTATATCAGTTGAAAATCTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGAGAT 3682
Qy      3100 GGAAGTC 3106
Db      3683 GGAAGTC 3689

```

RESULT 9
US-10-669-920-590

```

; Sequence 590, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004, 113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052, 482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997, 722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034, 650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085, 117
; PRIOR FILING DATE: 2002-02-27

```

```

; PRIOR APPLICATION NUMBER: US 10/087, 192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322, 281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322, 696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 4472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-590

Query Match      90.9%; Score 2824.2; DB 6; Length 4472;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2970; Conservative 0; Mismatches 63; Indels 28; Gaps 8;

Qy      1 CCGGAGAGCAAGTTGTTGAGAGCAAG-CAAGCTGATCTTCTCTCTCTCC 59
Db      578 CTGGCAGCAAGTTGTTGAGAGCAAGCTGATGCTTCTCTCTCTCTCC 637
Qy      60 CCAATCCGAGGAGCAGCCCGCGGCGTCATG--GCGCTCTCCGAGCTGCGGTAAGC 116
Db      638 CCAATCCGAGGAGCAGCCCGCGGCGTCATGCGCGCTCTCCGAGCTGCGGTAAGC 697
Qy      117 GTGAAGCCCGGAGGCTTGGCGCCGCGCAAGACCAAGACCAACTTCTGCGTTGAG 176
Db      698 GTGAAGCCCGGAGGCTTGGCGCCGCGCAAGACCAAGACCAACTTCTGCGTTGAG 757
Qy      177 TTGCTCCCGCAACCCCGGCGTGTGCTTTCTCATCCGACCCAGCGGCGG-CGG6G 235
Db      758 TTGCTCCCAACCCCGGCGTGTGCTTTCTCATCCGACCCAGCGGCGG-817
Qy      236 ACAACACAGTCCGCGAGAGAGCGTCCATTCAGTCACTGACAGCAGC-GCAGCGCT 294
Db      818 ACAACACAGTCCGCGAGAGAGCGTCCATTCAGTCACTGACAGCAGCAGCGCGC 877
Qy      295 TCGGTTCTGAGCCCAACCGCA-CTGAAAGCATTTGGCGCTTATCCATGCGCGTGAAGAA 353
Db      878 TCGGTTCTGAGCCCAACCGCACTGAAAGCATTTGGCGCTTATCCATGCGCGTGAAGAA 937
Qy      354 GTGTGAGATGGGATTAAGCTCAATGAGATATGAGAGAGAGACCGGAGATTGTACCG 413
Db      938 GTGTGAGATGGGATTAAGCTCAATGAGATATGAGAGAGAGACCGGAGATTGTACCG 997
Qy      414 TAACCATGTCACTGGGCTGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Db      998 TAACCATGTCACTGGGCTGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
Qy      474 CCTGGCCCGGCGCTCTCTCACTTATGTTAGATATCCATTTAGAGCCAGAGACCCAC 533
Db      1058 CCTGGCCCGGCGCTCTCTCACTTATGTTAGATATCCATTTAGAGCCAGAGACCCAC 1117
Qy      534 CAACCAATATCAAAATCTTCAACCAAGAGTGAAGTGTGCTGCGCAGGAGAGTGTGCTAG 593
Db      1118 CAACCAATATCAAAATCTTCAACCAAGAGTGAAGTGTGCTGCGCAGGAGAGTGTGCTAG 1177
Qy      594 AGGTGCGTCTGCTTGAAGATGCCCGGTATCATGTTGATGATGAGATGGGTCCT 653
Db      1178 AGGTGCGTCTGCTTGAAGATGCCCGGTATCATGTTGATGATGAGATGGGTCCT 1237
Qy      654 TGGGCGCCAAATAGAGCAGTGTCTTATTTGGGAGTACTTGACATTAAGGCGCCACAC 713
Db      1238 TGGGCGCCAAATAGAGCAGTGTCTTATTTGGGAGTACTTGACATTAAGGCGCCACAC 1297
Qy      714 CTAGAGACTCGGCGCTTATGCTTGAATCGCAGTGAAGCTGTAAGCACTGTAACCTTGTGT 773
Db      1298 CTAGAGACTCGGCGCTTATGCTTGAATCGCAGTGAAGCTGTAAGCACTTGTGT 1357
Qy      774 ACTTCATGTGATATGATCAGATGCTCATCTCAGATGATGATGATGATGATGATGATGATG 833
Db      1358 ACTTCATGTGATATGATCAGATGCTCATCTCAGATGATGATGATGATGATGATGATGATG 1417

```

834 GTGCGGAAGATTGTCAGTGAAGAACGTAAACAAGAGACACATACCTGAGCAACA 893
1418 GTGCGGAAGATTGTCAGTGAAGAACGTAAACAAGAGACACATACCTGAGCAACA 1477
894 CAGAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCGCAACATGCAAGTTGCGT 953
1478 CAGAAAGATGGAAGAGCGGCTCCATGCTGTGCTGCGGCGCAACATGCAAGTTGCGT 1537
954 GCCAGCGCGGAGGAACCAATGCCAACCATGCGGTGCTGAAAAACGGAGAGAGTTTA 1013
1538 GCCAGCGCGGAGGAACCAATGCCAACCATGCGGTGCTGAAAAACGGAGAGAGTTTA 1597
1014 AGCAGAGCATGCAATTGAGGCTCAAGAGTACGAACCAAGCATGAGAGCTCATTTAG 1073
1598 AGCAGAGCATGCAATTGAGGCTCAAGAGTACGAACCAAGCATGAGAGCTCATTTAG 1657
1074 AAGGTGTGTCCTCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGATACGGGT 1133
1658 AAGGTGTGTCCTCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGATACGGGT 1717
1134 CCATCAATCAACAGTACCACTGATGTGTGAGCGATCGCTCACCGGCGCATCTCC 1193
1718 CCATCAATCAACAGTACCACTGATGTGTGAGCGATCGCTCACCGGCGCATCTCC 1777
1194 AAGCGGACCTGCGGCAATGCTCTCCACAGTGTGAGAGAGACGTAGATTGTCTGCA 1253
1778 AAGCGGACCTGCGGCAATGCTCTCCACAGTGTGAGAGAGACGTAGATTGTCTGCA 1837
1254 AGGTTTACGTATGCCAGGCCCAATCAGTGTGATCAAGCAGCGGAAAAAGACGGCA 1313
1838 AGGTTTACGTATGCCAGGCCCAATCAGTGTGATCAAGCAGCGGAAAAAGACGGCA 1897
1314 GTAATACCGGCGCCGACGCGGCTGACCTAACGTTCTCAAGACACTCGGAGATTAATA 1373
1898 GTAATACCGGCGCCGACGCGGCTGACCTAACGTTCTCAAGGCGCGGATTAACA 1957
1374 GTTCCAGTGCAGAGTGTGCTGT-----TCAATGTACCGAGCGGATGCTGGG 1427
1958 CCACGGACAAGAGATTGAGTTCCTATATTCGGAATGTAACTTTTGAGGACGCTGGG 2017
1428 AATATATATGTAAGGTCCATTAATATAGGCAAGGCCAACAGTGTGCTGATCACTG 1487
2018 AATATATGTTGCTGGGTGATATCTATGTGAGATATCTTTCACTGTGATGTTGAAG 2077
1488 TCTTCGCAAAACAGCAAGCGCTGAGAGAGAAAGAGATTACAGTTCCCGACATACC 1547
2078 TCTTCG-----AGCGCTGAGAGAGAAAGAGATTACAGTTCCCGACATACC 2128
1548 TGAAGATGCAATTAATGTCATAGGGGTCTTTTAATGCGCTGTATGTGTAAAGTCA 1607
2128 TGAAGATGCAATTAATGTCATAGGGGTCTTTTAATGCGCTGTATGTGTAAAGTCA 2188
1608 TCTGTGCGGAGTGAAGAACAGACCAAGAGCGAATTACAGCGCGCGGCTGTGC 1667
2188 TCTGTGCGGAGTGAAGAACAGACCAAGAGCGAATTACAGCGCGCGGCTGTGC 2248
1668 ACAAGGTGACAAACGTATCCCTGCGGAGACAGGTAAAGTTTCGCTGATCCAGCT 1727
2248 ACAAGGTGACAAACGTATCCCTGCGGAGACAG-----GTTTCGCTGATCCAGCT 2302
1728 CCTTCATGAATCTCAACACCCCGCTGTGTGAAGTAAACAAGCGCTCTTCAAGCGAG 1787
2303 CCTTCATGAATCTCAACACCCCGCTGTGTGAAGTAAACAAGCGCTCTTCAAGCGAG 2362
1788 ACAACCCCATGCTGCGAGGGGTCCGAGATGAATTCACAGAGACCAAAATGGAGAT 1847
2363 ACAACCCCATGCTGCGAGGGGTCCGAGATGAATTCACAGAGACCAAAATGGAGAT 2422
1848 TTCAGAGATTAAGTGAACACTGTGAGCAAGCCCTGTGAGAGAGGTTGCTTTGGGCAAGTGG 1907
2423 TTCAGAGATTAAGTGAACACTGTGAGCAAGCCCTGTGAGAGAGGTTGCTTTGGGCAAGTGG 2482

1908 TCATGCGGAAGCAGTGGGAATTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCG 1967
2483 TCATGCGGAAGCAGTGGGAATTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCG 2542
1968 TGAAGATGTTGAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTCAAGATGG 2027
2543 TGAAGATGTTGAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTCAAGATGG 2602
2028 AGATGATGAAGATGATGGGAACAACAAGATATCATTAATCTTTCTTGGAGCTGCACAC 2087
2603 AGATGATGAAGATGATGGGAACAACAAGATATCATTAATCTTTCTTGGAGCTGCACAC 2662
2088 AGATGAGGCTCTCATGTGCTAAGTGTGATGCTCTTAAAGGCAACCTCCGAGAAATAC 2147
2663 AGATGAGGCTCTCATGTGCTAAGTGTGATGCTCTTAAAGGCAACCTCCGAGAAATAC 2722
2148 TCCAGCGCGGAGGCCAACCCGGAGTGAAGTACTCTTAATGAATTAACGTTGCTGAGG 2207
2723 TCCAGCGCGGAGGCCAACCCGGAGTGAAGTACTCTTAATGAATTAACGTTGCTGAGG 2782
2208 AGCAGATGACCTTCAAGGACTTGTGTGATGCACTTACAGCTGTGGCCAGAGATGAGT 2267
2783 AGCAGATGACCTTCAAGGACTTGTGTGATGCACTTACAGCTGTGGCCAGAGATGAGT 2842
2268 ACTTGGCTTCCCAAAATGATATTCATGAGATTAGAGACCAAGAAATGTTTGGTAAACAG 2327
2843 ACTTGGCTTCCCAAAATGATATTCATGAGATTAGAGACCAAGAAATGTTTGGTAAACAG 2902
2328 AAAACAATGTGATGAATAATGACAGACTTTGAGCTGCGCAGAGATTAACAATATTAAGT 2387
2903 AAAACAATGTGATGAATAATGACAGACTTTGAGCTGCGCAGAGATTAACAATATTAAGT 2962
2388 ATTACAAAAACACCACTAATGGGCGCTTCCAGTCAAGTGAATGGCTCCAGAAACCCCTGT 2447
2963 ATTACAAAAACACCACTAATGGGCGCTTCCAGTCAAGTGAATGGCTCCAGAAACCCCTGT 3022
2448 TTGATGAGTATACATCATGATGATGATGTCGATCTGCGGCTGTGATATGTGGAGA 2507
3023 TTGATGAGTATACATCATGATGATGATGTCGATCTGCGGCTGTGATATGTGGAGA 3082
2508 TCTTCACTTTAGGGGCGCTCGCCTTACCCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGC 2567
3083 TCTTCACTTTAGGGGCGCTCGCCTTACCCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGC 3142
2568 TGAAGAAAGACACAGATGATTAAGCCAGCCAACTGACCAACAAGACTGTACATGATGA 2627
3143 TGAAGAAAGACACAGATGATTAAGCCAGCCAACTGACCAACAAGACTGTACATGATGA 3202
2628 TGAAGGACTGTTGGCATGCAATGCGCTCCAGAGACCAAGCTTCAAGCAAGTTGGTAGAG 2687
3203 TGAAGGACTGTTGGCATGCAATGCGCTCCAGAGACCAAGCTTCAAGCAAGTTGGTAGAG 3262
2688 ACTTGATGCAATTTCTCACTCTCAACAACAAATGAAGATTAATTGGAACCTGACCAACTG 2747
3263 ACTTGATGCAATTTCTCACTCTCAACAACAAATGAAGATTAATTGGAACCTGACCAACTG 3322
2748 TCGAAGCATATTAACCTGATACCTGACACAAGAGTTCTTGTCTTCAAGAGATGATT 2807
3323 TCGAAGCATATTAACCTGATACCTGACACAAGAGTTCTTGTCTTCAAGAGATGATT 3382
2808 CTGTTTTTCTCGAGACCCAGCTTACGAACCAATGCAATGCTCTCATGATACCAATTA 2867
3383 CTGTTTTTCTCGAGACCCAGCTTACGAACCAATGCAATGCTCTCATGATACCAATTA 3442
2868 ACGGAGGTAAACATGAATGAATGTGTGCTGTGCCCTCCCAACAGAGACAGACTGGG 2927
3443 ACGGAGGTAAACATGAATGAATGTGTGCTGTGCCCTCCCAACAGAGACAGACTGGG 3502
2928 AACCTAGTAACTGAGAGGAGACCAATGCTCTCCAGAGCTTGTGTCTTCACTTGAT 2987
3503 AACCTAGTAACTGAGAGGAGACCAATGCTCTCCAGAGCTTGTGTCTTCACTTGAT 3562
2988 ATATGATCAAGAGATTAATTAATTGAAAGTAAATGATGATGTGTAAGATTATAC 3047

Db 3563 AATGATGATGAGAGTAAATTAATTGAAAGAAATGATGATGATTAATAC 3622
Qy 3048 A 3048
Db 3623 A 3623

RESULT 10
US-10-669-920-598
Sequence 598, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Moritz, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 598
LENGTH: 5080
TYPE: DNA
ORGANISM: Homo sapiens
US-10-669-920-598

Query Match 89.5%; Score 2780.2; DB 6; Length 5080;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 3028; Conservative 0; Mismatches 63; Indels 120; Gaps 9;

Qy 1 CCGGAGAGCAAACTTGTGTGAGGCAACG-CAGGCTGAGTCTTCTTCTGCTCC 59
Db 578 CTGCGAGCAAAATTTGTGTGAGGCAACGCGAAGCTGAGTCTTCTTCTTCTGCTCC 637
Qy 60 CCAAAATCCGAGGAGGCAAGCCGCGGCGTCAATG--GCGCTCTCCGAGCTGTGGGTAACG 116
Db 638 CCAAAATCCGAGGAGGCAAGCCGCGGCGTCAATG--GCGCTCTCCGAGCTGTGGGTAACG 697
Qy 117 GTGAAGCCCGGAGGCTTGGCGCGGAGAAAGACCAACCACTCTTCTGCGTTTGAG 176
Db 698 GTGAAGCCCGGAGGCTTGGCGCGGAGAAAGACCAACCACTCTTCTGCGTTTGAG 757
Qy 177 TTGCTCCCGGCAACCCCGGCTGTGCTTTCTCAATCCGACCAAGCGGAGGCG 235
Db 758 TTGCTCCCGCAACCCCGGCTGTGCTTTCTCAATCCGACCAAGCGGAGGCG 817
Qy 236 ACAACACAGGTCCGAGAGAGCGTTGCAATTCAGTGAATGACGACAGACG-CGACGCGC 294
Db 818 ACAACACAGGTCCGAGAGAGCGTTGCAATTCAGTGAATGACGACAGCGCAGCGCC 877
Qy 295 TCGGTTCTTGAAGCCCAAGCGA-GCTGAAGCATTTGGCGTGAATGCGCCGTAAGAGAA 353
Db 878 TCGGTTCTTGAAGCCCAAGCGAAGCGTGAAGCATTTGGCGTGAATGCGCCGTAAGAGAA 937
Qy 354 GTGTGAGAGTGGATTAAGCTCAATGAGATATGAGAGAGACCGGAGATGTGACCG 413

Db 938 GTGTGAGATGGATTAAGTCCACATGAGAGATATGAGAGAGACCGGAGATTGTACCG 997
Qy 414 TAACCATGTGAGCGGGGATGCTTTCATCTGCTGTGTGTGTGATGCAATGCAACTGT 473
Db 998 TAACCATGTGAGCGGGGATGCTTTCATCTGCTGTGTGTGTGATGCAATGCAACTGT 1057
Qy 474 CCTGGCCCGGCTCTTCAAGTTAGTGAAGATACCAATTAAGCCGAGAGGCAAC 533
Db 1058 CCTGGCCCGGCTCTTCAAGTTAGTGAAGATACCAATTAAGCCGAGAGGCAAC 1117
Qy 534 CAACCAATTAACCAATCTCTCAACCAAGATGATGCTGCGCAGGAGGATGCTGAG 593
Db 1118 CAACCAATTAACCAATCTCTCAACCAAGATGATGCTGCGCAGGAGGATGCTGAG 1177
Qy 594 AGTGGCGCTGCTGTGAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGAT 653
Db 1178 AGTGGCGCTGCTGTGAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGAT 1237
Qy 654 TGGGCGCCCAACATAGAGCAGTGTATTTGGGAGTACTTGCAGATTAAGGCGCACAC 713
Db 1238 TGGGCGCCCAACATAGAGCAGTGTATTTGGGAGTACTTGCAGATTAAGGCGCACAC 1297
Qy 714 CTAGAGACTCGGCTCTATGCTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
Db 1298 CTAGAGACTCGGCTCTATGCTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1357
Qy 774 ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
Db 1358 ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
Qy 834 GTGCGAAGATTTTGTCACTGAGAGAACATTAACCAAGAGAGACCAATTAAGTGAACAA 893
Db 1418 GTGCGAAGATTTTGTCACTGAGAGAACATTAACCAAGAGAGACCAATTAAGTGAACAA 1477
Qy 894 CAGAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
Db 1478 CAGAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1537
Qy 954 GCCGAGCCCGGAGGAGAACCAATGCCAATGCCGAGGCTGAGAAACGGAAGAGATT 1013
Db 1538 GCCGAGCCCGGAGGAGAACCAATGCCAATGCCGAGGCTGAGAAACGGAAGAGATT 1597
Qy 1014 AGCAGAGCATGCTGAGAGGCTCAAGGTACGAACCAAGCAGCAGTCAATTAAG 1073
Db 1598 AGCAGAGCATGCTGAGAGGCTCAAGGTACGAACCAAGCAGCAGTCAATTAAG 1657
Qy 1074 AAGGTGTGCTCCATCTGACAAAGGAAATTAATCTGTGTATGAGAAATTAATGCGGT 1133
Db 1658 AAGGTGTGCTCCATCTGACAAAGGAAATTAATCTGTGTATGAGAAATTAATGCGGT 1717
Qy 1134 CCATCAATCAACGTAACCTGATGATGTTGTGAGACGATGCTCAACCGGCCCATCTCC 1193
Db 1718 CCATCAATCAACGTAACCTGATGATGTTGTGAGACGATGCTCAACCGGCCCATCTCC 1777
Qy 1194 AAGCGGACTGCGGCAATGCTCCTCAAGTGTGAGAGAGACGTAAGATTGTCTGCA 1253
Db 1778 AAGCGGACTGCGGCAATGCTCCTCAAGTGTGAGAGAGACGTAAGATTGTCTGCA 1837
Qy 1254 AAGTTTACAGTATGCCAGGCCCATCTCAATGATGATCAAGCAGTGAAGAAACGCGCA 1313
Db 1838 AAGTTTACAGTATGCCAGGCCCATCTCAATGATGATCAAGCAGTGAAGAAACGCGCA 1897
Qy 1314 GTTAATTAAGGAGCGGAGCGGCTGCTCAAGTTCTCAAGCACTCGGGGATTAATA 1373
Db 1898 GTTAATTAAGGAGCGGAGCGGCTGCTCAAGTTCTCAAGCACTCGGGGATTAATA 1957
Qy 1374 GTTCAATGAGAGTGTGCTGCTGT-----TCAATGTGACCGAGCGGATGCTGCGG 1427
Db 1958 CCAAGGCAAAAGATGAGGTTCTCTAATTTGGAATGATTAATTTTGAAGAGCGTGGGG 2017
Qy 1428 AATATATATATGATGATGCTTCAATTAATTAAGGAGCGCAACAGTGTGCTGCTCACTG 1487
Db 2018 AATATATGCTGTGGGCGGATTAATCTAATGAGATATCTTTCACTGTGATGATGACAG 2077

! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO: 600
! LENGTH: 4697
! TYPE: DNA
! ORGANISM: Homo sapiens
US-10-669-920-600

Query Match 89.0%; Score 2765.8; DB 6; Length 4697;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 3024; Conservative 0; Mismatches 67; Indels 128; Gaps 9;

QY 1 CCCGAGCAAAAGTTGGTGGAGGCAACG-CAAGCCGAGTCTTCTCTCTCTCTCC 59
DB 187 CTGCGAGCAAAATTTGGTGGAGGCAACGCCAGCTGAGTCTTCTCTCTCTCTCTCC 246
QY 60 CCAAAATCCGAGGCAAGCCCGGCGCTCATG---GCGCTCTCCGAGCCCTGGGATACG 116
DB 247 CCAAAATCCGAGGCAAGCCCGGCGCTCATGCGCGCTCTCTCTCTCTCTCTCTCTCC 306
QY 117 GTGAAGCCCGGAGGCTTGGCCGCGGAGAAACCCAAAGACCACTTCTCTCTCTCTCTCT 176
DB 307 GTGAAGCCCGGAGGCTTGGCCGCGGAGAAACCCAAAGACCACTTCTCTCTCTCTCTCT 366
QY 177 TTGCTCCCGCAACCCCGGCGCTGCTGCTTCTCAATCCGCAACCGCGGAGC-CGGAG 235
DB 367 TTGCTCCCGCAACCCCGGCGCTGCTGCTTCTCAATCCGCAACCGCGGAGC-CGGAG 426
QY 236 ACAACACAGGTCCGAGGAGCGCTTGCATTCAAGTACTGACGACGACG-CCAGCGCC 294
DB 427 ACAACACAGGTCCGAGGAGCGCTTGCATTCAAGTACTGACGACGACG-CCAGCGCC 486
QY 295 TCGGTTCTGAGCCCGACCGCA-GCTGAAGCATTGGCGCTGATGCCCTCTCTCTCTCTCT 353
DB 487 TCGGTTCTGAGCCCGACCGCAAGGCTGAAGCATTGGCGCTGATGCCCTCTCTCTCTCT 546
QY 354 GTGTGAGAGTGGATTAACTCCACATGAGATATGAGAGAGAGACCGGGGATTGGTACG 413
DB 547 GTGTGAGAGTGGATTAACTCCACATGAGATATGAGAGAGAGACCGGGGATTGGTACG 606
QY 414 TAAACATGTCAGCTGGGGTCTTTTCACTGCTGGTCTGTCACATGACCACTTGT 473
DB 607 TAAACATGTCAGCTGGGGTCTTTTCACTGCTGGTCTGTCACATGACCACTTGT 666
QY 474 CCTTGGCCCGGCTCTCTCTGATTGATGAGATACCACTTGAAGCCAGAAAGCCAC 533
DB 667 CCTTGGCCCGGCTCTCTCTGATTGATGAGATACCACTTGAAGCCAGAAAGCCAC 726
QY 534 CAACCAAAATCAAAATCTCTCAACGAGGTGACGTGCTGGCGGAGGAGTGGCTAG 593
DB 727 CAACCAAAATCAAAATCTCTCAACGAGGTGACGTGCTGGCGGAGGAGTGGCTAG 786
QY 594 AGGTGGCTGCTCTGTTGAAGATGCGCGCTGATCACTTGAAGTGGGTCACCT 653
DB 787 AGGTGGCTGCTCTGTTGAAGATGCGCGCTGATCACTTGAAGTGGGTCACCT 846
QY 654 TGGGGCCCAACAAATAGGACAGTCTTATGGGAGATCTTGAAGTAAAGGCGCCACG 906
DB 847 TGGGGCCCAACAAATAGGACAGTCTTATGGGAGATCTTGAAGTAAAGGCGCCACG 906
QY 714 CTGAAGACTCCGGCTCTATGCTTGTATCTGSCAGTGAAGCTGAGCAAGTGAACCTTGT 773
DB 907 CTGAAGACTCCGGCTCTATGCTTGTATCTGSCAGTGAAGCTGAGCAAGTGAACCTTGT 966
QY 774 ACTTCAATGTAATGTCAAGATGCACTCATCCGAGATGATGAGATGACCCGATG 833
DB 967 ACTTCAATGTAATGTCAAGATGCACTCATCCGAGATGATGAGATGACCCGATG 1026
QY 834 GTGGGAAAGATTTTGTCAATGAGAACATTAACAAGAGAGCACTACTGACCAACA 893
DB 1027 GTGGGAAAGATTTTGTCAATGAGAACATTAACAAGAGAGCACTACTGACCAACA 1086
QY 894 CAGAAAAGATGAAAAGCGGCTCATGCTGCTGGCGCAACGTCAGATTTTGGCT 953

DB 1087 CAGAAAAGATGAAAAGCGGCTCATGCTGTGCTCGCGCCCAACATCTGTCAATTTGCT 1146
QY 954 GCCCAGCCCGGGGAGAACCAATGCCAATGCGGTGCTGAAAACGGGAAGAGTTTA 1013
DB 1147 GCCCAGCCCGGGGAGAACCAATGCCAATGCGGTGCTGAAAACGGGAAGAGTTTA 1206
QY 1014 AGCAGAGCATGCTGATTTGAGGCTCAAGATACGAACCAAGCATGAGCCCTCATTAATG 1073
DB 1207 AGCAGAGCATGCTGATTTGAGGCTCAAGATACGAACCAAGCATGAGCCCTCATTAATG 1266
QY 1074 AAAGTGTGTCCCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGATTAATCGGCT 1133
DB 1267 AAAGTGTGTCCCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGATTAATCGGCT 1326
QY 1134 CCATCAATCAACGTAACCTGATGTTTGTGAGACCATGCTCAACCGGCCCATCTCC 1193
DB 1327 CCATCAATCAACGTAACCTGATGTTTGTGAGACCATGCTCAACCGGCCCATCTCC 1386
QY 1194 AAGCGGACTGCGGCAATGCTCCACAGTGTGAGAGAGCGTAGGTTGTCTGCA 1253
DB 1387 AAGCGGACTGCGGCAATGCTCCACAGTGTGAGAGAGCGTAGGTTGTCTGCA 1446
QY 1254 AGGTTTACAGTATGCCAGCCCAATCCAGTGAATCAAGCATGGAAGAAACGCA 1313
DB 1447 AGGTTTACAGTATGCCAGCCCAATCCAGTGAATCAAGCATGGAAGAAACGCA 1506
QY 1314 GTAAATAGGGGCGGACCGGCTGCTTACCTCAAGTTCTCAAGCATCTGGGATTAATA 1373
DB 1507 GTAAATAGGGGCGGACCGGCTGCTTACCTCAAGTTCTCAAGCATCTGGGATTAATA 1566
QY 1374 GTTCAATGCA-----GAAGTGTGCTGTTCAATGTGACCGAGCGGA 1419
DB 1567 GTTCAATGCAACCGGCAAAAGAGATTAAGTTCTTATATTCGAGATGTAATCTTTGAGA 1626
QY 1420 TCGTGGGAAATATATATGTAAGTCTCCATTAATTAAGGAGGCAACCAAGTCTGCTG 1479
DB 1627 CGCTGGGAAATATATGTAAGTCTCCATTAATTAAGGAGATATCTTTCACTGACATG 1686
QY 1480 GCTCATGCTCTGCGCAAAACGACGAGCGCTGGAAGAAAGAGATTAACGCTTCCC 1539
DB 1687 GCTCATGCTCTGCGCAAAACGACGAGCGCTGGAAGAAAGAGATTAACGCTTCCC 1737
QY 1540 AGACTACCTGAGATGACATTTATCTGATAGGAGTCTTCTTAATCGCTGATGATGAT 1599
DB 1738 AGACTACCTGAGATGACATTTATCTGATAGGAGTCTTCTTAATCGCTGATGATGAT 1797
QY 1600 AACAGTCACTCTGTCCGATGAGATGAAGACGACCAAGAACCGCATTCAGACGCAAGC 1659
DB 1798 AACAGTCACTCTGTCCGATGAGATGAAGACGACCAAGAACCGCATTCAGACGCAAGC 1857
QY 1660 GGCTGTGCAACAGCTGACCAACGTAATCCCTCTGCGGAGACAGGTAACGTTTGGCTGA 1719
DB 1858 GGCTGTGCAACAGCTGACCAACGTAATCCCTCTGCGGAGACAG-----GTTTGGCTGA 1911
QY 1720 GTCCAGCTCTCTCATGAAGCTCCACACCGCGCTGATGAGATTAACAACGCTCTCTTC 1779
DB 1912 GTCCAGCTCTCTCATGAAGCTCCACACCGCGCTGATGAGATTAACAACGCTCTCTTC 1971
QY 1780 AACGGCAGACACCCCATGCTGCGAGGGGTCTCCAGATGAATCTTCCAGAGACCCAAA 1839
DB 1972 AACGGCAGACACCCCATGCTGCGAGGGGTCTCCAGATGAATCTTCCAGAGACCCAAA 2031
QY 1840 ATGGAGATTTCCAGAGATTAAGCTGACATGCGGCAAGCCCTGCGGAGAAAGTTGCTTGG 1899
DB 2032 ATGGAGATTTCCAGAGATTAAGCTGACATGCGGCAAGCCCTGCGGAGAAAGTTGCTTGG 2091
QY 1900 GCAAGTGTCAATGGGGAAGCAAGTGGGAATTGAACAAGCAAGCCCAAGAGCGGTAC 1959
DB 2092 GCAAGTGTCAATGGGGAAGCAAGTGGGAATTGAACAAGCAAGCCCAAGAGCGGTAC 2151
QY 1960 CGTGGCCGTGAAGATTTGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGATGTC 2019
DB 2152 CGTGGCCGTGAAGATTTGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGATGTC 2211

OY	2020	AGAAATGAGATGATGTAAGATGATTGGGAAACACAAATATATCAATTAATCTCTTGAGC	2079
Db	2212	AGAGATGAGATGATGTAAGATGATTGGGAAACACAAATATATCAATTAATCTCTTGAGC	2271
OY	2080	CTGCACACAGATGAGGCGCTCTATATGTCATATGTTAGTATGCTTAAAGGCAACCTCCG	2139
Db	2272	CTGCACACAGATGAGGCGCTCTATATGTCATATGTTAGTATGCTTAAAGGCAACCTCCG	2331
OY	2140	AGAAATCTCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCCATATGACATTTAAACGTGT	2199
Db	2332	AGAAATCTCTCCGAGCCCGGAGGCCACCCGGGATGAGTACTCCATATGACATTTAAACGTGT	2391
OY	2200	TCTGAGGAGACAGATGACCTTCAAGGACTTGGTGTCAATGCACTTACCCAGCTGGCCAGC	2259
Db	2332	TCTGAGGAGACAGATGACCTTCAAGGACTTGGTGTCAATGCACTTACCCAGCTGGCCAGC	2451
OY	2260	GATGAGATTACTGGCTTCCCAAAAATGATTAATCATGAGATTTAGACCCAGAAATGTTTT	2319
Db	2452	CATGAGATTACTGGCTTCCCAAAAATGATTAATCATGAGATTTAGACCCAGAAATGTTTT	2511
OY	2330	GGTAAACAAAAACATGATGATGAAAAATGACGACTTGGACTCGCCAGAGATATCAAA	2379
Db	2512	GGTAAACAAAAACATGATGATGAAAAATGACGACTTGGACTCGCCAGAGATATCAAA	2571
OY	2380	TATAGACTATTACAAAAGAACCACCAATGAGCGGCTTCACTCAAGTGGATGCTCCAGA	2439
Db	2572	TATAGACTATTACAAAAGAACCACCAATGAGCGGCTTCACTCAAGTGGATGCTCCAGA	2631
OY	2440	AGCCCTGTTTGTATATAGATATACATCATACAGATGATGTCGTGGCGGTGAT	2499
Db	2632	AGCCCTGTTTGTATATAGATATACATCATACAGATGATGTCGTGGCGGTGAT	2691
OY	2500	GTGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGATTCCTCGTAGAGACTTTT	2559
Db	2692	GTGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGATTCCTCGTAGAGACTTTT	2751
OY	2560	TAACTGCTGAAGAAAGACACAGATGATTAAGCAGACCACTGACCAACGAACTGTA	2619
Db	2752	TAACTGCTGAAGAAAGACACAGATGATTAAGCAGACCACTGACCAACGAACTGTA	2811
OY	2620	CATGATGATGAGGGACTGTGGGCAAGCAGTGGCCCTCCAGAGACCAAGCTTCAAGCACTT	2679
Db	2812	CATGATGATGAGGGACTGTGGGCAAGCAGTGGCCCTCCAGAGACCAAGCTTCAAGCACTT	2871
OY	2680	GGTAGAAAGCTTGGATTCGAATTTCTCACTCTCAACAACATG-----	2720
Db	2872	GGTAGAAAGCTTGGATTCGAATTTCTCACTCTCAACAACATGAGAACTTGGACCTCAG	2931
OY	2721	-----	2720
Db	2932	TCAGCCTCTCGAACCGTATTCACCTTGTATTCCTGACCCAGATGAAATAAACGTCTCT	2991
OY	2721	-----AGAAATACTTGGACCTCAGCCAACTCTTGGACAGTATTCACCTAGT	2767
Db	2992	CTTCCCTTCTTTCAGGAATACTTGGACCTCAGCCAACTCTTGGACAGTATTCACCTAGT	3051
OY	2768	TACCTCGACACAAAGACTTCTGTCTTCAAGAGATGATCTGTTTTTCTCCAGACCCC	2827
Db	3052	TACCTCGACACAAAGACTTCTGTCTTCAAGAGATGATCTGTTTTTCTCCAGACCCC	3111
OY	2828	ATGCCCTTAGAACCATGCTCTCTCAGTATCCACATTAACGGCAGGTTTAAACATGA	2887
Db	3112	ATGCCCTTAGAACCATGCTCTCTCAGTATCCACATTAACGGCAGGTTTAAACATGA	3171
OY	2888	ATGACTGTGTCTGCTGTCTGCCAACAAGACAGCACTGGGAACTTACCTACCTGACGAG	2947
Db	3172	ATGACTGTGTCTGCTGTCTGCCAACAAGACAGCACTGGGAACTTACCTACCTGACGAG	3231
OY	2948	GGAGACCAAGCCCTCCAGAGCTTGTGTCCTCACTTGTATATATGATATCAGAGAGTAA	3007
Db	3232	GGAGACCAAGCCCTCCAGAGCTTGTGTCCTCACTTGTATATATGATATCAGAGAGTAA	3291

```

QY 3008 TAATTGAAAAAGTATACGACTANGTGTAAAGATTTPADACGTGAAACCTGTAACTT 3067
Db 3292 TAAATTGAAAAAGTATACGACTATGTGTAAAGATTTPADACGTGAAACCTGTAACTT 3351
QY 3068 CCCGAGGAGGAGAAAGATTCTGTGAGCAGTGTGACTGC 3106
Db 3352 CCCGAGGAGGAGAAAGATTCTGTGAGCAGTGTGACTGC 3390

RESULT 12
US-10-669-920-582
; Sequence 582, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT FILING DATE: US/10/669,920
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 582
; LENGTH: 5088
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-582

Query Match      89.0%; Score 2765.8; DB 6; Length 5088;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 3024; Conservative 0; Mismatches 67; Indels 128; Gaps 9

QY 1 CCCGGAGCAAGCTTTGGGAGGGAAG-CAAGCTGAGTCCCTTCTCTCTCGTTC 59
Db 578 CTCGGAGCAAGTTTGGGAGGGAAGCCCAAGCTTGAATCTTCTCTCTCTCTTC 637
QY 60 CCAAAATCGAGGAGCAGCCCGCGGCGTCATG---GCGCTCTCTCGCAGCTGAGGATAGCG 116
Db 638 CCAAAATCGAGGAGCAGCCCGCGGCGTCAATGCCGCGCTCTCTCGGAGCTGAGGATAGCG 697
QY 117 GTGAAGCCCGGAGGCTTGGCGCCCGCGGAGAACCCAGACCAAGACCACTCTTTCTGCGTTTGGAG 176
Db 698 GTGAAGCCCGGAGGCTTGGCGCCCGCGGAGAACCCAGACCAAGACCACTCTTTGTGGTTGGAG 757
QY 177 TTGCTCCCCGGAACCCCGGCGCTCGTCGCTTTCTCCATCCGACCCACCGCGGAGG-C-CGGAG 235
Db 758 TTGCTCCCCGAACCCCGGCGCTCGTCGCTTTCTCCATCCGACCCACCGCGGAGGCGCGGAG 817
QY 236 ACAACACAGGTGCGGAGGAGCGTTGCCATTGAAGTACTGACGACGAGC-GCAGCGCC 294
Db 818 ACAACACAGGTGCGGAGGAGCGTTGCCATTGAAGTACTGACGACGAGCAGCGGAGCGCC 877
QY 295 TCGGTTCTTGAAGCCACGCA-GCTGAAGCAATTGCGGTAAGTCCATGCCCCGTAGAGAA 353
Db 878 TCGGTTCTTGAAGCCACGCAAGGCTGAAGCAATTGCGGTAAGTCCATGCCCCGTAGAGAA 937
QY 354 GTGTGCAATGGGATTAACTCCATGTGAGAGATATGAAGAGAGACCGGGGATTTGGTACCG 413

```

Db	938	GTGTGCAGATGGGANTTAACCTTCACATGGAGATATGAAAGGAGCCGGGGATTGTACCG	997
Qy	414	TAAACATGGTCAGCGTGGGGTGGTTTCATCTGCTGGTGTGTGATCAACATGGCACTTGT	473
Db	998	TAAACATGGTCAGCGTGGGGTGGTTTCATCTGCTGGTGTGTGATCAACATGGCACTTGT	1057
Qy	474	CCCTGGCCCGGCCCTCTCTCAAGTTTATGTAGATACCACTTAAGCCAGAAAGCCAC	533
Db	1058	CCCTGGCCCGGCCCTCTCTCAAGTTTATGTAGATACCACTTAAGCCAGAAAGCCAC	1117
Qy	534	CAACCAATATCCAAATCTTCTCAACGAAAGTGTACGTGGCTGGCCAGGGGATGCTGAC	593
Db	1118	CAACCAATATCCAAATCTTCTCAACGAAAGTGTACGTGGCTGGCCAGGGGATGCTGAC	1177
Qy	594	AGTGGCGGTGCTGTGTGAAGAATGCCGGCGGATACAGTTGGAATTAAGGATGGGGTGA	653
Db	1178	AGTGGCGGTGCTGTGTGAAGAATGCCGGCGGATACAGTTGGAATTAAGGATGGGGTGA	1237
Qy	654	TGGGGCCCAACATATGAGCAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGCGCCAC	713
Db	1238	TGGGGCCCAACATATGAGCAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGCGCCAC	1297
Qy	714	CTAGAGACTCCGGCTCTATGTCTGTACTGCCAGTAGGACTGTAGACAGTGAATCTTGT	773
Db	1298	CTAGAGACTCCGGCTCTATGTCTGTACTGCCAGTAGGACTGTAGACAGTGAATCTTGT	1357
Qy	774	ACTTCATGTGTAAATTCACAGATGTCATCTATCCGAGATGATGAGGATGACCCGAT	833
Db	1358	ACTTCATGTGTAAATTCACAGATGTCATCTATCCGAGATGATGAGGATGACCCGAT	1417
Qy	834	GTGCGGAAGATTTTGTTCAGTGAAGAACATTAACAACAAGAGACACATATCTGACCA	893
Db	1418	GTGCGGAAGATTTTGTTCAGTGAAGAACATTAACAACAAGAGACACATATCTGACCA	1477
Qy	894	CAGAAAGATGAAAAAGCGGCTCCATGCTGTGCTGGCCCAACCTGTCAAGTTTGCT	953
Db	1478	CAGAAAGATGAAAAAGCGGCTCCATGCTGTGCTGGCCCAACCTGTCAAGTTTGCT	1537
Qy	954	GCCGACCCGGGGGAAACCCATATGCCAACATTCGGTGGCTGAAAAACGGGAAGAGTTTA	1013
Db	1538	GCCGACCCGGGGGAAACCCATATGCCAACATTCGGTGGCTGAAAAACGGGAAGAGTTTA	1597
Qy	1014	AGCAGAGCATGCACTTGGAGGCTTCAAGGTACGAAACACAGACTGAGAGCTCATTTATG	1073
Db	1598	AGCAGAGCATGCACTTGGAGGCTTCAAGGTACGAAACACAGACTGAGAGCTCATTTATG	1657
Qy	1074	AAAGTGTGGTCCCATCTGACAAAGGAAATTAATCTGTGTATGTGAGAAATTAACGGGT	1133
Db	1658	AAAGTGTGGTCCCATCTGACAAAGGAAATTAATCTGTGTGTGAGAAATTAACGGGT	1717
Qy	1134	CCATCAATACACGTAACCACTGGATGTTTGTGAGACCATCCCTCACCGGCCCATCTCC	1193
Db	1718	CCATCAATACACGTAACCACTGGATGTTTGTGAGACCATCCCTCACCGGCCCATCTCC	1777
Qy	1194	AAGCCGACCTGGCCGCAATGCTCCACAGTGTGGAGAGACGTAGAGTTTGTCTGCA	1253
Db	1778	AAGCCGACCTGGCCGCAATGCTCCACAGTGTGGAGAGACGTAGAGTTTGTCTGCA	1837
Qy	1254	AGGTTTACAGTATGCCAGCCCAACATCCACATGATCAAGCACTGTGAAAAAGACGGCA	1313
Db	1838	AGGTTTACAGTATGCCAGCCCAACATCCACATGATCAAGCACTGTGAAAAAGACGGCA	1897
Qy	1314	GTAATATCGGGGCGGACGGGCTGCCCTTACCTCAAGTTCTACAGCACTCCGGGATTAATA	1373
Db	1898	GTAATATCGGGGCGGACGGGCTGCCCTTACCTCAAGTTCTACAGCACTCCGGGATTAATA	1957
Qy	1374	GTTCCAAATGCA-----GAAGTGTGGCTCTGTTCATGTGACCGAGGCGGCA	1419
Db	1958	TGTTAAACACGAGCAAAAGATTTGAGTTTCTTAATATCGGAATGTAACTTTTGAAGA	2017
Qy	1420	TGCTGGGAAATATATATGTAAAGTCTCAATTAATATAGGACGACCAACAGTCTGCTG	1479

Db	2018	CGCTGGGGAATATATACGTGCTTGGGGGGTAATCTATTTGGGATATCTTTCACTGTGATG	2017
Qy	1480	GCTCACTGCTCTGGCAAAAACAGCAAGCGCCCTGGAGAGAAAAGAGATTACAGCTTCCC	1539
Db	2078	GTTGACAGTTCTGGC-----AGGCGCTGGAAAGAAAAGAGATTACAGCTTCCC	2128
Qy	1540	AGACTACCTGGAGATAGCCATTATCTGCTATPAGGGGTCTTCTTAATGCCCTGTAATGATG	1599
Db	2129	AGACTACCTGGAGATAGCAATTATCTGCTATPAGGGGTCTTCTTAATGCCCTGTAATGATG	2188
Qy	1600	AAACGTCACTCTGGCCGGAATGAAGAACAGACCAAGAAAGCCAGACTTCAGCAGCAGCC	1659
Db	2189	AAACGTCACTCTGGCCGGAATGAAGAACAGACCAAGAAAGCCAGACTTCAGCAGCAGCC	2248
Qy	1660	GGCTGTGCAACAGCTGACCAACCGTATCCCCCTGGAGACAGGTGACAGTTTCGGCTGA	1719
Db	2249	GGCTGTGCAACAGCTGACCAACCGTATCCCCCTGGAGACAG-----GTTTCGGCTGA	2302
Qy	1720	GTCACGCTCTTCATGAATCTGCAACCCCGCTGGTAGGATTAACAACGCTCTCTTC	1779
Db	2303	GTCACGCTCTTCATGAATCTGCAACCCCGCTGGTAGGATTAACAACGCTCTCTTC	2362
Qy	1780	AAACGGACACACCCCAATGCTGGAGAGGGGTCTCGAGATGAATCTTCAGAGACCCAAA	1839
Db	2363	AAACGGACACACCCCAATGCTGGAGAGGGGTCTCGAGATGAATCTTCAGAGACCCAAA	2422
Qy	1840	ATGGAGATTCCAAAGAGATTAAGCTGACACTGGCAAGCCCTGGAGAGAGGTTGCTTTGG	1899
Db	2423	ATGGAGATTCCAAAGAGATTAAGCTGACACTGGCAAGCCCTGGAGAGAGGTTGCTTTGG	2482
Qy	1900	GCAGGTGTCATGGCGGAGAGCATGGGAAATTGACAAAGACAGGCCCAAGAGGGGTCTAC	1959
Db	2483	GCAGGTGTCATGGCGGAGAGCATGGGAAATTGACAAAGACAGGCCCAAGAGGGGTCTAC	2542
Qy	1960	CGTGGCCGTGAAGATGTTGAAGAATGATGCCACAGAGAAAGACCTTCTGATCTGGTGTG	2019
Db	2543	CGTGGCCGTGAAGATGTTGAAGAATGATGCCACAGAGAAAGACCTTCTGATCTGGTGTG	2602
Qy	2020	AGAGATGAGATGATGAAGATGATTTGGGAAAACAAGAAATATCATAAATCTTCTTGAGC	2079
Db	2603	AGAGATGAGATGATGAAGATGATTTGGGAAAACAAGAAATATCATAAATCTTCTTGAGC	2662
Qy	2080	CTGCACACAGATGGGCTCTCTATATGTCATATGTTGAATATCCTCTTAAAGCAACTTCG	2139
Db	2663	CTGCACACAGATGGGCTCTCTATATGTCATATGTTGAATATCCTCTTAAAGCAACTTCG	2722
Qy	2140	AGAAATCTCCGAGCCCGGAGAGCCACCCGGGATGGAATGATCACTCTATGACATTAACGGT	2199
Db	2723	AGAAATCTCCGAGCCCGGAGAGCCACCCGGGATGGAATGATCACTCTATGACATTAACGGT	2782
Qy	2200	TCTTGAGAGACGATGACCTTCAAGGACTTGGTGTCACTGCACTTACCAAGCTGGCCAGAGC	2259
Db	2783	TCTTGAGAGACGATGACCTTCAAGGACTTGGTGTCACTGCACTTACCAAGCTGGCCAGAGC	2842
Qy	2260	GATGAGATCTTGGCTTCCAAAATGTATTCATCGAGATTTAGCAAGCAAAATGTTTT	2319
Db	2843	CATGAGATCTTGGCTTCCAAAATGTATTCATCGAGATTTAGCAAGCAAAATGTTTT	2902
Qy	2320	GGTAAACAAAAACAATGTATGAAAATATGACACTTGGACTCGCCAGAGATATCAACAA	2379
Db	2903	GGTAAACAAAAACAATGTATGAAAATATGACACTTGGACTCGCCAGAGATATCAACAA	2962
Qy	2360	TATAGACTATTACAAAAGAACCAACCAATGGCGGCTTCAGTCAAGTGAATGGCTCCAGA	2439
Db	2963	TATAGACTATTACAAAAGAACCAACCAATGGCGGCTTCAGTCAAGTGAATGGCTCCAGA	3022
Qy	2440	AGCCCTGTTGATATGATATACCTCATCAGATGATGTCTGGTCTTTCGGGGTGTAAAT	2499
Db	3023	AGCCCTGTTGATATGATATACCTCATCAGATGATGTCTGGTCTTTCGGGGTGTAAAT	3082
Qy	2500	GTGGAGATCTTCACTTTAAGGGGGCTGGCCCTACCGAGGATTCGCGTGAAGAACTTTT	2559
Db	3083	GTGGAGATCTTCACTTTAAGGGGGCTGGCCCTACCGAGGATTCGCGTGAAGAACTTTT	3142

QY	2560	TAACCTGTGAAGGAAGGACACACAAATGATTAAGCCAGCCAACTGACACAAAGAACTGTA	2619
Db	3143	TAAGCTGTGAAGGAAGGACACACAAATGATTAAGCCAGCCAACTGACACAAAGAACTGTA	3202
QY	2620	CATGATGATGAGGGACCTGTGGCAATGCAGTSCCCTCCAGAGAACCAAGTTCAAGCACTT	2679
Db	3203	CATGATGATGAGGGACCTGTGGCAATGCAGTSCCCTCCAGAGAACCAAGTTCAAGCACTT	3262
QY	2660	GGTAGAGACCTTGGATCGAATTTCTCACTCTCAACAACCAATG-----	2720
Db	3263	GGTAGAGACCTTGGATCGAATTTCTCACTCTCAACAACCAATG-----	3322
QY	2721	-----	2720
Db	3323	TCAGCTCTCGAACCGTATTCACTTGTATTCTCGAACCCAAAGATGAATAAAGCTCTCT	3382
QY	2721	-----AGAAATTACTTGGACCTCAGCCCAACTCTCGAACAGTATTCACTAGT	2767
Db	3383	CTTCCCTCTCTTACAGAAATTACTTGGACCTCAGCCCAACTCTCGAACAGTATTCACTAGT	3442
QY	2768	TACCTGTACACAGAAAGTTCTTGTCTTCAAGAGATGATTTCTGTTTTTCTCCGAGACCC	2827
Db	3443	TACCTGTACACAGAAAGTTCTTGTCTTCAAGAGATGATTTCTGTTTTTCTCCGAGACCC	3502
QY	2828	ATGCCTTACGAAACCAATGCTCTCAGTATCCACATCAATAAACGAGAGTTTAAACATGA	2887
Db	3503	ATGCCTTACGAAACCAATGCTCTCAGTATCCACATCAATAAACGAGAGTTTAAACATGA	3562
QY	2888	ATGACTGTGTCTGCTCTGTCTCCCAACAGGACAGCACTGGGAACTAGTACACTGAGCAG	2947
Db	3563	ATGACTGTGTCTGCTCTGTCTCCCAACAGGACAGCACTGGGAACTAGTACACTGAGCAG	3622
QY	2948	GGAAGACATGCTCTCCCAAGCTTGTGTCTCCACTTGTATATATAGATCAAGAGAGTAA	3007
Db	3623	GGAAGACATGCTCTCCCAAGCTTGTGTCTCCACTTGTATATATAGATCAAGAGAGTAA	3682
QY	3008	TAAATGGAAAAGTAATCAGCATATGTGTAAAGATTATACAGTTGAAAACCTGTATCTT	3067
Db	3683	TAAATGGAAAAGTAATCAGCATATGTGTAAAGATTATACAGTTGAAAACCTGTATCTT	3742
QY	3068	CCCCAGAGAGAGAGAGGTTTCTGAGACAGTGAGCTGC	3106
Db	3743	CCCCAGAGAGAGAGAGGTTTCTGAGACAGTGAGCTGC	3781
RESULT 13			
; US-10-669-920-602			
; Sequence 602, Application US/10669920			
; Publication No. US2006019425A1			
GENERAL INFORMATION:			
APPLICANT: Morris, David W.			
APPLICANT: Malandino, Marc S.			
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER			
FILE REFERENCE: 20366-066001			
CURRENT APPLICATION NUMBER: US/10/669,920			
CURRENT FILING DATE: 2003-09-23			
PRIOR APPLICATION NUMBER: US 10/004,113			
PRIOR FILING DATE: 2001-10-23			
PRIOR APPLICATION NUMBER: US 10/052,482			
PRIOR FILING DATE: 2001-11-08			
PRIOR APPLICATION NUMBER: US 09/997,722			
PRIOR FILING DATE: 2001-11-30			
PRIOR APPLICATION NUMBER: US 10/034,650			
PRIOR FILING DATE: 2001-12-20			
PRIOR APPLICATION NUMBER: US 10/085,117			
PRIOR FILING DATE: 2002-02-27			
PRIOR APPLICATION NUMBER: US 10/087,192			
PRIOR FILING DATE: 2002-03-01			
PRIOR APPLICATION NUMBER: US 10/322,281			
PRIOR FILING DATE: 2002-12-17			
PRIOR APPLICATION NUMBER: US 10/322,696			
PRIOR FILING DATE: 2002-12-17			

Query Match	85.0%	Score 2641.4	DB 6	Length 3241
Beat Local Similarity	99.4%	Pred. No. 0		
Matches 2716	Conservative	0	Mismatches	6
NUMBER OF SEED ID NOS: 1441 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 602 ; LENGTH: 3241 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-669-920-602				
1	CCCGGAGCAAGTTTGGTGAAGGCAACG-CAGACCTGAGTCTTCTTCTCTGTTCC	59		
187	CTCGGACCAAGTTTGGTGAAGGCAACGCCAAGCTGAGTCTTCTTCTCTGTTCC	246		
60	CCAAATCCGAGGAGAGCCCGCGGGCGTCAATG--GCGCTCTCCGACCTGGGGTACGC	116		
247	CCAAATCCGAGGAGAGCCCGCGGGCGTCAATG--GCGCTCTCCGACCTGGGGTACGC	306		
117	GTGAAGCCCGGAGAGCTTGGGCGCGGCGAAGACCCAAAGAACACTCTCTCTGGTTGAG	176		
307	GTGAAGCCCGGAGAGCTTGGGCGCGGCGAAGACCCAAAGAACACTCTCTCTGGTTGAG	366		
177	TTTGCCTCCGAGAACCCCGGGGCTCGTGGTTTCTCATCCGACCCGACCGCGGGG-CGGGG	235		
367	TTTGCCTCCGAGAACCCCGGGGCTCGTGGTTTCTCATCCGACCCGACCGCGGGG-CGGGG	426		
236	ACAACACAGTTCGCGGAGAGAGGTTGCCATTCAAGTGACTGACGAGAGC-GCAGCGCC	294		
427	ACAACACAGTTCGCGGAGAGAGGTTGCCATTCAAGTGACTGACGAGAGC-GCAGCGCC	486		
295	TGGTTTCTGAGCCCAACGCA-GCTGAAGGCAATTGGCGGTATGCTCATGCGGTAGAGAA	353		
487	TGGTTTCTGAGCCCAACGCA-GCTGAAGGCAATTGGCGGTATGCTCATGCGGTAGAGAA	546		
354	GGTGCACATGGGAAATTAAAGTCAATGAGAGATATGAGAAAGAGACCGGGGATTGGTACCG	413		
547	GGTGCACATGGGAAATTAAAGTCAATGAGAGATATGAGAAAGAGACCGGGGATTGGTACCG	606		
414	TAAACATGGTCAAGTGGGGTGGTTTCACTGCGTGGTGGTCAATGCAACTTGT	473		
607	TAAACATGGTCAAGTGGGGTGGTTTCACTGCGTGGTGGTCAATGCAACTTGT	666		
474	CCCTGGCCCGGCCCTTCCTTCACTTTAGTTGAGAGATACCAATTAAAGCCAAAGAGCCAC	533		
667	CCCTGGCCCGGCCCTTCCTTCACTTTAGTTGAGAGATACCAATTAAAGCCAAAGAGCCAC	726		
534	CAACCAAAATCAAAATCTCTCAACAGAGATGATGATGGCTGCGCGCAGGGGAGTGGCTAG	593		
727	CAACCAAAATCAAAATCTCTCAACAGAGATGATGATGGCTGCGCGCAGGGGAGTGGCTAG	786		
594	AGGTGGCTGCTGTTTGAAGAATGGCGCCGTATCACTTGAAGTGAAGTGGGGTGGTCACT	653		
787	AGGTGGCTGCTGTTTGAAGAATGGCGCCGTATCACTTGAAGTGAAGTGGGGTGGTCACT	846		
654	TGGGGCCCAAAATGAGACAGTGGCTTATTGGGAGATCTTGCAGATTAAGGGCGCCACAC	713		
847	TGGGGCCCAAAATGAGACAGTGGCTTATTGGGAGATCTTGCAGATTAAGGGCGCCACAC	906		
714	CTAGAGACTCCGCGCTTATGCTGTGATCTGCACTGAGTGAAGCTGTAAGCACTTGGT	773		
907	CTAGAGACTCCGCGCTTATGCTGTGATCTGCACTGAGTGAAGCTGTAAGCACTTGGT	966		
774	ACTTCAATGGTGAATGTCAGATGACCATCTCATCCGAGATGATGAGATGACCCGATG	833		
967	ACTTCAATGGTGAATGTCAGATGACCATCTCATCCGAGATGATGAGATGACCCGATG	102		
834	GTGCGGAGAGATTTGTCACTGAGAACAGTAAACAACAAGAGACCACTACTGAGCCAAAC	893		
1027	GTGCGGAGAGATTTGTCACTGAGAACAGTAAACAACAAGAGACCACTACTGAGCCAAAC	108		
894	CAGAAAAGATGAAAAAGCGGCTCAATGCTGTGCTGCGGCAACAATGTCAAATTTGGCT	953		

1087 CAGAAAGATGAAAGCGGCTCCATCTGTGCTTCGCGCAACATCTGCAAGTTTGGCT 1146
1087 CAGAAAGATGAAAGCGGCTCCATCTGTGCTTCGCGCAACATCTGCAAGTTTGGCT 1146
954 GCCCAGCCGCGGGGGAACCCATGCGCAACATGCGGTGCTGAAAAACGGAAGAGTTTA 1013
1147 GCCCAGCGGGGGGAACCCATGCGCAACATGCGGTGCTGAAAAACGGAAGAGTTTA 1206
1014 AGCAGAGCATGCGATTGGAAGCTACAGATGAGAAACGACATGAGACCTCATATTAG 1073
1207 AGCAGAGCATGCGATTGGAAGCTACAGATGAGAAACGACATGAGACCTCATATTAG 1266
1074 AAGGTGTGCTCCATCTGCAAGAGGAAATTAACCTGTAGTGAAGATGATACGGGT 1133
1267 AAGGTGTGCTCCATCTGCAAGAGGAAATTAACCTGTGTGAGATGATACGGGT 1326
1134 CCATCAATGACATGACATGCTGATGTTGTGAGAGCATGCGCTCAACCGGACCATCTTC 1193
1327 CCATCAATGACATGACATGCTGATGTTGTGAGAGCATGCGCTCAACCGGACCATCTTC 1386
1194 AAGCGGATCTGCGGCAATGCTTCCATGCTGCTGAGAGACATGATAGTTTGTCTGCA 1253
1387 AAGCGGATCTGCGGCAATGCTTCCATGCTGCTGAGAGACATGATAGTTTGTCTGCA 1446
1254 AAGTTTACGATGATGCGGCAACCCCATGCAATGATGATCAAGCACGAGGAAAGACGGCA 1313
1447 AAGTTTACGATGATGCGGCAACCCCATGCAATGATGATCAAGCACGAGGAAAGACGGCA 1506
1314 GTAATATACGGGCGCGGCTGCTGCTCACTCAAGTTTCTCAAGCATCTCGGGATTAATA 1373
1507 GTAATATACGGGCGCGGCTGCTGCTCACTCAAGTTTCTCAAGCATCTCGGGATTAATA 1566
1374 GTTCCATGACAGAGTGTGCTGCTGCTCAATGATGATGATGATGATGATGATGATGAT 1433
1567 GTTCCATGACAGAGTGTGCTGCTGCTCAATGATGATGATGATGATGATGATGATGAT 1626
1434 TATGTAGAGTCTCAATTAATTAAGGAGGAGGCAACCATGCTGCTGCTCACTGCTGCTG 1493
1627 TATGTAGAGTCTCAATTAATTAAGGAGGAGGCAACCATGCTGCTGCTCACTGCTGCTG 1686
1494 CAAAACAGCAGCGCTGAGAGGAAAGAAAGATTAACGCTTCCCGACATCACTGAGAGA 1553
1687 CAAAACAGCAGCGCTGAGAGGAAAGAAAGATTAACGCTTCCCGACATCACTGAGAGA 1746
1554 TAGCCATTTACTGATAGGAGGCTTCTTAATGCTGCTGATGATGATGATGATGATGAT 1613
1747 TAGCCATTTACTGATAGGAGGCTTCTTAATGCTGCTGATGATGATGATGATGATGAT 1806
1614 GCGGATGAGAGCAAGACCAAGAACGACCTTCAAGCAGCGGCGCTGAGCAAGC 1673
1807 GCGGATGAGAGCAAGACCAAGAACGACCTTCAAGCAGCGGCGCTGAGCAAGC 1866
1674 TAGCCAAAGATATCCCTGCTGCGGAGACAGATTAAC---AGTTTCGCTGATGCTGAGCTCC 1729
1867 TAGCCAAAGATATCCCTGCTGCGGAGACAGATTAACAGTTTCCGCTGATGCTGAGCTCC 1926
1730 TCCATGATCTCAACACCCCGCTGCTGAGATTAACACGCTCTCTTCAACGCGCAGC 1789
1927 TCCATGATCTCAACACCCCGCTGCTGAGATTAACACGCTCTCTTCAACGCGCAGC 1986
1790 ACCCCGATGCTGAGAGGCTTCCGAGTATGAACTTCAAGAGACCCCAAAATGAGAGTTT 1849
1987 ACCCCGATGCTGAGAGGCTTCCGAGTATGAACTTCAAGAGACCCCAAAATGAGAGTTT 2046
1850 CCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1909
2047 CCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2106
1910 ATGCGGAAAGCATGAGAAATGACAAAGACAGCCCAAGAGGCGCTCACTGCGCGCTG 1969
2107 ATGCGGAAAGCATGAGAAATGACAAAGACAGCCCAAGAGGCGCTCACTGCGCGCTG 2166
1970 AAGATTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2029

2167 AAGATTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226
2030 ATGATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2089
2227 ATGATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
2090 GATGAGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
2287 GATGAGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
2150 CGAGCCCGGAGGCAACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2209
2347 CGAGCCCGGAGGCAACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2406
2210 CAGATGACCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2269
2407 CAGATGACCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2466
2270 TTGCTTCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2329
2467 TTGCTTCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2526
2330 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2389
2527 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2586
2390 TACAAAAGACCAACCAATGAGGCGGCTTCCAGTCAAGTGAATGAGCTGCAAGAGCCCTGTTT 2449
2587 TACAAAAGACCAACCAATGAGGCGGCTTCCAGTCAAGTGAATGAGCTGCAAGAGCCCTGTTT 2646
2450 GAT 2509
2647 GAT 2706
2510 TTCACTTTAGGAGGCTGCGCTTCAACGAGGATTTCCCGTGAAGAACTTTTAAGCTGCTG 2569
2707 TTCACTTTAGGAGGCTGCGCTTCAACGAGGATTTCCCGTGAAGAACTTTTAAGCTGCTG 2766
2570 AAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2629
2767 AAGAGAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2826
2630 AGGAGCTGTTGAGCAGTGCCTGCGGAGAGACCAAGTTCAACAGTGTGATGAGAGC 2689
2827 AGGAGCTGTTGAGCAGTGCCTGCGGAGAGACCAAGTTCAACAGTGTGATGAGAGC 2886
2690 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2722
2887 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2919

RESULT 14
US-10-669-920-626
Sequence 626, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192


```

; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 626
; LENGTH: 3632
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-669-920-626

Query Match      85.0%; Score 2641.4; DB 6; Length 3632;
                  99.4%; Pred. No. 0;
Matches 2716; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

OY 1 CCCCAGACAAAGTTGGTGGAGGCAAG-CAGGCTAGTCCCTTCTCTCTCTCTCC
DB 578 CTCGGACAAAGTTGGTGGAGGCAAGCCAAAGCTTAGTCTTCTCTCTCTCTCTCC
OY 60 CCAATCCGAGGAGGAGCCGCGGCGGCGTATG---GCGCTCTCCGACGCTTGGGTACGC
DB 638 CCAATCCGAGGAGGAGCCGCGGCGGCGTATGCGCGCGCTCTCTCCGACGCTTGGGTACGC
OY 117 GTGAAGCCCGGAGGCTTGGCGCGCGGAGAGCCCAAGACCACTTCTGCGTTGGAG
DB 698 GTGAAGCCCGGAGGCTTGGCGCGCGGAGAGCCCAAGACCACTTCTGCGTTGGAG
OY 177 TTGCTCCCGGAGCCCGCGGCGTCTGCTTCTCATCCGACCGCGGAGGCGCGGAG
DB 758 TTGCTCCCGGAGCCCGCGGCGTCTGCTTCTCATCCGACCGCGGAGGCGCGGAG
OY 226 ACAACAGAGTGGCGGAGGAGGCTTGCATTCAAGTGACTGAGAGAGAGC-GCAGCGC
DB 818 ACAACAGAGTGGCGGAGGAGGCTTGCATTCAAGTGACTGAGAGAGAGCGCGC
OY 295 TCGGTTCTGAGCCCAACGCGA-GCTGAAGGCAATGGCGGTAGTCCATGCGGTAGAGAA
DB 878 TCGGTTCTGAGCCCAACGCGAAGGCAATGGCGGTAGTCCATGCGGTAGAGAA
OY 354 GTGTGCAATGGAGTTTAAGTCCATGAGATATGAGAAAGAGACCGGAGATTTGGTACG
DB 938 GTGTGCAATGGAGTTTAAGTCCATGAGATATGAGAAAGAGACCGGAGATTTGGTACG
OY 414 TAAACATGGTACGTGGGTCGTTTCATCTGCTGGTCTGCTGCAACATGAGCACTTGT
DB 998 TAAACATGGTACGTGGGTCGTTTCATCTGCTGGTCTGCTGCAACATGAGCACTTGT
OY 474 CCTGGCCCGGCGCTCTCTCAAGTTTAGTTGAGAGATACCAATTAGAGCCAGAAAGCCAC
DB 1058 CCTGGCCCGGCGCTCTCTCAAGTTTAGTTGAGAGATACCAATTAGAGCCAGAAAGCCAC
OY 534 CAACCAAAATACCAAAATCTCAACCAAGAGTGAAGTGGCTGGCCAGGGAGTGGCTAG
DB 1118 CAACCAAAATACCAAAATCTCAACCAAGAGTGAAGTGGCTGGCCAGGGAGTGGCTAG
OY 594 AGGTGGCTGCTGTTGAAAGATGCGCGGTGATCAGTTGGACTAAGATGGGGTGCAT
DB 1178 AGGTGGCTGCTGTTGAAAGATGCGCGGTGATCAGTTGGACTAAGATGGGGTGCAT
OY 654 TGGGGCCCAATAGAGAGTCTTATTTGGGGAGTACTTGGAGATTAAGGGCGCACAC
DB 1238 TGGGGCCCAATAGAGAGTCTTATTTGGGGAGTACTTGGAGATTAAGGGCGCACAC
OY 714 CTAGAGACTCCGGCTCTATGCTTGTATGCGGAGTGAAGTGAAGTGAAGTGAAGT
DB 1298 CTAGAGACTCCGGCTCTATGCTTGTATGCGGAGTGAAGTGAAGTGAAGTGAAGT
OY 774 ACTTCAATGGATGTCAGAGATGCAATCCGAGATGATGAGATGACACCGATG
DB 1358 ACTTCAATGGATGTCAGAGATGCAATCCGAGATGATGAGATGACACCGATG

```

```

OY 834 GTGGGAAGATTTTGTCAGTGAGAGCAAGTAAACAAGAGAGCACTATGAGCCAA
DB 1418 GTGGGAAGATTTTGTCAGTGAGAGCAAGTAAACAAGAGAGCACTATGAGCCAA
OY 894 CAGAAAAGATGAAAAAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT
DB 1478 CAGAAAAGATGAAAAAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTTGGCT
OY 954 GCCAGCGGGGGAGAACCCCAATGCCAACATGCGGTGCTGAAAAAGGGAAGATTTA
DB 1538 GCCAGCGGGGGAGAACCCCAATGCCAACATGCGGTGCTGAAAAAGGGAAGATTTA
OY 1014 AGCAGAGCATTCGATTGGAGGCTACGAAGGTACGAACACAGACTGAGCTCTATATG
DB 1598 AGCAGAGCATTCGATTGGAGGCTACGAAGGTACGAACACAGACTGAGCTCTATATG
OY 1074 AAGGTGTGCTCCATCTGACAGGGAATTATACCTGTGTATGTGAGAAATGATACGGT
DB 1658 AAGGTGTGCTCCATCTGACAGGGAATTATACCTGTGTGTGAGAAATGATACGGT
OY 1134 CCATCAATCAGACGTACCTGGAATGTTGTGAGCGATGCGCTCACCGGCGCATCTCC
DB 1718 CCATCAATCAGACGTACCTGGAATGTTGTGAGCGATGCGCTCACCGGCGCATCTCC
OY 1194 AAGCGGACTGCGGCAAAATGCTTCCAGAGTGTGCGAGAGAGAGCTAGAGTTTGTGCA
DB 1778 AAGCGGACTGCGGCAAAATGCTTCCAGAGTGTGCGAGAGAGAGCTAGAGTTTGTGCA
OY 1254 AAGTTTACAGATGATGCCAGGCGCCACATCCAGTGAATCAAGACTGGAAGAAAGCGCA
DB 1898 AAGTTTACAGATGATGCCAGGCGCCACATCCAGTGAATCAAGACTGGAAGAAAGCGCA
OY 1314 GTAATATCGGGCCGAGCGGCTGCGCTTACCTCAAGTTCACACACTCGGGGATTAATA
DB 1898 GTAATATCGGGCCGAGCGGCTGCGCTTACCTCAAGTTCACACACTCGGGGATTAATA
OY 1374 GTTCCAAATGAGAGTGTGCTGCTCAATGTGACCGAGGCGGATGCTGGGATTAATA
DB 1958 GTTCCAAATGAGAGTGTGCTGCTCAATGTGACCGAGGCGGATGCTGGGATTAATA
OY 1434 TATGTAAAGTCTCCAAATTAATTAAGGCGAGGCAACAGTCTGCTGCTCACTGCTGC
DB 2018 TATGTAAAGTCTCCAAATTAATTAAGGCGAGGCAACAGTCTGCTGCTCACTGCTGC
OY 1494 CAATAACAGACCGCTGGAAGAGAAAGAGATTAAGCTTCCCAAGACTACCTGAGGA
DB 2078 CAATAACAGACCGCTGGAAGAGAAAGAGATTAAGCTTCCCAAGACTACCTGAGGA
OY 1554 TAGCCATTACTGCAATAGGGGCTTCTTAATCGCCTGTATGTGTGTAACATGATCTGT
DB 2138 TAGCCATTACTGCAATAGGGGCTTCTTAATCGCCTGTATGTGTGTAACATGATCTGT
OY 1614 GCCGAATGAGAAACGACCAAGAAAGCCAGACTTCAAGAGCCAGCGGCTGTGCAAGC
DB 2198 GCCGAATGAGAAACGACCAAGAAAGCCAGACTTCAAGAGCCAGCGGCTGTGCAAGC
OY 1674 TGAACCAACGTATCCCTCTGGGAGAGACAGTAAAC---AGTTTGGCGTGAAGTCCAGCTCC
DB 2258 TGAACCAACGTATCCCTCTGGGAGAGACAGTAAAGTTTGGCTGAAGTCCAGCTCC
OY 1730 TCCATGAATCTCAACACCCGCTGGTGTAGAGATTAACACACGCTCTCTTCAACGAGAC
DB 2318 TCCATGAATCTCAACACCCGCTGGTGTAGAGATTAACACACGCTCTCTTCAACGAGAC
OY 1790 ACCCCATGCTGGCAGGGGCTCTCCAGATAGAACTTCCAGAGACCCAAATATGGAGTTT
DB 2378 ACCCCATGCTGGCAGGGGCTCTCCAGATAGAACTTCCAGAGACCCAAATATGGAGTTT
OY 1850 CCAAGAGATTAAGCTTACACTGGGCAAGCCCTCGGAGAGAGTTGTTGGCAATGGTGC
DB 2438 CCAAGAGATTAAGCTTACACTGGGCAAGCCCTCGGAGAGAGTTGTTGGCAATGGTGC
OY 1910 ATGGGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGGCGGTCAACGTTGCGGTG

```

Db	2498		ATGGGGAGACGATGGGATTGACAAAGACAAAGCCCAAGAGGGGGTCAAGCTGGCCGTG	2557
Qy	1970		AAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGCAGAGATGGAG	2029
Db	2558		AAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGCAGAGATGGAG	2617
Qy	2030		ATGATGAAGATGATTTGGGAAAACAAGAAATTCATAAATCTTTCTTGGAGCTGCACACAG	2089
Db	2618		ATGATGAAGATGATTTGGGAAAACAAGAAATTCATAAATCTTTCTTGGAGCTGCACACAG	2677
Qy	2090		GATGGGACCTCTCTAATGTCATAGTTGAGATGCGCTCTAAAGGCAACCTCCAGAAATACCTC	2149
Db	2678		GATGGGACCTCTCTAATGTCATAGTTGAGATGCGCTCTAAAGGCAACCTCCAGAAATACCTC	2737
Qy	2150		CGAGCCCGGAGGCGCACCCGGGATGAGATCTCTATGACATTTAACCGTGCTCTGAGGAG	2209
Db	2738		CGAGCCCGGAGGCGCACCCGGGATGAGATCTCTATGACATTTAACCGTGCTCTGAGGAG	2797
Qy	2210		CAGATGACCTTTCAAGGACTTGGTGTGATGCACCTTACACAGCTGGCCAGACGATGGAGTAC	2289
Db	2798		CAGATGACCTTTCAAGGACTTGGTGTGATGCACCTTACACAGCTGGCCAGACGATGGAGTAC	2857
Qy	2270		TTGGCTTCCCAAAAATGATTCATCCGAATTTAGAGCCAGAAATGTTTGGTAAACGAA	2329
Db	2858		TTGGCTTCCCAAAAATGATTCATCCGAATTTAGAGCCAGAAATGTTTGGTAAACGAA	2917
Qy	2330		AACAATGTGATGAAAATATAGCAGACTTTGGACTCCGCAAGATATTCACAAATATAGACTAT	2389
Db	2918		AACAATGTGATGAAAATATAGCAGACTTTGGACTCCGCAAGATATTCACAAATATAGACTAT	2977
Qy	2390		TACAAAAAGACCAACCAATGGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAACCCCTGTT	2449
Db	2978		TACAAAAAGACCAACCAATGGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAACCCCTGTT	3037
Qy	2450		GATAGAGATATACATCATCACAAGATATGTCTGTCTCTCCGGGCTTAAATGCGGAGATC	2509
Db	3038		GATAGAGATATACATCATCACAAGATATGTCTGTCTCTCCGGGCTTAAATGCGGAGATC	3097
Qy	2510		TTCACTTTAGGGGGCTCGCCCTTCCCAAGGAGATCCCGTGGAGGAACTTTTAAAGCTGCTG	2569
Db	3098		TTCACTTTAGGGGGCTCGCCCTTCCCAAGGAGATCCCGTGGAGGAACTTTTAAAGCTGCTG	3157
Qy	2570		AAGGAAGACACAGAAATGATTAAGCCAGCCAACTGCACCAACGAACTGTACATGATGATG	2629
Db	3158		AAGGAAGACACAGAAATGATTAAGCCAGCCAACTGCACCAACGAACTGTACATGATGATG	3217
Qy	2630		AGGACTGTGGCATGCAATGCGCTTCCCAAGACCAACGTTCAAGCACTTGGTGAAGAAC	2689
Db	3218		AGGACTGTGGCATGCAATGCGCTTCCCAAGACCAACGTTCAAGCACTTGGTGAAGAAC	3277
Qy	2690		TTGATCGAATTTCTCACTCTGCACACCAATGAG	2722
Db	3278		TTGATCGAATTTCTCACTCTGCACACCAATGAG	3310
RESULT 15				
US-10-669-920-570				
Sequence 570, Application US/10669920				
Publication No. US20060194265A1				
GENERAL INFORMATION:				
APPLICANT: Moritz, David W.				
APPLICANT: Malandro, Marc S.				
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER				
FILE REFERENCE: 20366-066001				
CURRENT APPLICATION NUMBER: US/10/669,920				
CURRENT FILING DATE: 2003-09-23				
PRIOR APPLICATION NUMBER: US 10/004,113				
PRIOR FILING DATE: 2001-10-23				
PRIOR APPLICATION NUMBER: US 10/052,482				
PRIOR FILING DATE: 2001-11-08				
PRIOR APPLICATION NUMBER: US 09/997,722				
PRIOR FILING DATE: 2001-11-30				

[illegible]

QY	774	ACTCTAATGCTAAATGTCACAGATGTCATCTCAATCCGAGATGATGAGATGACACCGATG	893
Db	967	ACTCTAATGCTAAATGTCACAGATGTCATCTCAATCCGAGATGATGAGATGACACCGATG	1026
QY	834	GTGCGGAAGATTTTGTCTGATGAGAAAGATTAACAAGAGAGACCAATCTGACCAACA	893
Db	1027	GTGCGGAAGATTTTGTCTGATGAGAAAGATTAACAAGAGAGACCAATCTGACCAACA	1086
QY	894	CAGAAAAGATGAAAAGCGGCTCCATGCTGTGCTCGCGCCACACTGTCAAGTTTCCT	953
Db	1087	CAGAAAAGATGAAAAGCGGCTCCATGCTGTGCTCGCGCCACACTGTCAAGTTTCCT	1146
QY	954	GCCGAGCGGGGGGAAACCAATGCGCAACATGCGGTGCTGAAAACCGGAGAGATTAA	1013
Db	1147	GCCGAGCGGGGGGAAACCAATGCGCAACATGCGGTGCTGAAAACCGGAGAGATTAA	1206
QY	1014	AGCAGAGACATCGATTTGAGAGCTTACAAGTACGAAACAGCACTGAGGCTCATTAATG	1073
Db	1207	AGCAGAGACATCGATTTGAGAGCTTACAAGTACGAAACAGCACTGAGGCTCATTAATG	1266
QY	1074	AAAGTGTGCTCCCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGAAATGAATACGGCT	1133
Db	1267	AAAGTGTGCTCCCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGAAATGAATACGGCT	1326
QY	1134	CCATCAATCACACGTAACCACTGTGATGTTGAGAGCGATCGCTACCGGCGCATCTCTCC	1193
Db	1327	CCATCAATCACACGTAACCACTGTGATGTTGAGAGCGATCGCTACCGGCGCATCTCTCC	1386
QY	1194	AAAGCCGAGCTGCGGCAAAATGCTCTCACAGTGTGTGAGAGAGAGTGAATTTGTCTGCA	1253
Db	1387	AAAGCCGAGCTGCGGCAAAATGCTCTCACAGTGTGTGAGAGAGAGTGAATTTGTCTGCA	1446
QY	1254	AGGTTTACAGTGAATCCGAGCCCAACATCCAGTGAATCAAGCAGTGAAGAAAGACGGCA	1313
Db	1447	AGGTTTACAGTGAATCCGAGCCCAACATCCAGTGAATCAAGCAGTGAAGAAAGACGGCA	1506
QY	1314	GTAATTAACGGGCCCCGACGGGCTGCCCCCTCACTCAAGTTCTCAGCACTCGGGGTAATA	1373
Db	1507	GTAATTAACGGGCCCCGACGGGCTGCCCCCTCACTCAAGTTCTCAGCACTCGGGGTAATA	1566
QY	1374	GTTCCAAATGCAAGAGTGTGCTGTCTGT-----TCAATGTGACCGAGCGGAGTCTGAGG	1427
Db	1567	CCACGGACAAAGAGATGAAGGTTCTCTAATTCGGAATGTAACTTTTGAGACGCTGAGG	1626
QY	1428	AATATATATGTAAAGTCTTCAATTAATATAGGCGAGGCCAACAGTCTGCTGCTCACTG	1487
Db	1627	AATATATATGTAAAGTCTTCAATTAATATAGGCGAGGCCAACAGTCTGCTGCTCACTG	1686
QY	1488	TCCTGCCAAAAACGCAAGCGCTGGAAGAGAAAGAGATTAACAGCTTCCCCACACTAAC	1547
Db	1687	TCCTGCC-----AGCGCTGTGAAAGAAAGAGATTAACAGCTTCCCCACACTAAC	1737
QY	1548	TGGAATATAGCACTTAATCTGCAATAGGGGCTCTTAAATGAGCTGTATGATGTTGTAACATCA	1607
Db	1738	TGGAATATAGCACTTAATCTGCAATAGGGGCTCTTAAATGAGCTGTATGATGTTGTAACATCA	1797
QY	1608	TCCTGTGCGGATGAAGAACAGACCAAGAACCGACCTTACAGACCGACGCGCTGTGC	1667
Db	1798	TCCTGTGCGGATGAAGAACAGACCAAGAACCGACCTTACAGACCGACGCGCTGTGC	1857
QY	1668	ACAACTGACCAAAGGTATCCCCCTGCGAGACAGATTAACAGAAAGTTTGGCTGAATCC	1723
Db	1858	ACAACTGACCAAAGGTATCCCCCTGCGAGACAGATTAACAGAAAGTTTGGCTGAATCC	1917
QY	1724	AGCTCTCCATGAACTCCACACACCCGCTGTGTGAGATTAACACACGCTCTCTTCAACG	1783
Db	1918	AGCTCTCCATGAACTCCACACACCCGCTGTGTGAGATTAACACACGCTCTCTTCAACG	1977
QY	1784	GCAGACACCCCATATGCTGGCAGGGGTCTTCCAGTATGAATTTCCAGAGAACCCAAAATG	1843
Db	1978	GCAGACACCCCATATGCTGGCAGGGGTCTTCCAGTATGAATTTCCAGAGAACCCAAAATG	2037

QY	1844	GAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTTGGAGAGAGGTGCTTTGGGCAA	1903
Db	2038	GAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTTGGAGAGAGGTGCTTTGGGCAA	2097
QY	1904	GTGGTCATGGCGGAGCAGTGGGAAATTGACAAACACAGCCCAAGAGGCGCGTCAACCGTG	1963
Db	2098	GTGGTCATGGCGGAGCAGTGGGAAATTGACAAACACAGCCCAAGAGGCGCGTCAACCGTG	2157
QY	1964	GCCGTGAAGATGTTGAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGGTCCAGAG	2023
Db	2158	GCCGTGAAGATGTTGAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGGTCCAGAG	2217
QY	2024	ATGGAAGATGAAGAAGATGATGGGAAACACAAGAATATCATPAAATCTTCTGGAGCCCTGC	2083
Db	2218	ATGGAAGATGAAGAAGATGATGGGAAACACAAGAATATCATPAAATCTTCTGGAGCCCTGC	2277
QY	2084	ACACAGATGGGCGCTCTCTATGTCAATGTTAGTATGGCTCTTAAGCCAACTTCGAGAA	2143
Db	2278	ACACAGATGGGCGCTCTCTATGTCAATGTTAGTATGGCTCTTAAGCCAACTTCGAGAA	2357
QY	2144	TACCTCCGAGCCCGGAGGCCACCCGGGATGGAATCTCCATGACATTTAACCGTGTTCT	2203
Db	2338	TACCTCCGAGCCCGGAGGCCACCCGGGATGGAATCTCCATGACATTTAACCGTGTTCT	2397
QY	2204	GAGGAGCAGATGACCTTTCAGAGACTTGGTGTTCATGACCTTACCACTGGGCCAGACGAGTG	2263
Db	2398	GAGGAGCAGATGACCTTTCAGAGACTTGGTGTTCATGACCTTACCACTGGGCCAGAGCAGTG	2457
QY	2284	GAGTACTTGGCTTCCCAAAAATGTAATTCATGGAATTTAGAGGACAGAAAATGTTTGSTA	2323
Db	2458	GAGTACTTGGCTTCCCAAAAATGTAATTCATGGAATTTAGAGGACAGAAAATGTTTGSTA	2517
QY	2324	ACAGAAAACAATGTGATGAATAATAGCAGACTTTGGACTCGCCAGAGATATCAACATATA	2383
Db	2518	ACAGAAAACAATGTGATGAATAATAGCAGACTTTGGACTCGCCAGAGATATCAACATATA	2577
QY	2384	GACTATTAACAAAAGACCACTATGGCGGCTTCCAGTCAAGTGAATGGCTCCGAAGCC	2443
Db	2578	GACTATTAACAAAAGACCACTATGGCGGCTTCCAGTCAAGTGAATGGCTCCGAAGCC	2637
QY	2444	CTGTTTGAATAGATTAACACTCATCAGAGTGAATGTCTGGTCCCTTCGAGGTGTATCTGG	2503
Db	2638	CTGTTTGAATAGATTAACACTCATCAGAGTGAATGTCTGGTCCCTTCGAGGTGTATCTGG	2697
QY	2504	GAGATCTTCACTTTAAGGGGGCTCGCCCTTACCAGGGAATCCCGTGAAGAACTTTTAAG	2562
Db	2698	GAGATCTTCACTTTAAGGGGGCTCGCCCTTACCAGGGAATCCCGTGAAGAACTTTTAAG	2757
QY	2564	CTGCTGAAGGAAGGACACAGAAATGATTAAGCAGCACTGACCAAGAAAGAACTGTACATG	2622
Db	2758	CTGCTGAAGGAAGGACACAGAAATGATTAAGCAGCACTGACCAAGAAAGAACTGTACATG	2811
QY	2624	ATGATGAGGAGACTGTTGGCATGCACTGGCCCTCCAGAGACCAAGCTTCAAGCAGTTGGTA	2683
Db	2818	ATGATGAGGAGACTGTTGGCATGCACTGGCCCTCCAGAGACCAAGCTTCAAGCAGTTGGTA	2877
QY	2684	GAAAGCTTGAATGCAATTTCTCACTCTCAACAACATGAG	2722
Db	2878	GAAAGCTTGAATGCAATTTCTCACTCTCAACAACATGAG	2916

Search completed: October 2, 2006, 18:47:12
Job time : 1108 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:04:22 ; Search time 14063 Seconds
(without alignments)
12350.526 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaagtttgctg.....tttcgcgagcagtgacgcgc 3106

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc3:*
3: gb_esc4:*
4: gb_esc5:*
5: gb_esc6:*
6: gb_esc7:*
7: gb_esc8:*
8: gb_esc9:*
9: gb_esc10:*
10: gb_esc11:*
11: gb_esc12:*
12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2305.4	74.2	2460	14	DD037912 Homo sapi
2	2166	69.7	3523	6	BC096749 Homo sapi
3	1384.4	44.6	2817	6	CR857280 Pongo pyg
4	1177.2	37.9	2295	14	DD037913
5	1086.4	35.0	3513	6	CR859698 Pongo pyg
6	1050.2	33.8	4050	6	AK049704 Mus muscu
7	1001.4	32.2	3259	6	AK028354 Mus muscu
8	906.6	29.2	4150	6	AK143552 Mus muscu
9	905.4	29.2	3761	6	AK163495 Mus muscu
10	777.4	25.0	885	3	BQ438964 AGENCOURT
11	759.6	24.5	898	1	DN102332 AGENCOURT
12	755.6	24.3	898	1	DN102332 AGENCOURT
13	735	23.7	757	5	CD643272 AGENCOURT
14	728	23.4	3146	6	AK084850 Mus muscu
15	719	23.1	2218	6	AK081810 Mus muscu
16	705.2	22.7	818	10	CB217005 NISC_rq11
17	704.4	22.7	772	9	CB217005 NISC_rq11
18	704.4	22.5	924	2	CB217005 NISC_rq11
19	700.4	22.5	924	2	CB217005 NISC_rq11

20	697.2	22.4	834	2	BG698600 Mus muscu
21	693.6	22.3	3133	6	AK085723 Mus muscu
22	693.4	22.3	1013	3	B1656483 Mus muscu
23	692.8	22.3	905	2	B1655023 Mus muscu
24	692.4	22.3	791	2	B1656640 Mus muscu
25	692	22.3	692	2	CB758275 AGENCOURT
26	690	22.2	726	8	CN345543 AGENCOURT
27	687.6	22.1	909	2	B1661393 AGENCOURT
28	685.8	22.1	837	9	DN822797 UMC-Dentil
29	684.8	22.0	946	2	B1558570 Mus muscu
30	682.4	22.0	729	2	DR002343 Mus muscu
31	677.2	21.8	693	3	BM792391 K-EST0072
32	676.8	21.8	680	5	CD675167 Mus muscu
33	672.2	21.6	720	9	DR001520 Mus muscu
34	671.6	21.6	879	2	B1854011 Mus muscu
35	664.8	21.4	797	4	CA318181 Mus muscu
36	664.2	21.4	836	2	B1853502 Mus muscu
37	661.4	21.3	836	2	B1858079 Mus muscu
38	660.8	21.3	787	2	B1661662 Mus muscu
39	660.4	21.3	774	2	B1660473 Mus muscu
40	660.4	21.3	826	2	B1658887 Mus muscu
41	660	21.2	852	2	B1853362 Mus muscu
42	659.8	21.2	808	2	BG864499 Mus muscu
43	658.4	21.2	771	8	CR629587 Mus muscu
44	658.4	21.2	910	2	BC916151 Mus muscu
45	657.8	21.2	965	2	B1659067 Mus muscu

ALIGNMENTS

RESULT 1
DD037912
LOCUS DD037912 2460 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens FGFR2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DD037912
VERSION DD037912.1 GI:66889121

KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 2460)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,

Hubisz, M.J., Pedel-Alon, A., Tanenbaum, D.M., Civejello, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees
(et) Plos Biol. 3 (6), E170 (2005)

JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325

AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Pedel-Alon, A., Tanenbaum, D.M., Civejello, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES location/Qualifiers

source 1..2460

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="10"

<1..>2460

/gene="FGFR2"

/locus_tag="HC7772"

ORIGIN

Query Match	74.2%	Score 2305.4;	DB 14;	Length 2460;
Best Local Similarity	96.7%;	Pred. No. 0;		
Matches 2393;	Conservative 0;	Mismatches 61;	Indels 21;	Gaps 3;

OY	419	ATGTCAGCTGAGGAGCGTTTATCATCTGACCTGGTCGAGTCAACAATGGCAACCTTGCTCCTG	478
Db	1	ATGGCTACAGTGGGAGCGTTTATCTGCTCGGTGGTGGTCAACAATGGCAACCTTGCTCCTG	60
OY	479	GCCCGGCGCTCTTTCAGTTTATGTTAGAGATACCACTTATGAGCCGAAAGACCAACAAC	538
Db	61	GCCCGGCGCTCTTTCAGTTTATGTTAGAGATACCACTTATGAGCCGAAAGACCAACAAC	120
OY	539	AAATATCCAAATCTCTCAACCAAGATGTACGTGGTCGACAGGGGAGTGGCTTGAAGGTG	598
Db	121	AAATATCCAAATCTCTCAACCAAGATGTACGTGGTCGACAGGGGAGTGGCTTGAAGGTG	180
OY	599	CGCTGCGCTGTGAAAGATGCGCGCGTGCATGATTGGACTTAAGGATGGGGTCACTTGGGG	658
Db	181	CGCTGCGCTGTGAAAGATGCGCGCGTGCATGATTGGACTTAAGGATGGGGTCACTTGGGG	240
OY	659	CCCAACCAATAGGACAGTGCCTTATTTGGGAGATCTTGCAATTAAGGGCGCCACACTTGA	718
Db	241	CCCAACCAATAGGACAGTGCCTTATTTGGGAGATCTTGCAATTAAGGGCGCCACACTTGA	300
OY	719	GACCTCGGCGCTCTATGCTTTGTATCTGCGCAGTTAGGACTGTAGACAGTGAACCTTGGAATCTTC	778
Db	301	GACCTCGGCGCTCTATGCTTTGTATCTGCGCAGTTAGGACTGTAGACAGTGAACCTTGGAATCTTC	360
OY	779	ATGTGTAATGTCAACGATGCCATCTCATCCGGAGATGATAGAGATGACACCGATGGTGG	838
Db	361	ATGTGTAATGTCAACGATGCCATCTCATCCGGAGATGATAGAGATGACACCGATGGTGG	420
OY	839	CAAGATTTTGTGACGTGAGAACATATACCAAGAGAGACCACTACTGSAACCAACACAA	898
Db	421	CAAGATTTTGTGACGTGAGAACATATACCAAGAGAGACCACTACTGSAACCAACACAA	480
OY	899	AAGATGAGAAAGCGGCTCATGCTGTGCTGCGGCGCAACACTGTCAAGTTTGTGCTGCCA	958
Db	481	AAGATGAGAAAGCGGCTCATGCTGTGCTGCGGCGCAACACTGTCAAGTTTGTGCTGCCA	540
OY	959	GCCGGGGGGAAACCAATGCGCAACATGCGGTGGCTTGAAGAAACGGGAAGAGTTTAAAGAG	1018
Db	541	GCCGGGGGGAAACCAATGCGCAACATGCGGTGGCTTGAAGAAACGGGAAGAGTTTAAAGAG	600
OY	1019	GAGCATCCGATTTGGAGGCTCAAGAGTACGAAACCAAGCATGAGGCTCATTTATGGAAAGT	1078
Db	601	GAGCATCCGATTTGGAGGCTCAAGAGTACGAAACCAAGCATGAGGCTCATTTATGGAAAGT	660
OY	1079	GTGGTCCCATCTGACAGAGGAAATTTATCCTGTGTATGTGAGAAATGAATACGGGTCTATC	1138
Db	661	GTGGTCCCATCTGACAGAGGAAATTTATCCTGTGTGTGAGAAATGAATACGGGTCTATC	720
OY	1139	AATCAACAGTACCAACCTGATGTTGTGAGGCAATGCTCAACGGCCATCTCCAAAGC	1198
Db	721	AATCAACAGTACCAACCTGATGTTGTGAGGCAATGCTCAACGGCCATCTCCAAAGC	780
OY	1199	GGAATCGCCGGCAAAATGCTCCACAGTGGTCGAGAGAGAGATGAAGTTTGTCTGCAAGGT	1258
Db	781	GGAATCGCCGGCAAAATGCTCCACAGTGGTCGAGAGAGAGATGAAGTTTGTCTGCAAGGT	840
OY	1259	TACAGTATGCCCCAGGCCCACTCACTGATGATCAAGCACTGTGAAAAGAACCGCAGTAA	1318
Db	841	TACAGTATGCCCCAGGCCCACTCACTGATGATCAAGCACTGTGAAAAGAACCGCAGTAA	900
OY	1319	TACGGGCGCGACGGGCTGCCCTACTCAAGGTTCTCAGCACTCGGGATTAATATGTTCC	1378
Db	901	TACGGGCGCGACGGGCTGCCCTACTCAAGGTTCTCAGCACTCGGGATTAATATGTTCC	960
OY	1379	AATGCAAGAGTGCCTGGCTGTG-----TCAATGTGACCGAAGCGGAGATCTGGGGAAATAT	1438
Db	961	GAACAAGAAATGAGGTTCTCTATATTTGCGAAATGTACTTTTGAAGAGACCTGGGGAAATAT	1022
OY	1433	AATATGAAGTCTCCAAATTTATATAGGCAAGGCCAACAGTCTGCTGCTCACTGTCTTG	1498

Db	1021	ACGCTTGGCGGGTAATTCATTGGGATATCCCTTTCACCTCGATGATGGTGAAGATTCTG	1080
OY	1493	CCAAAAAGCAAGGCGCTCGGAAGAGAAAAGAGATTACAGCTTCCCGACATACCTGGAG	1552
Db	1081	CC-----AGCGCTGGAAAGAAAAGAAAGATTACAGCTTCCCGACATACCTGGAG	1131
OY	1553	ATAGCCATTATCTGCATAGGGGCTTCTTATATCGCTGTATATGGTGTAAAGTCAATCTTG	1612
Db	1132	ATAGCCATTATCTGCATAGGGGCTTCTTATATCGCTGTATATGGTGTAAAGTCAATCTTG	1191
OY	1613	TGCGGATATGAAGAACAGAACCAAGAACCCAGCTTACAGCGCAGCGCGCTGTGCAAG	1672
Db	1192	TGCGGATATGAAGAACAGAACCAAGAACCCAGCTTACAGCGCAGCGCGCTGTGCAAG	1251
OY	1673	CTGACCAAAAGTATCCCCCTGCGGAGACAGGTAAACATTTTCGCTGTAGTCAAGCTCTCC	1732
Db	1252	CTGACCAAAAGTATCCCCCTGCGGAGACAG-----GTTTCGCTGTAGTCAAGCTCTCC	1305
OY	1733	ATGAATCTCCACACCCCGCTGGTGAAGATTAACAACGCGCTCTCTTCAACGGCAGACAC	1792
Db	1306	ATGAATCTCCACACCCCGCTGGTGAAGATTAACAACGCGCTCTCTTCAACGGCAGACAC	1365
OY	1793	CCCATGCTGGCAGGGGCTCTCCGAGTATGAACCTTCCAGAGAACCCAAATGGGATTTCCA	1852
Db	1366	CCCATGCTGGCAGGGGCTCTCCGAGTATGAACCTTCCAGAGAACCCAAATGGGATTTCCA	1425
OY	1853	AGAGATTAAGCTGAACCTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCAATG	1912
Db	1426	AGAGATTAAGCTGAACCTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCAATG	1485
OY	1913	GCGAAGCAGTGGGAAATTGACAAAGCAAGCCCAAGAGGCGAGTCACTGGCCGTGAAG	1972
Db	1486	GCGAAGCAGTGGGAAATTGACAAAGCAAGCCCAAGAGGCGAGTCACTGGCCGTGAAG	1545
OY	1973	ATGTTGAAAAGTGAATGCCACAGAGAAAAGCCTTTCTGATCTGGTGTCAAGATGGGAATG	2032
Db	1546	ATGTTGAAAAGTGAATGCCACAGAGAAAAGCCTTTCTGATCTGGTGTCAAGATGGGAATG	1605
OY	2033	ATGAAGATGATTGGGAAACAACAAGAAATCATTAATCTCTTGGAGCCTGACACAGGAT	2092
Db	1606	ATGAAGATGATTGGGAAACAACAAGAAATCATTAATCTCTTGGAGCCTGACACAGGAT	1665
OY	2093	GGGCCTCTCTATGTCTATAGTTGAATATGCTCTTAAAGGCAACCTCCGAAATACCTCCGA	2152
Db	1666	GGGCCTCTCTATGTCTATAGTTGAATATGCTCTTAAAGGCAACCTCCGAAATACCTCCGA	1725
OY	2153	GCCCGGAGGCAACCCGGGATGGAGTATCTCTATGACATTTAACCGTGTCTCTGAGAGCAG	2212
Db	1726	GCCCGGAGGCAACCCGGGATGGAGTATCTCTATGACATTTAACCGTGTCTCTGAGAGCAG	1785
OY	2213	ATGACCTTCAAGGACTTGGTGTCAATGACACCAACAGCTGGGCAACCGATGGAGTACTTG	2272
Db	1786	ATGACCTTCAAGGACTTGGTGTCAATGACACCAACAGCTGGGCAACCGATGGAGTACTTG	1845
OY	2273	GCTTCCCAAAATGTAATCATCGAAGTTTACAGCCAGAAATGTTTTGGTAAACAGAAAAC	2332
Db	1846	GCTTCCCAAAATGTAATCATCGAAGTTTACAGCCAGAAATGTTTTGGTAAACAGAAAAC	1905
OY	2333	AAATGATGAATAATGACAGCTTTGGACTGGCCAGAGATATCAACATATAGACTATTTAC	2392
Db	1906	AAATGATGAATAATGACAGCTTTGGACTGGCCAGAGATATCAACATATAGACTATTTAC	1965
OY	2393	AAAAAGACCAACAAATGGGCGGCTTCCATCAAGTGAAGGCTCCAGAAAGCCCTGTTGAT	2452
Db	1966	AAAAAGACCAACCAATGGGCGGCTTCCATCAAGTGAAGGCTCCAGAAAGCCCTGTTGAT	2025
OY	2453	AGAGATTAACATCATCAGATGAATGTCTGGTCTCTTCCGGGCTGTTAATGTGGAGATCTTC	2512
Db	2026	AGAGATTAACATCATCAGATGAATGTCTGGTCTCTTCCGGGCTGTTAATGTGGAGATCTTC	2085
OY	2513	ACTTTAGGGGGCTCGCCCTTACCCAGGATTCCTGGTGAAGAACTTTTAACTGCTGAAG	2572


```

Db      2086 ACTTTAGGGGGCTCGCCCTACCCAGGAGTCCCGTGAGAGACTTTTAACTGCTGAG 2145
Qy      2573 GAAGACACAGAAATGATTAAGCCAGCACTGCAACCAAGAACTGTATGATGAGG 2632
Db      2146 GAAGACACAGAAATGATTAAGCCAGCACTGCAACCAAGAACTGTATGATGAGG 2205
Qy      2633 GACTGTGGCAATGAGTGGCCCTCCAGAGACCAAGCTTCAAGCAGTGGTAAAGACTTG 2692
Db      2206 GACTGTGGCAATGAGTGGCCCTCCAGAGACCAAGCTTCAAGCAGTGGTAAAGACTTG 2265
Qy      2693 GATCGAATTCCTCACTCTCAACAACCAATGAGAACTTGAACCTCAAGCCACTTCGA 2752
Db      2266 GATCGAATTCCTCACTCTCAACAACCAATGAGAACTTGAACCTCAAGCCACTTCGA 2325
Qy      2753 CAGTATTCACCTGATTAACCTTCAACAAGAACTTGTGTTCTTCAAGAGATGATTTCT 2812
Db      2326 CAGTATTCACCTGATTAACCTTCAACAAGAACTTGTGTTCTTCAAGAGATGATTTCT 2385
Qy      2813 TTTTCTCCAGACCCCAATGCTTACGAGCAATGCTTCCAGATTCACACATTAACGCG 2872
Db      2386 TTTTCTCCAGACCCCAATGCTTACGAGCAATGCTTCCAGATTCACACATTAACGCG 2445
Qy      2873 AGTGTTAAACATGA 2887
Db      2446 AGTGTTAAACATGA 2460

RESULT 2
BC096749 3523 bp mRNA linear HTC 21-JUL-2005
LOCUS Homo sapiens cDNA clone IMAGE:5265147, containing frame-shift
DEFINITION
ERRORS
ACCESSION BC096749 GI:66911819
VERSION BC096749.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 3523)
AUTHORS Strusberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Sherman,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhac,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stalcioen,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Uedlin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Rabe,S.S., Loggellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shcherbenko,Y.,
Boutard,G.G., Blakesley,R.W., Touchman,D.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,
Scherer,A., Schein,J.B., Jones,S.J., and Marra,M.A.
CONSTRM Mammalian Gene Collection Program Team
TITLE human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 3523)
AUTHORS NIH MGC Project
CONSTRM Direct Submision
TITLE Submitted (01-JUN-2005) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov

```

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil@stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILLUM at: <http://image.illum.gov>
 Series: IMAK Plate: 198 Row: d Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 13186239
 This clone has the following problem: frame shifted.

FEATURES
 source
 location/Qualifiers
 1..3523
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5265147"
 /tissue_type="Brain, hippocampus"
 /clone_id="NIH_MGC_95"
 /lab_host="DH10B"
 /note="Vector: pBluescriptR"

ORIGIN
 Query Match 69.7%; Score 2166; DB 6; Length 3523;
 Best Local Similarity 84.4%; Pred. No. 0;
 Matches 2750; Conservative 0; Mismatches 10; Indels 498; Gaps 8;

```

Qy      1 CCCGCGAGCAAAAGTTGGTGAAGGCAAG-CAAGCTGAGTCTTTCTCTCTGTTCC 59
Db      178 CTCGCGAGCAAAAGTTGGTGAAGGCAAGCCAGAGCTTGAATCTTCTCTCTGTTCC 237
Qy      60 CCAATCCGAGGGGAGCCCGGGGGGCTCATG---GGGCTCCCGGAGCGTGGGGTAAGC 116
Db      238 CCAATCCGAGGGGAGCCCGGGGGGCTCATGCGCGGCTCTCCGAGCTGGGGTAAGC 297
Qy      117 GTGAAGCCCGGAGGCTTGGCGCCGCGAGAACCCAGAGACCACTTTCTGCGTTTGAG 176
Db      298 GTGAAGCCCGGAGGCTTGGCGCCGCGAGAACCCAGAGACCACTTTCTGCGTTTGAG 357
Qy      177 TTGCTCCCGCAACCCCGGGCTGTGCTTTCTCATCTCCGACCGCGGGGC-CGGGG 235
Db      358 TTGCTCCCGCAACCCCGGGCTGTGCTTTCTCATCTCCGACCGCGGGGC-CGGGG 417
Qy      236 ACAACACAGTGGCGGAGAGAGCGTTGCCATCAAGTGAAGTGAAGAGAGC-GCAGCGCC 294
Db      418 ACAACACAGTGGCGGAGAGAGCGTTGCCATCAAGTGAAGTGAAGAGAGC-GCAGCGCC 477
Qy      295 TCGGTTCTGAGCCACCGCA-GCTGAAGGCAATTCGGGTAGTCCATGCGCGTAGAGAA 353
Db      478 TCGGTTCTGAGCCACCGCAAGCGAGCTGAAGGCAATTCGGGTAGTCCATGCGCGTAGAGAA 537
Qy      414 TAAACATGTCAGTGGGTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Db      598 TAAACATGTCAGTGGGTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Qy      474 CCTGAGCCGCGCCCTCTTCAAGTTAGTTAGAGATACATTAAGAGCCAGAGCCAC 533
Db      658 CCTGAGCCGCGCCCTCTTCAAGTTAGTTAGAGATACATTAAGAGCCAGAG----- 711
Qy      534 CAACCAATACCAAAATCTCTCAACCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 593
Db      712 ----- 711

```

QY 594 AGGTGCGCTGCTGTGTAAGATGCGCGGTGATCAATTGACCTAAGAGATGGGCTGCACT 653
 Db 712 ----- 711
 QY 654 TGGGGCCCAACAATAGACAGTGTCTATTGGGAGACTTGGCAAGTAAGGGCGCACAC 713
 Db 712 ----- 711
 QY 714 CTAGAGACTCGGCTCTATGCTTGTACTGCGAGTAGAGACTGTAGACAGTGAACCTTGGT 773
 Db 712 ----- 711
 QY 774 ACTTCATGTGTGATGTCAACAATGCCATCTCATCCGAGATGATGAGATGACACCGATG 833
 Db 712 ----- 711
 QY 834 GTGCGGAAGATTTTGTCACTGATGAGAACAGTAACAACAAGAGACCACTATCTGGAACCA 893
 Db 712 ----- 732
 QY 894 CAGAAAAGATGAAAAAGCGGCTCACTGCTGTGCTGCGGCCCAACACTGTCAAGTTTCGCT 953
 Db 733 CAGAAAAAATGAAAAAGCGGCTCACTGTGTGCTGCGGCCCAACACTGTCAAGTTTCGCT 792
 QY 954 GCCCAGCCGGGGGAAACCCATGCCACCATGCGGTGCTGAATAACGGAAAGAGTTTA 1013
 Db 793 GCCCAGCCGGGGGAAACCCATGCCACCATGCGGTGCTGAATAACGGAAAGAGTTTA 852
 QY 1014 AGCAGAGACATGCGATTGGAAGGCTACAAGGTACGAAACAGACCTGGAACCTCATTAAG 1073
 Db 853 AGCAGAGACATGCGATTGGAAGGCTACAAGGTACGAAACAGACCTGGAACCTCATTAAG 912
 QY 1074 AAAGTGTGTCCCATCTGACAAAGGAAATTAATCTGTGTAGTGAAGATGAATAACGGGT 1133
 Db 913 AAAGTGTGTCCCATCTGACAAAGGAAATTAATCTGTGTGTGAGATGAATAACGGGT 972
 QY 1134 CCATCAATCAACGTACCACTGTGATGTTGTGAGAGATGCGCTCAACGGGCCCATCTTC 1193
 Db 973 CCATCAATCAACGTACCACTGTGATGTTGTGAGAGATGCGCTCAACGGGCCCATCTTC 1032
 QY 1194 AAGCCGAGCTGCGGCAAAATGCTCCACAGTGTGAGAGAGACGTGAAGTTGTCTGCA 1253
 Db 1033 AAGCCGAGCTGCGGCAAAATGCTCCACAGTGTGAGAGAGACGTGAAGTTGTCTGCA 1092
 QY 1254 AGGTTTACAGTATGCCAGCCCAATCCAGTGTCAAGCACTGGAAGAAAGACGCA 1313
 Db 1093 AGGTTTACAGTATGCCAGCCCAATCCAGTGTCAAGCACTGGAAGAAAGACGCA 1152
 QY 1314 GTAATATCGGGCCCCAGCGGGCTGCCCTCAAGGTTCTCAAGCACTGCGGGATTAATA 1373
 Db 1153 GTAATATCGGGCCCCAGCGGGCTGCCCTCAAGGTTCTCAAGCACTGCGGGATTAATA 1212
 QY 1374 GTTCCAAATGCAAGAGTGTGGCTGTGTTCAATGTGACGAGGCGGATGCTGGGGATTAATA 1433
 Db 1213 GTTCCAAATGCAAGAGTGTGGCTGTGTTCAATGTGACGAGGCGGATGCTGGGGATTAATA 1272
 QY 1434 TATGTAAAGTCTTCAATTATATATAGGCAAGCCCAAGTCTGCTGGTCACTGTCTTC 1493
 Db 1273 TATGTAAAGTCTTCAATTATATATAGGCAAGCCCAAGTCTGCTGGTCACTGTCTTC 1332
 QY 1494 CAAAAACGCA----- 1503
 Db 1333 CAAAAACGCAAGGCGCGGTGTTAACAACAAGCAAAAGATTAAGGTTCTTAATAT 1392
 QY 1504 ----- 1503
 Db 1393 CGGAATGTAACTTTGAGGACGCTGGGGATTAATCTGCTGGCGGGTAACTTAATTGG 1452
 QY 1504 ----- AGCGCTTGAAGAGAAAAAGAGATT 1528
 Db 1453 AATATCTTTCACTGTGATGTTGAAGATTCTGCGAGCGCTGGAGAGAAAAAGAGATT 1512
 QY 1529 AAGATCTTCCCAAGATTAAGATGAGCAATTAATCTGCAATAGGGGTCTTTTAATGCGC 1588

Db 1513 AAGCTTCCCAAGATTAAGTGAATGCAATTAATCTGCAATAGGGGTCTTTAATGCGC 1572
 QY 1589 TGTATGTGTGTAAACATCATCTGTGCGGAATGAAGAACAGACAAAGAACGACATTC 1648
 Db 1573 TGTATGTGTGTAAACATCATCTGTGCGGAATGAAGAACAGACAAAGAACGACATTC 1632
 QY 1649 AGCAGCCAGCGGCTGTGCAACAGCTGAACCAAGTATCCCTCGCGGAGACAGGTAA 1708
 Db 1633 AGCAGCCAGCGGCTGTGCAACAGCTGAACCAAGTATCCCTCGCGGAGACAGGTAA 1692
 QY 1709 GTTTCGGGTAGTCAAGTCACTCCCAACACCCGCTGTGAGATTAACA 1768
 Db 1693 GTTTCGGGTAGTCAAGTCACTCCCAACACCCGCTGTGAGATTAACA 1752
 QY 1769 CGCCTCTCTTCAACGAGACACACCCATGTGCGAGGGGTCTTCGAGTATGA 1828
 Db 1753 CGCCTCTCTTCAACGAGACACACCCATGTGCGAGGGGTCTTCGAGTATGA 1812
 QY 1829 GAGAACCAAAATGGAGTTTCCAAAGATTAAGTGAACCTGGGCAAGCCCTGGGAGAA 1888
 Db 1813 GAGAACCAAAATGGAGTTTCCAAAGATTAAGTGAACCTGGGCAAGCCCTGGGAGAA 1872
 QY 1889 GATTGCTTTGGGCAAGTGTCAATGGCGGAAGCAATGGGAAATTAACAAGCCGAG 1948
 Db 1873 GATTGCTTTGGGCAAGTGTCAATGGCGGAAGCAATGGGAAATTAACAAGCCGAG 1932
 QY 1949 GAGGCGGTCAACGTGCGGTGAAGATGTAAGATGATGCAACAGAAAGACCTTTCT 2008
 Db 1933 GAGGCGGTCAACGTGCGGTGAAGATGTAAGATGATGCAACAGAAAGACCTTTCT 1992
 QY 2009 GATCTGTGTCAAGATGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 2068
 Db 1993 GATCTGTGTCAAGATGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 2052
 QY 2069 CTTCTTGAAGCTGCAACAGAGATGGGCTCTCATATGCTATGATGATGATGATGATGAT 2128
 Db 2053 CTTCTTGAAGCTGCAACAGAGATGGGCTCTCATATGCTATGATGATGATGATGATGAT 2112
 QY 2129 GGCACCTCGAGAAATCTTCGAGCCCGGAGGCCACCCGGGATGAGATCTCTTAATGAC 2188
 Db 2113 GGCACCTCGAGAAATCTTCGAGCCCGGAGGCCACCCGGGATGAGATCTCTTAATGAC 2172
 QY 2189 ATTAAACGTGTCTGTGAGAGACATGATGATGATGATGATGATGATGATGATGATGAT 2248
 Db 2173 ATTAAACGTGTCTGTGAGAGACATGATGATGATGATGATGATGATGATGATGATGAT 2232
 QY 2249 CTGCGCAGACGAGATGAGATCTTGGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCC 2308
 Db 2233 CTGCGCAGACGAGATGAGATCTTGGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCC 2292
 QY 2309 AGAAATGTTTTGTAAACAGAAACATGTGATGAATAATGACACTTTGACTGCGCAGA 2368
 Db 2293 AGAAATGTTTTGTAAACAGAAACATGTGATGAATAATGACACTTTGACTGCGCAGA 2352
 QY 2369 GATATCAACATTAATGAATTAACAAAGACCAATGCGGCTTCCAGTCAAGTGG 2428
 Db 2353 GATATCAACATTAATGAATTAACAAAGACCAATGCGGCTTCCAGTCAAGTGG 2412
 QY 2429 ATGCTCCAGAAAGCCTGTTGATGAGATTAACCTCATGAGATGTCTGTCTTC 2488
 Db 2413 ATGCTCCAGAAAGCCTGTTGATGAGATTAACCTCATGAGATGTCTGTCTTC 2472
 QY 2489 GGGGTGTAAATGTGAGATCTTCACTTAAGGGGCTGCGCTTACCGAGATTCCTG 2548
 Db 2473 GGGGTGTAAATGTGAGATCTTCACTTAAGGGGCTGCGCTTACCGAGATTCCTG 2532
 QY 2549 GAGAACTTTTAACTGTGAAGAGACAGCAAGATGAAGCAAGCAAGCAAGCAAGCAAGCA 2608
 Db 2533 GAGAACTTTTAACTGTGAAGAGAGACAGCAAGATGAAGCAAGCAAGCAAGCAAGCAAGCA 2592
 QY 2609 AAGCACTGTATGATGATGAGAGATGTTGCAATGAGTGCCTTCCAGAGACCAAG 2668

Db 2593 AACGACGTGTACATGATGATGAGGAGCTGTGGACATGACGTGCTCCAGAGACCAAGC 2652
 QY 2669 TTCAAGCACTTGTGTAGAAAGCTTGGATCGAATTTCTCATCTCTCAACAACCAATGAGGAATAC 2728
 Db 2653 TTCAAGCACTTGTGTAGAAAGCTTGGATCGAATTTCTCATCTCTCAACAACCAATGAGGAATAC 2712
 QY 2729 TTGGAACCTGAGCAACCTCTCCAGAGATTAACCTGATTAACCTGAGCAACAAGATTCT 2788
 Db 2713 TTGGAACCTGAGCAACCTCTCCAGAGATTAACCTGATTAACCTGAGCAACAAGATTCT 2772
 QY 2789 TGTCTTTCAGAGATGATTCGTGTTTCTCCAGACCCCATGCTTACCAACCATGCTT 2848
 Db 2773 TGTCTTTCAGAGATGATTCGTGTTTCTCCAGACCCCATGCTTACCAACCATGCTT 2831
 QY 2849 CCTCATGATTCACACATTAACCGCAGGTGTTAAACATGATATGCTGTCTGCTGCTCC 2908
 Db 2832 CCTCATGATTCACACATTAACCGCAGGTGTTAAACATGATATGCTGTCTGCTGCTCC 2891
 QY 2909 CAACAGGACAGACAGCTGGAACCTACTCACTGACAGAGAGACCATGCTCCAGAGC 2968
 Db 2892 CAACAGGACAGACAGCTGGAACCTACTCACTGACAGAGAGACCATGCTCCAGAGC 2951
 QY 2969 TGTGTTCTTCCACTTGTATATGATCAGAGAGATTAATTAATGAGAAAGTATCAGCA 3028
 Db 2952 TGTGTTCTTCCACTTGTATATGATCAGAGAGATTAATTAATGAGAAAGTATCAGCA 3011
 QY 3029 TATGTGTAAGATTATTAACAGTTGAAACTTGTATCTTCCAGAGAGAGAAAGTAT 3088
 Db 3012 TATGTGTAAGATTATTAACAGTTGAAACTTGTATCTTCCAGAGAGAGAAAGTAT 3071
 QY 3089 TCTGAGCAGTGTGACCTGC 3106
 Db 3072 TCTGAGCAGTGTGACCTGC 3089

RESULT 3
 CR857280 2817 bp mRNA linear HTC 12-NOV-2004
 LOCUS CR857280
 DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp469H1521 (from clone DKFZp469H1521).
 ACCESSION CR857280
 VERSION CR857280.1 GI:55725423
 KEYWORDS HTC.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pongo.
 REFERENCE 1 (bases 1 to 2817)
 AUTHORS Bahrt, A., Lauber, J., Mewes, H. W., Weil, B., Amid, C., Oesanger, A.,
 Fobo, G., Han, M., and Wiemann, S.
 CONSRTM The German CDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr. 1, D-85764
 Neuberberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 This clone (DKFZp469H1521) is available at the RZPD Deutsches
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKFZp469H1521
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 Location/Qualifiers
 1..2817
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp469H1521"
 /issue_type="kidney"
 /clone_id="469 (synonym: pkid1). Vector psport1_sfi; host
 DH10B; sites SfiIa + SfiIb"

/dev_stage="adult"
 /note="fibroblast growth factor receptor 2 precursor (Homo sapiens), differentially spliced"
 1..2817
 /gene="DKFZp469H1521"
 132..1286
 /gene="DKFZp469H1521"
 /codon_start=1
 /product="hypothetical protein"
 /protein_id="CAH89576.1"
 /db_xref="GI:55725424"
 /translation="MNSNTPVLRITRLSTADTPMLAGVSEYELPEDPKPEPPDKL
 LKGLGEGCFQGVVMAAVGIDDKPKRAVAVAKMLKDAATERDLSDLVSEMMK
 MIGKKNILINLLAGCTODGPIYVIVEYSKGLREYLARRPGMEYSDIRVVEEQ
 MTFKDIIVCTYQIOLARGMEYLASOKIHDIAARVLYENNNMKIADGLADINND
 YKKTINRRLPYRKMAAPALPDYVTHSDVWSRGVLMELFTTGSSPYPGIPIVELF
 KLKLGHHMDPRANCTNELYMKRDKMAVSRFTFQQLVEDLRILTLTNEEYLD
 LSPLEQYSPSPYDTRSSSSGSDSVFSPDPMPYEPCLPQYPHINGSYKT"
 ORIGIN

Query Match 44.6%; Score 1384.4; DB 6; Length 2817;
 Best Local Similarity 99.2%; Pred. No. 0; Mismatches 1391; Conservative 0; Indels 11; Gaps 0;
 Matches 1391; Conservative 0; Mismatches 1391; Conservative 0; Indels 11; Gaps 0;
 QY 1705 AACAGTTTCGAGTCAAGTCCAGCTCCTCCATGATTCACCAACCCCGCTGTGAGATTAAC 1764
 Db 104 AAAAGTTTCGAGTCAAGTCCAGCTCCTCCATGATTCACCAACCCCGCTGTGAGATTAAC 163
 QY 1765 AACAGCTCTCTTCAACGGCAGACACCCCAATGCTGAGGGGTCTCCGATGAACT 1824
 Db 164 AACAGCTCTCTTCAACGGCAGACACCCCAATGCTGAGGGGTCTCCGATGAACT 223
 QY 1825 TCCAGAGACCCCAATGAGATTTCCAGATTAAGTCACTGAGGGCAAGCCCTGAG 1884
 Db 224 TCCAGAGACCCCAATGAGATTTCCAGATTAAGTCACTGAGGGCAAGCCCTGAG 283
 QY 1885 AGAAGTTTCGTTGGGCAAGTGTGATGCGGAGACAGTGGGATTTGACCAAGACAGCC 1944
 Db 284 AGAAGTTTCGTTGGGCAAGTGTGATGCGGAGACAGTGGGATTTGACCAAGACAGCC 343
 QY 1945 CAAGAGGCGGTCAACGTTGCGGTGAAGATGTTGAAGATGATGCCACAGAGAACCT 2004
 Db 344 CAAGAGGCGGTCAACGTTGCGGTGAAGATGTTGAAGATGATGCCACAGAGAACCT 403
 QY 2005 TTCTGATTCGTGTCAAGATGAGATGATGAAGATTTGGGAAACAAGAAATTCAT 2064
 Db 404 TTCTGATTCGTGTCAAGATGAGATGATGAAGATTTGGGAAACAAGAAATTCAT 463
 QY 2065 AATCTCTTGGAGCCTGCAACAGATGGGCTCTATGTCTATGTTGAGTATGCTC 2124
 Db 464 AATCTCTTGGAGCCTGCAACAGATGGGCTCTATGTCTATGTTGAGTATGCTC 523
 QY 2125 TAAAGCAACCTCCAGAAATACCTCCAGACCCCGAGGCCACCCGGATGAGTACTCTTA 2184
 Db 524 TAAAGCAACCTCCAGAAATACCTCCAGACCCCGAGGCCACCCGGATGAGTACTCTTA 583
 QY 2185 TGAATTAACGTTGTTCTGAGAGACATGATACCTTCAAGAGCTTGTTCACTGACCTTA 2244
 Db 584 TGAATTAACGTTGTTCTGAGAGACATGATACCTTCAAGAGCTTGTTCACTGACCTTA 643
 QY 2245 CCAGCTGGCAGACGAGATGAGTATCTGCTCCCAAAATGATTCATCGAGATTAGC 2304
 Db 644 CCAGCTGGCAGACGAGATGAGTATCTGCTCCCAAAATGATTCATCGAGATTAGC 703
 QY 2305 AACCAAAATGTTTGGTAAAGAAAACAATGTGATGAATATGACAGCTTTGACTCCG 2364
 Db 704 AACCAAAATGTTTGGTAAAGAAAACAATGTGATGAATATGACAGCTTTGACTCCG 763
 QY 2365 CAGATATCAACATATGATCTATTTAACAAGAACCAATGAGCGGCTCCAGTCA 2424
 Db 764 CAGATATCAACATATGATCTATTTAACAAGAACCAATGAGCGGCTCCAGTCA 823
 QY 2425 GTGATGCTCCAGAACCCCTGTTTGAATGAGATTAACCTCATCAGATGATGTCTGTC 2484

Db	824	GTGATATGGCTTCAGAAAGCCCTGTTTGAATAGATATACATCATCAAGATATGTCTGTCT	883
QY	2485	CTTGGGGGTGTTAAATGTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCCAGGGATTC	2544
Db	884	CTTGGGGGTGTTAAATGTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCCAGGGATTC	943
QY	2545	CGTGGAGGAATCTTTTAAAGTCGCTGAAGGAACACAGAAATGGATTAAGCAGCAACTG	2604
Db	944	CGTGGAGGAATCTTTTAAAGTCGCTGAAGGAACACAGAAATGGATTAAGCAGCAACTG	1003
QY	2605	CACCAACGAACCTGTATACATGATGATGAGGGACTGTGGCATGCACTGCGCTCCAGAAC	2664
Db	1004	CACCAACGAACCTGTATACATGATGATGAGGGACTGTGGCATGCACTGCGCTCCAGAAC	1063
QY	2665	AACGTTCAAGCAGTTGGTAGAAGACTGGATCGAATTCATCTCTCACACCAATGAGGA	2724
Db	1064	AACGTTCAAGCAGTTGGTAGAAGACTGGATCGAATTCATCTCTCACACCAATGAGGA	1123
QY	2725	ATACTGGACCTCAGCCCACTCTCGAACAATATTCACCTAGTTACCTGTACACAAAG	2784
Db	1124	ATACTGGACCTCAGCCCACTCTCGAACAATATTCACCTAGTTACCTGTACACAAAG	1183
QY	2785	TTCTTGTTCTTCAGAGATGATTCGTTTTTCTCCAGACCCCAATGCTTACGAACATG	2844
Db	1184	TTCTTGTTCTTCAGAGATGATTCGTTTTTCTCCAGACCCCAATGCTTACGAACATG	1243
QY	2845	CCTTCCTCAGATCCACACATTAACCGCAGTGTAAACATGAATGACTGTCTGCTG	2904
Db	1244	CCTTCCTCAGATCCACACATTAACCGCAGTGTAAACATGAATGACTGTCTGCTG	1303
QY	2905	TCCCCAACAAGACAGCACTGGGAACCTAGCTACACTGACGAGGAAACATGCTCCCA	2964
Db	1304	TCCCCAACAAGACAGCACTGGGAACCTAGCTACACTGACGAGGAAACATGCTCCCA	1363
QY	2965	GAGCTGTGTGCTCCACTGTATATATGATCAGAGGAGTAATATATGAAAAAGTATC	3024
Db	1364	GAGCTGTGTGCTCCACTGTATATATGATCAGAGGAGTAATATATGAAAAAGTATC	1423
QY	3025	AGCATATGTGTAAAGATTTATACAGTTGAAAACTGTATCTTCCCGAGAGAGAAAGAA	3084
Db	1424	AGCATATGTGTAAAGATTTATACAGTTGAAAACTGTATCTTCCCGAGAGAGAAAGAA	1483
QY	3085	GGTTTCTGGAGCAGTGAAGCTG 3106	
Db	1484	GGTTTCTGGAGCAGTGAAGCTG 1505	
RESULT 4			
DQ037913		2295 bp DNA linear GSS 02-JUN-2005	
LOCUS		Pan troglodytes FGFR2 gene, VIRTUAL TRANSCRIPT, partial sequence,	
DEFINITION		genomic survey sequence.	
ACCESSION		DQ037913.1 GI:66889122	
KEYWORDS		GSS.	
SOURCE		Pan troglodytes (chimpanzee)	
ORGANISM		Pan troglodytes (chimpanzee)	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
		Homnidae; Pan.	
		1 (bases 1 to 2295)	
		Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,	
		Hubsiz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,	
		White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	
		A Scan for Positively Selected Genes in the Genomes of Humans and	
		Chimpanzees	
		(er) PLOS Biol. 3 (6), E170 (2005)	
JOURNAL		15869325	
PUBMED		2 (bases 1 to 2295)	
REFERENCE		Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,	
AUTHORS		Hubsiz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,	
		White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	

TITLE		Direct Submission	
JOURNAL		Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
FEATURES		Location/Qualifiers	
source		1..2295	
		/organism="Pan troglodytes"	
		/mol_type="genomic DNA"	
gene		/db_xref="taxon:9598"	
		<1..>2295	
		/gene="FGR2"	
ORIGIN		/locus_tag="HC7772"	
Query Match	37.9%	Score 1177.2;	DB 14; Length 2295;
Best Local Similarity	52.4%	Pred. No. 0;	
Matches 1208;	Conservative 0;	Mismatches 1087;	Indels 9; Gaps 2;
QY	419	ATGTGCACTGGGGTCCGTTTCATCTGCGTGGTGGTCAACATGGGCAACCTGCTCGT	478
Db	1	ATGTGCACTGGGGTCCGTTTCATCTGCGTGGTGGTCAACATGGGCAACCTGCTCGT	60
QY	479	GCCGGGCGCTCTTCAGTTTGTGAGAGATACCACTATGAGCCAGAAGCCACCAACC	538
Db	61	GCCGGGCGCTCTTCAGTTTGTGAGAGATACCACTATGAGCCAGAAGGNNNNNNNNNN	120
QY	539	AAATACCAATCTCTCAACGAGAAGTGTACGTGGCTGCGCAGGGAGATCGCTAGAGTG	598
Db	121	NN	180
QY	599	CGCTGCTGTTGAAAGATGCCCGCGTATCAAGTTGGAATAAGATGGGGTCACTTGGGG	658
Db	181	NN	240
QY	659	CCCAACAATAGAGACAGTGCTTATTGGGAGATCTTGACATAAAGGCGCCACACTAGA	718
Db	241	NN	300
QY	719	GACTCCGGCTCTATGCTTGTATCTGCAGTAGAGACTGAGACGTGAACCTTGACTTC	778
Db	301	NN	360
QY	779	ATGTGAATGTCAAGATGCCATCTCATCCGAGATGATGAGATGACACCGATGCTCG	838
Db	361	NN	420
QY	839	GAAAGTTTGTCAGTGAGAAACAGTAAACAAGAGACCACTATGACCAACACAGAA	898
Db	421	NN	480
QY	899	AAGATGAGAAAAGCGGCTCCATGCTGTGCTGGCGCAACACTGTCMACTTGCCTGCCA	958
Db	481	NN	540
QY	959	GCCGGGGGGAACCAATGCCAACAATCGGTGGCTGAAAAACGGGAAGAATTAAAGCAG	1018
Db	541	NN	600
QY	1019	GAGCATCGCATTTGAGAGCTACAAAGTATGAGAAACGACACTGAGGCTCATTTATGAAAGT	1078
Db	601	NN	660
QY	1079	GTGTGCCATCTGACAGAGGAAATTATACCTGTGTAGTGAAGATGAATAACGGGTCAATC	1138
Db	661	GTGTGCCATCTGACAGAGGAAATTATACCTGTGTGTGAGAAATGAATACGGGTCAATC	720
QY	1139	AATCAACGTACACCTGATTTGTGAGCGATGCTCAACGGGCCATCTCTCAAGCC	1199
Db	721	AATCAACGTACACCTGATTTGTGTGAGCGATGCTCAACGGGCCATCTCTCAAGCC	780
QY	1199	GGAATGCCGGAATATGCTTCCACATGCTGTGGAAGAGACGTAGATTTGTCTGCAAGGTT	1258

```

Db      781 GGAATGCGCCGGAATATCTCTCAAGTGTGAGAGAGAGTAGAGTTTCTGCAAGTT 840
Qy      1259 TACAGTATGATGCCAGGCCCAATCTCAGTGTATCAACACGTGAAAAAAGCGCACTAA 1318
Db      841 TACAGTATGATGCCAGGCCCAATCTCAGTGTATCAACACGTGAAAAAAGCGCACTAA 900
Qy      1319 TACGGGCCCCGAGCGGCTGCCCTTCAAGTGTCTCAAGCATCTCGGGGATAAATAGTTCC 1378
Db      901 TACGGGCCCCGAGCGGCTGCCCTTCAAGTGTCTCAAG--NNNNNNNNNNNNNNNNNN 957
Qy      1379 AATGCAAGATGTGCTGTCTGTTCAATGTGACGAGCGGAGTCTGGGAAATATATATGT 1438
Db      958 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1017
Qy      1439 AAGGTCTCCAAATATATAGGGAGCGCAACAGTCTGCTGCTCACTGCTGCCAATA 1498
Db      1018 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1077
Qy      1499 CAGCAAGCGCTGGAGAGAGAAAGAGATTACAGTTTCCCGAGACTACCTGAGATAGCC 1558
Db      1078 NNNNNNNCCCTGGAGAGAGAAAGAGATTACAGTTTCCCGAGACTACCTGAGATAGCC 1137
Qy      1559 ATTATGATAGAGGCTCTTCTTAATGCTGATGATGATGATGATGATGATGATGATGATG 1618
Db      1138 ATTATGATAGAGGCTCTTCTTAATGCTGATGATGATGATGATGATGATGATGATGATG 1197
Qy      1619 ATGAGAGACACGACCAAGAGACGATTCAGAGAGCGGCTGTGCAAACTGATGCC 1678
Db      1198 ATGAGAGACACGACCAAGAGACGATTCAGAGAGCGGCTGTGCAAACTGATGCC 1257
Qy      1679 AAAAGTATCCCTCTGGGAGAGACGATTCAGATTCGCTGAGTCTGCTCTCATGAAC 1738
Db      1258 AAAAGTATCCCTCTGGGAGAGACG-----NNNNNNNNNNNNNNNNNNNNNNNNNN 1311
Qy      1739 TCCAAACACCCGCTGTGAGATATACAAACACGCTCTTCAACGAGACACCCCATG 1798
Db      1312 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1371
Qy      1799 CTGGCAGGGGTCTCCAGATATGAATTCTCAGAGACCCAAATATGAGATTCCAAGAT 1858
Db      1372 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1431
Qy      1859 AAGCTGACACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGGTCACTGGCGGA 1918
Db      1432 NNGCTGACACTGGGCAAGCCCTGGGAGAGAGTTGCTTTGGGCAATGGTCACTGGCGGA 1491
Qy      1919 GCAGTGGGAATTGACAAAGACAGCCCAAGAGAGCGGTCAAGTGGCCGTGAAGATGTTG 1978
Db      1492 GCAGTGGGAATTGACAAAGACAGCCCAAGAGAGCGGTCAAGTGGCCGTGAAGATGTTG 1551
Qy      1979 AAGATGATGTCACAGAGAAAGACTTTCTGATCTGCTGTCAGAGATGAGATGAAG 2038
Db      1552 AAGATGATGTCACAGAGAAAGACTTTCTGATCTGCTGTCAGAGATGAGATGAAG 1611
Qy      2039 ATGATTTGGGAAACACAGATATCATTAATCTTTGGAGCTGTGCAACAGATGGAGCT 2098
Db      1612 ATGATTTGGGAAACACAGATATCATTAATCTTTGGAGCTGTGCAACAGATGGAGCT 1671
Qy      2099 CTCTATGTCTACTGTGATGCTCTAAAGGCACTCCGAGAAATACCTCCGAGCCCG 2158
Db      1672 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1731
Qy      2159 AGGCAACCCGGATGAGATCTCTATGACATTAACCGTGTCTGAGAGACAGATGACC 2218
Db      1732 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1791
Qy      2219 TTCAAGACCTTGTGTCTACCTACCTGAGCGAGACGATGAGATCTTGGCTCC 2278
Db      1792 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1851
Qy      2279 CAAAAATGATATCATGAGATTAGCAGCAGAAATGTTTGGTAAACAGAAACAATGTC 2338

```

```

Db      1852 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1911
Qy      2339 ATGAAATAGCAGCTTTGAGATCTGCGAGAGATATCAAAATATGACTATTACAAAAG 2398
Db      1912 ATGAAATAGCAGCTTTGAGATCTGCGAGAGATATCAAAATATGACTATTACAAAAG 1971
Qy      2399 ACCACCAATGGCGGCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATG 2458
Db      1972 ACCACCAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2031
Qy      2459 TACACTCATCAGATGATGTCTGTCTTGGGCTGTTATGTGGAGATCTTCACTTTA 2518
Db      2032 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2091
Qy      2519 GGGGCTGCGCTTACCGAGGATTCGCGTGGAGAACTTTTATGCTGTGAGAGAGGA 2578
Db      2092 GGGGCTGCGCTTACCGAGGATTCGCGTGGAGAACTTTTATGCTGTGAGAGAGGA 2151
Qy      2579 CACAGAAATGATTAACCAAGCACTGCAACCAAGAACTGTACATGATGAGAGACTGT 2638
Db      2152 CACAGAAATGATTAACCAAGCACTGCAACCAAGAACTGTACATGATGAGAGACTGT 2211
Qy      2639 TGGCATGACAGTCCCTCCAGAGACCAAGTTCAGAGCTGTGAGAGACTGTGATGCA 2698
Db      2212 TGGCATGACAGTCCCTCCAGAGACCAAGTTCAGAGCTGTGAGAGACTGTGATGCA 2271
Qy      2699 ATTCTCATCTTCACAAACCAATGAG 2722
Db      2272 ATTCTCATCTTCACAAACCAATGAG 2295

RESULT 5
CR859698
LOCUS      CR859698      3513 bp      mRNA      linear      HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA, cDNA DKFp469L2025 (from clone DKFp469L2025).
ACCESSION CR859698
VERSION    CR859698.1 GI:55730268
KEYWORDS   HTC.
SOURCE      Pongo pygmaeus (orangutan)
ORGANISM   Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Pongo.
REFERENCE   1 (bases 1 to 3513)
AUTHORS    Wandute,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,W. and Wiemann,S.
CONSTRM    The German cDNA Consortium
JOURNAL    Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Agowa (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFp469L2025) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFp469L2025
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.

FEATURES
            source
            1..3513
            /organism="Pongo pygmaeus"
            /mol_type="mRNA"
            /db_xref="taxon:9600"
            /clone="DKFp469L2025"
            /cissue_type="kidney"
            /clone_lib="469 (anonymous: pkid). Vector pSport1_sfi; host
            DH10B; sites SfiIa + SfiIb"
            /dev_stage="adult"
            /note="fibroblast growth factor receptor (Homo sapiens)"
            1..3513
            /gene="DKFp469L2025"
            gene

```


CDS	126..2588	/gene="DKFZ469L2025"
		/codon_start=1
		/product="hypothetical protein"
		/protein_id="CAH91857.1"
		/db_xref="GI:55730269"
		/translation="MMSKCLFMVAIVTATLCTRAREPTLPEDQPWGAPVEYESPLVHPGDLQRLRLDDVDSIMVLRDGVGLAASNRTITGEEVEVDSPADSGIAYAC
		TSSPBGSDITTYFVSVSDALPSSBDDSSSEKPTDITKPNPAPVYTSPEKME
		KLHAIVPAKTVKFKCPSSGTPNPTLRMLKNGKEKPHRIIGKVRATMSIIMDSV
		VPSKGNVTCTIVENEYSINHTYOLDVERSPHRPILQAGLPANKTVLGSNVEBDA
		VYSDPQPIOWLKHTEUNSGKIGDNLRYNOILTKAGYNTDKMEVTLHANSPEDA
		GBYTLGANSIGLSHSAWLVLELBERPAVMTSPYLLEITICAGFPLSCWGSY
		IVYTKSGTKSDPHSOVAVHLAKSIPLRRQVTVSADSSANSGVILVPSRLSSS
		GTPLMAGSEVELPEDPRLMELPRDLVIGKPGEGCQVYLAENVGLDKPNRYTK
		VAVKMLKSDATEKDLSDLISEMENKMI GKHNIIINLIGACTODGLYIVIEYASKG
		LREYLOARPPGLEVCNPSHNPEEOLSKDLVSCAYOVAGMEYLAKKCIHRDLAA
		RNVLYTEBNVWKIADRGALRDIHNTDYKKTNGRLPYGMAPEALPRITHTOSDVV
		SFGVLWEIFTLGDSPIYGPVVEEELFKLLKSGHRDKSNCTNELJMMMRCHNAVPS
		QRPFKOLVEDLRIVALTSNOEYLDLSMPDYSPPDTRSTSSGSDSVSHEP
		LPEBPCLRHPAQLANGGILKRR"
ORIGIN		
Query Match	35.0%;	Score 1086.4; DB 6; Length 3513;
Best Local Similarity	68.8%;	Pred. No. 3.2e-307;
Matches 1578; Conservative	0;	Mismatches 681; Indels 33; Gaps 5;
QY	603	GCCTGTTAAAGATGCGCCGTGATCAGTTGACTAAGATGGGGTGAATTGGGGCCCA 662
DB	292	GGCTCGGAGCATGTGACAGACATCACTGGCTCGGAGCGGGTGAAGCTGGGAAA 351
QY	663	ACAATAGACAGTCTTATTGGGAGTACTTGACATTAAGGGCCCACTTAGAGACT 722
DB	352	GCAACCGCACCGCATCAAGGGGAGAGGTGAGGTGACGAGCTCACTGCCGAGACT 411
QY	723	CCGGCTCTATGCTGTACTGCACTGTAAGACAGTGAACCTTGACTCTCANGG 782
DB	412	CCGGCTCTATGCTGTAACCAAGACCCCTCGGAGGTGACACCACTACCTCTCCG 471
QY	783	TGAATGTCAAGATGCCATCTCATCC-----GAGATGATGAGATGACACCGATG 833
DB	472	TCAATGTTCAATGCTCTCCCTCTCGGAGGATGATGATGATGATGATGATGATG 531
QY	834	GTGGGAAAGATTTTGTCACTGAGAACAGTAAACAAGACACCAATCTGAGCCAA 893
DB	532	CAGAGAGAAAGAAACAGATTAACCAAAACCAACCCCTAGCTCATATTGACATCCC 591
QY	894	CAGAAAGATGGAAGAGCGCTCAATGCTGCTGCGGCGCAACACTGCAAGTTCCGT 953
DB	592	CAGAAAAATGGAAGAAATGCAATGCACTGCGGCTGCGCAAGACAGTGAAGTTCAAT 651
QY	954	GCCCAAGCCGGGGGAAACCAATGCAACCATGCGGTGCTGAAGAAACGGGAAGAGTTTA 1013
DB	652	GCCCTTCAAGTGGACCCCAACCCCACTGCGGTGTTGAAGAAATGCAAGATTTCA 711
QY	1014	AGCAGAGCATGCACTTGAAGGCTACAGGTACGAAACAGACCTGAGACCTCATTTATG 1073
DB	712	AACCTGACCAAGAAATGGAAGGCTACAGGTCCGTTATGCTACCTGAGACATCAATATG 771
QY	1074	AAAAGTGTGCTCCATGCAAGAGGAAATTAATCCTGTAGTGAAGATGAAATCGAGT 1133
DB	772	ACTCGGTGTGCTCTGACAGAGGCAATCACTGCAATGTGAGAAATGATATGGA 831
QY	1134	CCATCAATCAAGTACCACTGATGTTGTGAGAGCATGCGCTCAACCGGCCCATCTTCC 1193
DB	832	GATTAACAACAAGTACAGCTGATGTGTGAGAGGATCCCTTCAACGACCATCTTCC 891
QY	1194	AAGCGGAGTCCCGGCAATGCTTCAAGTGTGCGAGAGACCTGAGATTGTCTGCA 1253
DB	892	AAGCAGGGTGGCCCGCAACAGACAGTGGCCCTGGGTAGCAACGTGGAGTTCAATGTGTA 951
QY	1254	AGGTTTACAGTATGCGCAGCCCAATCAAGTATCAAGCAGTGGAAAGAACGGCA 1313

DB	952	AGGTGACAGATGATCCGACCGGCACATCCAGTGGCTAAAGACATCGAGGTGAACGGGA 1011
QY	1314	GTAATACGGGCCCGACGGGCTGCCCTACCTCAAGTTCTCAAGACATCGGGGATAATA 1373
DB	1012	GCAAGATTGGTCCAGACACCTGCTTATGTCAGATCTTGMAACATGCTGGAGTTATA 1071
QY	1374	GTTCCAAATGCAAGATGCTGGCTGTTC-----AATGTGACCGAGGCGGATGCTGGGG 1427
DB	1072	CCACCGACAAAGATAGAGGTGCTTCACTTAAGAAATGTCTCTTTGAGAGCGCAGGGG 1131
QY	1428	AATATATATGTAAGTCTCCATTAATATATAGAGCAGGCCAACCACTGCTCGTCACTG 1487
DB	1132	AGTATAGTGTGTGGCGGGTAATCTATCGGACTCTCCATCACTGCAATGTTGACCG 1191
QY	1488	TCCTGCCAAAACAGAACCGCTTGAAGAGAAAAGATTAACGCTTTCCCAAGACTAAC 1547
DB	1192	TTCT-----GGAAGCCCTGGAAGAGGCGGAGATGATGACCTCGCCCTGTAAAC 1242
QY	1548	TGGAGATAGCATTAATGCAATAGGGGTCTTAAATCGCCTGATGTGGTAAACAGTCA 1607
DB	1243	TGGAGATCATATCTAATTGTGCAAGGGGCTTTCCTCATCTCTGCAATGGTGGGTCCG 1302
QY	1608	TCCTGTGCGGAATGAAGAACGACCAAGAACCACTTCAAGACCGACCGGCTGTGC 1667
DB	1303	TGCTCTAACAGACGAAGGTGTATCAAGAAAGCAGACTTCAAGCAGATGGCTGTGC 1362
QY	1668	ACAAGCTGACCAACGTAATCCCTCTGGGAGACAGGTAAAGTTTCGGCTGAGTCAAGCT 1727
DB	1363	ACAAGCTGGCCMAAGACATCCCTCTGCGCAGACAGGTAAAGTGTGCTGATCTCAAGTG 1422
QY	1728	CCTCATGAATCTCCAAACCCCGCTGTGAGGATTAACAACGCGCTCTTCAACGCGAG 1787
DB	1423	CATCATGAATCTCTGAGATTTTCTGTGGTGGCCGCTCAAGGCTCTCTCAAGTGG---- 1478
QY	1788	ACACCCCATCTGAGCAGGGGTCTCCAGATTAAGACTTCAAGAGACCCAAATGGAGT 1847
DB	1479	--ACTCCATGCTAGCAGAGGGTCTCTGATGTAGACTTCCGAAGACCTCTGCTGGAGGC 1536
QY	1848	TTCCAGAGATTAAGTGAATCTGGGCAAGCCCCGTGGAGAAAGTTGCTTTGGGCAAGTG 1907
DB	1537	TGCTCGGAGCAGACTGTCTTAAGCAAAACCTCGGAGAGAGGCTGCTTTGGGCAAGTG 1586
QY	1908	TCATGCGGAGACAGTGGGAATTTGCAAAAGACAGACCCCAAGAGGCGGTCAACGTTGG 1967
DB	1597	TGTTGGCAGAGCTGTGCGGCTGAGACAGACCAACCAACCGTGTACCAAGTGGGTG 1656
QY	1968	TGAAGATGTTGAAGATGATGCCACAAGAAAGACTTTGTGATGTGTCTCAAGATGG 2027
DB	1657	TGAAGATGTTGAAGTGGGACCAACAGAAAGACTTGTCAAGACTGTCAAGAAATGG 1716
QY	2028	AGATGATGAAGATGATTTGGGAAACAAAGAAATATCAATCTTGGAGCCGTGCACAC 2087
DB	1717	AGATGATGAAGATGATCGGAGAGATGAAGATATATCAATCTGTGTGGGCGCTGCACGC 1776
QY	2088	AGGATGGGCTCTCTAATGTCTAATGTTAGTATGCTCTTAAGGCAACCTCCAGAAATAC 2147
DB	1777	AGGAGGTCCTCTGTATGTCACTGTGAGATATGCTCTCAAGGCAACCTGGGGAGTATAC 1836
QY	2148	TCCAGCCCGGAGGCAACCGGAGTGAAGTACTCTATGACATTAACGTTTCTCTGAG 2207
DB	1837	TGCAAGGCCCGGAGGCCCAAGGCTGGAATCTGTACAAACCCAGGCCAACCAACCAAG 1896
QY	2208	AGCAGATGACCTTCAAGGACTTTGGTGTCACTACCACTGGCCGACAGAGATGGAGT 2267
DB	1897	AGCAGCTCTCTCTCAAGGACCTGTGTCTGCTGCTCAAGAGTGGCCGAGGAGTGAAGT 1956
QY	2268	ACTTGCTTCCCAAAATGATATCAATGCAATTTAGCAGCCAGAAATGTTTGTGTAAG 2327
DB	1957	ATCTGGCTCTCAAGAGTGTATCAACCGAGACTGTGGCCGACAGAAATCTCTGGTGAAG 2016
QY	2328	AAAACATGTGATGAATATAGCAACTTTGACTGCAAGATATCAACATATAGACT 2387
DB	2017	AGGACAAATGTGATGAAGATGACACTTGGCTCTGCGACGGGACATTCACCAATCGACT 2076

```

QY 2388 ATTACAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGAGTCCAGAAAGCCCTGT 2447
DB 2077 ACTATATAAAGACCAACCAACGCGGCACTCTGTGAAGTGAATGGGCGGCAAGCAATTAT 2136
QY 2448 TTGATAGATATACACTCATCAGAGTGAATGTCTCTCGGAGGTGTATATGTGGAGAA 2507
DB 2137 TTGACCGGATCTACACCCACAGAGTGAATGTGTGTCTTTTGGGGTGTCTCTGTGGANA 2196
QY 2508 TCTTCACTTTAAGGGGCTCGCCCTTACCAAGGATTCCTCGTGAAGAACTTTTAAGCTGC 2567
DB 2197 TCTTCACTCTGGGTGGCTCCCGGTACCCGGTGTGTCTGTGAAGAGCTTTTCAAGCTGC 2256
QY 2568 TGAAGGAAGACACACAGATGATATAGCCCAACCTGCACCAACCACTGTCAATGATGA 2627
DB 2257 TGAAGGAAGGATCAACCGCATGACCAAGCCAGTAACTGACCAACGAGCTGTCAATGATGA 2316
QY 2628 TGAGGAGCTGTGGCATGAGTGGCTCTCCCAAGACCAAGCTTCAAGCAGTTGTGAGAA 2687
DB 2317 TCGGGAGCTGTGGCATGAGTGGCTCTCCCAAGACCAAGCTTCAAGCAGCTGTGAGAA 2376
QY 2688 ACTTGATGAAATTTCTCACTCTCAACCAATGAGGATATCTTGAACCTCAAGCAACTC 2747
DB 2377 ACTTGACCGCATCGTGGCTTGACCTCAACCAAGGATGACTGAGCTGTGCATGCCCC 2436
QY 2748 TCGAAGAGTATTCACCTAGTACCTGACCAAGAAATTTCT--TCTTCTTCAAGAGAG 2804
DB 2437 TGGACAGATACCTCCCACTCTTCCGACACCGGAGCTCTAGTCTCTTCAAGGAGAG 2496
QY 2805 ATTCTGTCTTCTTCTCCAGACCCCATGCTTCAAGCAACCATGCTCTCTCAAGTATCCACA 2864
DB 2497 ATTCTGTCTTCTTCTCAAGAGCCGCTCTCCGAGAGAGCCCTGCTGCCCAACCAAGCC 2556
QY 2865 TAAACGGCAGTG 2876
DB 2557 AGCTTGCCATG 2568

RESULT 6
AK049704 4050 bp mRNA linear HTC 02-SEP-2005
LOCUS AK049704.1 GI:26093593
DEFINITION Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
enriched library, clone: C530043G19 product: fibroblast growth factor
receptor 1, full insert sequence.
ACCESSION AK049704
VERSION AK049704.1 GI:26093593
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Scleroglossa; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carinci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carinci, P.,
Komuro, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Harada, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Watanabe, M.,
Yonekura, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format

```

```

JOURNAL sequencing pipeline with 384 multicapillary sequencer
PUBMED Genome Res. 10 (11), 1757-1771 (2000)
11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 7
AUTHORS The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
TITLE The Transcriptional Landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carinci, P.,
Fukuda, S., Furumoto, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T.,
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komuro, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, A.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshinori Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
source location/Qualifiers
1..4050
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:C530043G19"
/db_xref="taxon:10090"
/clone="C530043G19"
/tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
1..4050
/note="fibroblast growth factor receptor 1 (MGD|MG1:95522
GB|BC010200, evidence: BLASTN, 99%, match=3841)
putative"
ORIGIN
Query Match 33.8%; Score 1050.2; DB 6; Length 4050;
Best Local Similarity 68.2%; Pred. No. 1.5e-296;
Matches 1577; Conservative 0; Mismatches 698; Indels 38; Gaps 7;

```

Oy 568 CGTGGCTGCGCAGGAGAGTGCCTAGAGTGCCTGCTCTTGTGAAGAATGCCGCGT-- 625
 Db 856 CTTGGTCCACCTTGGCGACCTGCTACAGCTTGGCTGGCTTGGCGATGATGTCAGAG 915
 Oy 626 -ATCAGTTGACCTAAGATGGGGTGCACCTTGGGCGCCAACTAGAGACATGCTTATGG 684
 Db 916 CATCAATGCGCTGCGGATGGGGTGCACGCTGTGAGAGCAACGCTACCCGATCACAG 975
 Oy 685 GGAAGTCTTGAAGTAAGGGGCGCCACCTAGAGACTCCGGGCTCTATGCTTGTACTGC 744
 Db 976 GAGAGAGGTGAGAGTGGGAGTCCATCCGCTGACTTGGCTCTACGCTTGGTAC 1035
 Oy 745 CAGTAGACTGTAGACAGTGAACCTTGTACTTCAATGTGTGAATGTACAGATGCCATCTC 804
 Db 1036 CAGCAGCCCTCTGGCAGAGTACCACTACTTCCGCTCAATGCTCAGATGCACTCC 1095
 Oy 805 ATCCGAGATGATGAGATGACACCGATGTCGGAAGATTTTGTCACTGAGAACATGA 864
 Db 1096 ATCTCGGAGATGATGACGACGATGACTCTCTCGGAGGAGAAAGACGAGCA 1155
 Oy 865 CAACAG-----AGAGCAGTATCTGAGCAACACAGAAAGATGAGAAAGCGCT 915
 Db 1156 CACCAACCAAACTCTGATCTCTCTGACATCCGAGAGAAATGAGAGAAACT 1215
 Oy 916 CCATGCTGCTGCGGCAACATGTCAAGTTTCGCTGCCAGCGGCGGAGAACCAAT 975
 Db 1216 GCATCGGCTGCGGCTGCGCAACGCTGAAGTTCAAGTCCGCTGAGTGGGACACCA 1275
 Oy 976 GCCAACCATGCGGTGCTGAAGAACGGAGAGATTTAAGCAGAGCATGCGATTGGAG 1035
 Db 1276 CCCCCTGCTGCTGTTGAAAAATGGCAAGATTTAAGCTGACACCGAATTTGAGG 1335
 Oy 1096 CTACAAAGTACGAAACAGCAGCTGAGGCTCATTTAAGAAATGATGCTCCACTGACAA 1095
 Db 1336 CTACAAAGTTGCTATGCACTGAGACATCAATATGATTTGTGTGCTCC--TTGACAA 1393
 Oy 1096 GGGAAATTAATCCTGTGTAGTGAAGATGAATACGGGTTCATCAATCACTACACT 1155
 Db 1394 GGGCAACTACCTGATGTGAGAGATGATATGAGAGCATCAACCACTACACT 1453
 Oy 1156 GGAATTTGAGAGCATGCGCTCAACCGGCTCATCTCCAGAGCGGATCGCGGCAATGC 1215
 Db 1454 TGACGTGCTGGAACATCTCCGACCGAACCATCTTCAGGAGGCTGCTGCAACAA 1513
 Oy 1216 CTCACAGTGTGCGAGAGAGTGTGATGCTGTGCAAGTTTCAAGTATGCCAGCC 1275
 Db 1514 GACAGTGGCTTGGGAGCAATGTGAGTTCAATGTATGATGATGAGCATCCGAGCC 1573
 Oy 1276 CCACATCCAGTGTATCAGCAGTGAAGAAAGAAACGGCAGTAATAACGGGCGGAGCT 1335
 Db 1574 TCAATTTAGTGTGAGACATCACTGAGGTGAACGGAGTTAAGATGGGCCAGAACAT 1633
 Oy 1336 GCCCTTACTCAAGTTCTCAAGCATCTCGGGGATTAATGTTCCATGACGAA-----GT 1389
 Db 1634 GCCGATGTCCAGATCTCTGAAGACTGCTGAGTTATACACCGACAGAGAAATGAGGT 1693
 Oy 1390 GCTGCTGCTTCAATGTAGCAGAGCGAGCGGATGCTGGGAAATATATATGTAATGCTCA 1449
 Db 1694 GCTTCACTACGGAATGTCTCTTTGAGAGTGGGGGAGTATACGTGCTTGGCGGTGA 1753
 Oy 1450 TTATATAGGAGGAGCCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1509
 Db 1754 CTCTATCGGACTCTCCATCACTCTGATGTTGAACGTTCT-----GGAAGCCCT 1804
 Oy 1510 TGAAGAGAGAAAGAGATTAACAGCTTCCCACTACTGAGATGAGCAATTAATCTGAT 1569
 Db 1805 GGAAGAGAGACAGCTGTATGACCTTCAACCGCTTACCTGAGATATTAATTAATCTGAC 1864
 Oy 1570 AGGGGCTTCTTAATGCTGTATGTTGTTAAGATCATCTGTGCGAATGAGAACAC 1629
 Db 1865 CCGGCGCTTCTGATCTCTGCAATGTTGGCTCTGTCACTATTAATGATGAAGCGG 1924

Oy 1630 GACCAAGAACCAAGCTTTACAGCAGCGGCTGTGCAAGCTGACCAAGATATCC 1689
 Db 1925 CACCAAGAAAGGACATTTCAATAGCCAGATGGCTGTGCAAGCTGACCAAGATATCC 1984
 Oy 1690 CTTGCGGAGACAGGTAAACATTTTCCGCTGATGCTCAGCTCTCTCAATGATCAACACCC 1749
 Db 1985 TCTGCGAGACAGGTAAACATGTGATGCTCAAGTGCATTCATGAACTCTGGGTTCT 2044
 Oy 1750 GCTGTGAGGATTAACAACGCGCTCTCTTCAACGCGAGACACCCCATGCTGCGAGGGT 1809
 Db 2045 CTTGTTGCGGCGCTCAAGGCTC-----TCTCCAGCGGAGACCCCACTGTGCTGAGT 2098
 Oy 1810 CTCCGATTAAGAACTTCCAGAGGACCAAAATGGGAGTTTCAAGATTAAGCTGACAT 1869
 Db 2099 CTCCGATTAAGATCTCTGAGATGCCCGCTGAGACTGCCAGAGACAGATGCTGCTT 2158
 Oy 1870 GGGCAAGCCCTGAGAGAGATGCTTGTGGGCAAGTGTCAATGCGGAGCAAGTGGAA 1929
 Db 2159 AGGCAACCACTTGGCGAGGGCTGCTTGGGCAAGTGTGTGGCTGAGGCAATCGGCT 2218
 Oy 1930 TGACAAAGACAAAGCCCAAGAGCGGTCAACGTGCGGTGAAGATTTGAAGATGATGC 1989
 Db 2219 GATTAAGACCAACCAACGCTGTGACCAAGTGGCGGTGAAGATTTGAAGTCCAGCG 2278
 Oy 1990 CACGAGAAAGACCTTTCTGATCTGTGTGAGAGATGAGATGAGATGATTTGGGA 2049
 Db 2279 AACGAGAGAGCTGTGATGATGATGATGAGATGAGATGAGATGAGATGAGATGAG 2338
 Oy 2050 ACACAAAGATTAATTAATCTTTGAGAGCTGACACAGATGGGCTCTATGTCAT 2109
 Db 2339 GCACAAAGATTAATTAATCTTTGAGAGCTGACACAGATGGTCTCTTATGTCAT 2398
 Oy 2110 AGTTGATGATGCTCTTAAGGCAACCTTCCAGAAATCTCTGAGAGCTGAGAGGCTCA 2169
 Db 2399 TGTGAGATGACCTTCCAAAGGCAATCTCCGAGATTAATTAAGAGCTGAGAGCTCTG 2458
 Oy 2170 GATGAGATGACCTTATGATCAATTAACGATGTTCTGAGAGAGATGACCTTCAAGAT 2229
 Db 2459 GCTGAGATGATGCTTAATACCCAGCAGACACCCGAGAGACAGCTGCTTCCAAAGATCT 2518
 Oy 2230 GGTGTATGACCTTACAGAGCTGCGCAGACGAGATGATCTTGGCTTCCAAAGATGAT 2289
 Db 2519 GGTATCTGTGCTATAGAGTGTGCTCGGAGGATGAGATCTTCTCTTAAGATGAT 2578
 Oy 2290 TCAATGAGATTTAGAGCAGAAATGTTTGTGTAACAGAAACAAATGATGAATAGC 2349
 Db 2579 ACAAGAGACCTGCTGTAGAAAGTCTCTGTGACGAGATTAACGTAATGAAGATGCG 2638
 Oy 2350 AGACTTTGAGATCTGCGAGAGATTAACAATATGATTAATTAACAAAGACCAATGG 2409
 Db 2639 AGACTTTGAGATCTGCGAGAGATTAACAATATGATTAATTAACAAAGACCAATGG 2638
 Oy 2410 GCGGCTTCAAGTGAAGTGTGCTCAGAAAGCCCTGTTGATGATGATTAACATCATCA 2469
 Db 2639 CCAAGTGTGATGAGTGTGAGGAGGCGGAGGCTGTTAAGCGATCAACACACCA 2758
 Oy 2470 GAGTATGTCTGTCTTGTGGGATGATGATGAGATCTTCACTTTAAGGGGCTGCGC 2529
 Db 2759 GAGCAGATGTGTGATTTTGAAGTGTCTTGTGAGATCTTCACTTGTGGGCTGCGC 2818
 Oy 2530 CTACCAAGAGATCTGCGAGAGAACTTTAAGCTGTGAAGAGAGACAGAAATGGA 2589
 Db 2819 ATACCCGAGTGTGCTGTGAAGAACTTTCAAGCTGTGAAGAGAGTCAATCGAATGGA 2878
 Oy 2590 TAAAGCAGCACTGACCAACGAACTGTATGATGATGAGAGAGCTTGGCATGAGT 2649
 Db 2879 CAGGCTCAGTAATGATCAATGAGCTGTATGATGATGATGAGAGAGCTGCGCATGAGT 2938
 Oy 2650 GCGCTTCCAGAGCAACGTTCAAGCAAGTGTGTGAAGAACTTGAATTCGAACTCT 2709
 Db 2939 GCGCTTCAAGAGACCTTAAGCTTCAAGCAAGTGTGTGAAGAACTTGAAGCTGCGCATGAGCT 2998
 Oy 2710 CACAAACAAATGAGAAATCTTGAAGCTTCAAGCAAGCTTCAAGATTAATCACTAGTTA 2769

Db	2999	GACCTCCACACGAGATATCGAAGCTTCCATACCGCTGACACGACTACTACCCAGCTT	3058
Qy	2770	CCCTGACACAAAGATT---CTTGTCTTCAGAGAGATGATTTGTTTTTCTCCAGACCC	2826
Db	3059	TCCCGACACGCGAGCTCCACCTGCTCTCCAGGAGAGACTGTGTTCTTCATGAGACC	3118
Qy	2827	CATGCTTACGAAACATGCTTCTCTCATGATTC	2859
Db	3119	GTTACTGAGAGAGCCCTGTCTGCTCGACACC	3151
RESULT 7			
LOCUS	AK028354	3259 bp	mRNA
DEFINITION			linear
ACCESSION	AK028354		HTC 02-SEP-2005
VERSION	AK028354.1		GI:26390449
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
1	Carninci, P. and Hayashizaki, Y.		
2	High-efficiency full-length cDNA cloning		
3	High-efficiency full-length cDNA cloning		
4	High-efficiency full-length cDNA cloning		
5	High-efficiency full-length cDNA cloning		
6	High-efficiency full-length cDNA cloning		
7	High-efficiency full-length cDNA cloning		
8	High-efficiency full-length cDNA cloning		
9	High-efficiency full-length cDNA cloning		
10	High-efficiency full-length cDNA cloning		
11	High-efficiency full-length cDNA cloning		
12	High-efficiency full-length cDNA cloning		
13	High-efficiency full-length cDNA cloning		
14	High-efficiency full-length cDNA cloning		
15	High-efficiency full-length cDNA cloning		
16	High-efficiency full-length cDNA cloning		
17	High-efficiency full-length cDNA cloning		
18	High-efficiency full-length cDNA cloning		
19	High-efficiency full-length cDNA cloning		
20	High-efficiency full-length cDNA cloning		
21	High-efficiency full-length cDNA cloning		
22	High-efficiency full-length cDNA cloning		
23	High-efficiency full-length cDNA cloning		
24	High-efficiency full-length cDNA cloning		
25	High-efficiency full-length cDNA cloning		
26	High-efficiency full-length cDNA cloning		
27	High-efficiency full-length cDNA cloning		
28	High-efficiency full-length cDNA cloning		
29	High-efficiency full-length cDNA cloning		
30	High-efficiency full-length cDNA cloning		
31	High-efficiency full-length cDNA cloning		
32	High-efficiency full-length cDNA cloning		
33	High-efficiency full-length cDNA cloning		
34	High-efficiency full-length cDNA cloning		
35	High-efficiency full-length cDNA cloning		
36	High-efficiency full-length cDNA cloning		
37	High-efficiency full-length cDNA cloning		
38	High-efficiency full-length cDNA cloning		
39	High-efficiency full-length cDNA cloning		
40	High-efficiency full-length cDNA cloning		
41	High-efficiency full-length cDNA cloning		
42	High-efficiency full-length cDNA cloning		
43	High-efficiency full-length cDNA cloning		
44	High-efficiency full-length cDNA cloning		
45	High-efficiency full-length cDNA cloning		
46	High-efficiency full-length cDNA cloning		
47	High-efficiency full-length cDNA cloning		
48	High-efficiency full-length cDNA cloning		
49	High-efficiency full-length cDNA cloning		
50	High-efficiency full-length cDNA cloning		
51	High-efficiency full-length cDNA cloning		
52	High-efficiency full-length cDNA cloning		
53	High-efficiency full-length cDNA cloning		
54	High-efficiency full-length cDNA cloning		
55	High-efficiency full-length cDNA cloning		
56	High-efficiency full-length cDNA cloning		
57	High-efficiency full-length cDNA cloning		
58	High-efficiency full-length cDNA cloning		
59	High-efficiency full-length cDNA cloning		
60	High-efficiency full-length cDNA cloning		
61	High-efficiency full-length cDNA cloning		
62	High-efficiency full-length cDNA cloning		
63	High-efficiency full-length cDNA cloning		
64	High-efficiency full-length cDNA cloning		
65	High-efficiency full-length cDNA cloning		
66	High-efficiency full-length cDNA cloning		
67	High-efficiency full-length cDNA cloning		
68	High-efficiency full-length cDNA cloning		
69	High-efficiency full-length cDNA cloning		
70	High-efficiency full-length cDNA cloning		
71	High-efficiency full-length cDNA cloning		
72	High-efficiency full-length cDNA cloning		
73	High-efficiency full-length cDNA cloning		
74	High-efficiency full-length cDNA cloning		
75	High-efficiency full-length cDNA cloning		
76	High-efficiency full-length cDNA cloning		
77	High-efficiency full-length cDNA cloning		
78	High-efficiency full-length cDNA cloning		
79	High-efficiency full-length cDNA cloning		
80	High-efficiency full-length cDNA cloning		
81	High-efficiency full-length cDNA cloning		
82	High-efficiency full-length cDNA cloning		
83	High-efficiency full-length cDNA cloning		
84	High-efficiency full-length cDNA cloning		
85	High-efficiency full-length cDNA cloning		
86	High-efficiency full-length cDNA cloning		
87	High-efficiency full-length cDNA cloning		
88	High-efficiency full-length cDNA cloning		
89	High-efficiency full-length cDNA cloning		
90	High-efficiency full-length cDNA cloning		
91	High-efficiency full-length cDNA cloning		
92	High-efficiency full-length cDNA cloning		
93	High-efficiency full-length cDNA cloning		
94	High-efficiency full-length cDNA cloning		
95	High-efficiency full-length cDNA cloning		
96	High-efficiency full-length cDNA cloning		
97	High-efficiency full-length cDNA cloning		
98	High-efficiency full-length cDNA cloning		
99	High-efficiency full-length cDNA cloning		
100	High-efficiency full-length cDNA cloning		
101	High-efficiency full-length cDNA cloning		
102	High-efficiency full-length cDNA cloning		
103	High-efficiency full-length cDNA cloning		
104	High-efficiency full-length cDNA cloning		
105	High-efficiency full-length cDNA cloning		
106	High-efficiency full-length cDNA cloning		
107	High-efficiency full-length cDNA cloning		
108	High-efficiency full-length cDNA cloning		
109	High-efficiency full-length cDNA cloning		
110	High-efficiency full-length cDNA cloning		
111	High-efficiency full-length cDNA cloning		
112	High-efficiency full-length cDNA cloning		
113	High-efficiency full-length cDNA cloning		
114	High-efficiency full-length cDNA cloning		
115	High-efficiency full-length cDNA cloning		
116	High-efficiency full-length cDNA cloning		
117	High-efficiency full-length cDNA cloning		
118	High-efficiency full-length cDNA cloning		
119	High-efficiency full-length cDNA cloning		
120	High-efficiency full-length cDNA cloning		
121	High-efficiency full-length cDNA cloning		
122	High-efficiency full-length cDNA cloning		
123	High-efficiency full-length cDNA cloning		
124	High-efficiency full-length cDNA cloning		
125	High-efficiency full-length cDNA cloning		
126	High-efficiency full-length cDNA cloning		
127	High-efficiency full-length cDNA cloning		
128	High-efficiency full-length cDNA cloning		
129	High-efficiency full-length cDNA cloning		
130	High-efficiency full-length cDNA cloning		
131	High-efficiency full-length cDNA cloning		
132	High-efficiency full-length cDNA cloning		
133	High-efficiency full-length cDNA cloning		
134	High-efficiency full-length cDNA cloning		
135	High-efficiency full-length cDNA cloning		
136	High-efficiency full-length cDNA cloning		
137	High-efficiency full-length cDNA cloning		
138	High-efficiency full-length cDNA cloning		
139	High-efficiency full-length cDNA cloning		
140	High-efficiency full-length cDNA cloning		
141	High-efficiency full-length cDNA cloning		
142	High-efficiency full-length cDNA cloning		
143	High-efficiency full-length cDNA cloning		
144	High-efficiency full-length cDNA cloning		
145	High-efficiency full-length cDNA cloning		
146	High-efficiency full-length cDNA cloning		
147	High-efficiency full-length cDNA cloning		
148	High-efficiency full-length cDNA cloning		
149	High-efficiency full-length cDNA cloning		
150	High-efficiency full-length cDNA cloning		
151	High-efficiency full-length cDNA cloning		
152	High-efficiency full-length cDNA cloning		
153	High-efficiency full-length cDNA cloning		
154	High-efficiency full-length cDNA cloning		
155	High-efficiency full-length cDNA cloning		
156	High-efficiency full-length cDNA cloning		
157	High-efficiency full-length cDNA cloning		
158	High-efficiency full-length cDNA cloning		
159	High-efficiency full-length cDNA cloning		
160	High-efficiency full-length cDNA cloning		
161	High-efficiency full-length cDNA cloning		
162	High-efficiency full-length cDNA cloning		
163	High-efficiency full-length cDNA cloning		
164	High-efficiency full-length cDNA cloning		
165	High-efficiency full-length cDNA cloning		
166	High-efficiency full-length cDNA cloning		
167	High-efficiency full-length cDNA cloning		
168	High-efficiency full-length cDNA cloning		
169	High-efficiency full-length cDNA cloning		
170	High-efficiency full-length cDNA cloning		
171	High-efficiency full-length cDNA cloning		
172	High-efficiency full-length cDNA cloning		
173	High-efficiency full-length cDNA cloning		
174	High-efficiency full-length cDNA cloning		
175	High-efficiency full-length cDNA cloning		
176	High-efficiency full-length cDNA cloning		
177	High-efficiency full-length cDNA cloning		
178	High-efficiency full-length cDNA cloning		
179	High-efficiency full-length cDNA cloning		
180	High-efficiency full-length cDNA cloning		
181	High-efficiency full-length cDNA cloning		
182	High-efficiency full-length cDNA cloning		
183	High-efficiency full-length cDNA cloning		
184	High-efficiency full-length cDNA cloning		
185	High-efficiency full-length cDNA cloning		
186	High-efficiency full-length cDNA cloning		
187	High-efficiency full-length cDNA cloning		
188	High-efficiency full-length cDNA cloning		
189	High-efficiency full-length cDNA cloning		
190	High-efficiency full-length cDNA cloning		
191	High-efficiency full-length cDNA cloning		
192	High-efficiency full-length cDNA cloning		
193	High-efficiency full-length cDNA cloning		
194	High-efficiency full-length cDNA cloning		
195	High-efficiency full-length cDNA cloning		
196	High-efficiency full-length cDNA cloning		
197	High-efficiency full-length cDNA cloning		
198	High-efficiency full-length cDNA cloning		
199	High-efficiency full-length cDNA cloning		
200	High-efficiency full-length cDNA cloning		
201	High-efficiency full-length cDNA cloning		
202	High-efficiency full-length cDNA cloning		
203	High-efficiency full-length cDNA cloning		
204	High-efficiency full-length cDNA cloning		
205	High-efficiency full-length cDNA cloning		
206	High-efficiency full-length cDNA cloning		
207	High-efficiency full-length cDNA cloning		
208	High-efficiency full-length cDNA cloning		
209	High-efficiency full-length cDNA cloning		
210	High-efficiency full-length cDNA cloning		
211	High-efficiency full-length cDNA cloning		
212	High-efficiency full-length cDNA cloning		
213	High-efficiency full-length cDNA cloning		
214	High-efficiency full-length cDNA cloning		
215	High-efficiency full-length cDNA cloning		
216	High-efficiency full-length cDNA cloning		
217	High-efficiency full-length cDNA cloning		
218	High-efficiency full-length cDNA cloning		
219	High-efficiency full-length cDNA cloning		
220	High-efficiency full-length cDNA cloning		
221	High-efficiency full-length cDNA cloning		
222	High-efficiency full-length cDNA cloning		
223	High-efficiency full-length cDNA cloning		
224	High-efficiency full-length cDNA cloning		
225	High-efficiency full-length cDNA cloning		
226	High-efficiency full-length cDNA cloning		
227	High-efficiency full-length cDNA cloning		
228	High-efficiency full-length cDNA cloning		
229	High-efficiency full-length cDNA cloning		
230	High-efficiency full-length cDNA cloning		
231	High-efficiency full-length cDNA cloning		
232	High-efficiency full-length cDNA cloning		
233	High-efficiency full-length cDNA cloning		
234	High-efficiency full-length cDNA cloning		
235	High-efficiency full-length cDNA cloning		
236	High-efficiency full-length cDNA cloning		
237	High-efficiency full-length cDNA cloning		
238	High-efficiency full-length cDNA cloning		
239	High-efficiency full-length cDNA cloning		
240	High-efficiency full-length cDNA cloning		
241	High-efficiency full-length cDNA cloning		
242	High-efficiency full-length cDNA cloning		
243	High-efficiency full-length cDNA cloning		
244	High-efficiency full-length cDNA cloning		
245	High-efficiency full-length cDNA cloning		
246	High-efficiency full-length cDNA cloning		
247	High-efficiency full-length cDNA cloning		
248	High-efficiency full-length cDNA cloning		
249	High-efficiency full-length cDNA cloning		
250	High-efficiency full-length cDNA cloning		
251	High-efficiency full-length cDNA cloning		
252	High-efficiency full-length cDNA cloning		
253	High-efficiency full-length cDNA cloning		
254	High-efficiency full-length cDNA cloning		
255	High-efficiency full-length cDNA cloning		
256	High-efficiency full-length cDNA cloning		
257	High-efficiency full-length cDNA cloning		
258	High-efficiency full-length cDNA cloning		
259	High-efficiency full-length cDNA cloning		
260	High-efficiency full-length cDNA cloning		
261	High-efficiency full-length cDNA cloning		
262	High-efficiency full-length cDNA cloning		
263	High-efficiency full-length cDNA cloning		
264	High-efficiency full-length cDNA cloning		
265	High-efficiency full-length cDNA cloning		
266	High-efficiency full-length cDNA cloning		
267	High-efficiency full-length cDNA cloning		
268	High-efficiency full-length cDNA cloning		
269	High-efficiency full-length cDNA cloning		
270	High-efficiency full-length cDNA cloning		
271	High-efficiency full-length cDNA cloning		
272	High-efficiency full-length cDNA cloning		
273	High-efficiency full-length cDNA cloning		
274	High-efficiency full-length cDNA cloning		
275	High-efficiency full-length cDNA cloning		
276	High-efficiency full-length cDNA cloning		
277	High-efficiency full-length cDNA cloning		
278	High-efficiency full-length cDNA cloning		
279	High-efficiency full-length cDNA cloning		
280	High-efficiency full-length cDNA cloning		
281	High-efficiency full-length cDNA cloning		
282	High-efficiency full-length cDNA cloning		
283	High-efficiency full-length cDNA cloning		
284	High-efficiency full-length cDNA cloning		
285	High-efficiency full-length cDNA cloning		
286	High-efficiency full-length cDNA cloning		
287	High-efficiency full-length cDNA cloning		
288	High-efficiency full-length cDNA cloning		
289	High-efficiency full-length cDNA cloning		
290	High-efficiency full-length cDNA cloning		
291	High-efficiency full-length cDNA cloning		
292	High-efficiency full-length cDNA cloning		
293	High-efficiency full-length cDNA cloning		
294	High-efficiency full-length cDNA cloning		
295	High-efficiency full-length cDNA cloning		
296	High-efficiency full-length cDNA cloning		
297	High-efficiency full-length cDNA cloning		
298	High-efficiency full-length cDNA cloning		
299	High-efficiency full-length cDNA cloning		
300	High-efficiency full-length cDNA cloning		
301	High-efficiency full-length cDNA cloning		
302	High-efficiency full-length cDNA cloning		
303	High-efficiency full-length cDNA cloning		
304	High-efficiency full-length cDNA cloning		
305	High-efficiency full-length cDNA cloning		
306	High-efficiency full-length cDNA cloning		
307	High-efficiency full-length cDNA cloning		
308	High-efficiency full-length cDNA cloning		
309	High-efficiency full-length cDNA cloning		
310	High-efficiency full-length cDNA cloning		
311	High-efficiency full-length cDNA cloning		
312	High-efficiency full-length cDNA cloning		
313	High-efficiency full-length cDNA cloning		
314	High-efficiency full-length cDNA cloning		
315	High-efficiency full-length cDNA cloning		
316	High-efficiency full-length cDNA cloning		
317	High-efficiency full-length cDNA cloning		
318	High-efficiency full-length cDNA cloning		
319	High-efficiency full-length cDNA cloning		
320	High-efficiency full-length cDNA cloning		
321	High-efficiency full-length cDNA cloning		
322	High-efficiency full-length cDNA cloning		
323	High-efficiency full-length cDNA cloning		
324	High-efficiency full-length cDNA cloning		
325	High-efficiency full-length cDNA cloning		
326	High-efficiency full-length cDNA cloning		
327	High-efficiency full-length cDNA cloning		
328	High-efficiency full-length cDNA cloning		
329	High-efficiency full-length cDNA cloning		
330	High-efficiency full-length cDNA cloning		
331	High-efficiency full-length cDNA cloning		
332	High-efficiency full-length cDNA cloning		
333	High-efficiency full-length cDNA cloning		
334	High-efficiency full-length cDNA cloning		
335	High-efficiency full-length cDNA cloning		
336	High-efficiency full-length cDNA cloning		
337	High-efficiency full-length cDNA cloning		
338	High-efficiency full-length cDNA cloning		
339	High-efficiency full-length cDNA cloning		
340	High-efficiency full-length cDNA cloning		
341	High-efficiency full-length cDNA cloning		
342	High-efficiency full-length cDNA cloning		
343	High-efficiency full-length cDNA cloning		
344	High-efficiency full-length cDNA cloning		
345	High-efficiency full-length cDNA cloning		
346	High-efficiency full-length cDNA cloning		
347	High-efficiency full-length cDNA cloning		
348	High-efficiency full-length cDNA cloning		
349	High-efficiency full-length cDNA cloning		
350	High-efficiency full-length cDNA cloning		
351	High-efficiency full-length cDNA cloning		
352	High-efficiency full-length cDNA cloning		
353	High-efficiency full-length cDNA cloning		
354	High-efficiency full-length cDNA cloning		
355	High-efficiency full-length cDNA cloning		
356	High-efficiency full-length cDNA cloning		
357	High-efficiency full-length cDNA cloning		
358	High-efficiency full-length cDNA cloning		
359</			

FEATURES	COMMENT	TITLE	JOURNAL	AUTHORS	
source	<p>1. 3259</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="FANTOM,DB:3830408H21"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="3830408H21"</p> <p>/sex="female"</p> <p>/tissue_type="placenta and extra embryonic tissue"</p> <p>/clone_id="RIKEN full-length enriched mouse cDNA library"</p> <p>/dev_stage="18 days pregnant adult"</p> <p>200. 2401</p> <p>/note="unnamed protein product; fibroblast growth factor receptor 1 (MGD MG195522, evidence: Direct assignment) putative"</p> <p>/codon_start=1</p> <p>/protein_id="BAC25899.1"</p> <p>/db_xref="GI:26390450"</p> <p>/translation="MMGKCLFLNAVLTATCTAPAPTLPEDALPSSBDDDDDDSSSEBEGTNDTKNRPRVAPYPTSPERMEKKLAAVPATKCYSPGNPLRLMKRKEKREPRHRIGGYKRRATVMSITDMSVPSKQICVENEYSINTYQLDVYERVSHRPILOGLPANKTVALGSAVEFRCVYSDOPTIQLKAIENVGSKIGPNLPPVOLIKTAGVTTDKEMEVLAIRNVSPEADBYCYCLGNSIGLSHSAMLVLALEBERPAWTPYLEIITICGAFLISCMGSAVLIYMKSGTCKSDFSQAVHKLAKSIDPLRQVATYSAOSSASMSGVLVPSRLSSGTPMLAGSEYELPEDPMELEPRDLVGLGKPGDECPQGVYLAELGLDKMDPNVTYVAVMKASDAEKOLSDIISEMMKMKIKHNNITNLDACTQDPEPLYTIVERYASKGNLREYLQARRPGLRYCNPSPHREQLSSKDLVSAQYVARGMEYTLASRCKIHRDLAAENVLTEDNVKIDPGLARIDHIDYRKKTNGSLPVMKAPALFDRITHDSDVMSFVGLWEIPTLAGSPYGVPEVLEFKLLKEGRMDKPNENCTNELYMMRDCMAVPSORPFPKQVLEDLDRIVALTSDQYDLISIIPLDQYBSPFDTSTSCSSGSDSVFHSHEPLPEEPCLEPRHPTQANSLKRR"</p> <p>3243. 3248</p> <p>/note="putative"</p> <p>3259</p> <p>/note="putative"</p>	<p>Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-tesg@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.</p> <p>Please visit our web site for further details.</p> <p>URL: http://genome.gsc.riken.jp/</p> <p>URL: http://fantom.gsc.riken.jp/</p> <p>Location/Qualifiers</p>	<p>Direct Submission</p> <p>Hayashizaki, Y.</p> <p>Muramatsu, M. and Hayashizaki, Y.</p>		<p>Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carrinchi, P., Fukuda, S., Furuno, M., Hagiwara, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.</p>
ORIGIN					
polyA_signal					
polyA_site					
Query Match	32.2%;	Score 1001.4;	DB 6;	Length 3259;	
Best Local Similarly	70.4%;	Pred. No. 3.3e-282;			
Matches 1405;	Conservative	0;	Mismatches 566;	Indels 24; Gaps 4;	
874	AGGACCATCTCGGACCAACAGAAAGAGGAAAGAGGAGGAGCTGCTGCTGAGGCG	933			
385	AGCTCCCTATCTGACATCATCCCAAGAGAAATGAGAGAGAAATCTGATCATCGGATGCCGCTGC	444			

QY 934 CAACACTGTCAAGTTTGGCTGCTCCAGCCGGGGGAGAACCCAAATGCCAACATGCGGTGCT 993
 Db 445 CAAGACGGTGAAGTTCAAGTTGCTCCGTCCAGTGGGACACCCAACTCTGCGCTGCTT 504
 QY 994 GAAAAACGGGAAGAGTTTAAAGCAGAGAGATGTGCTTTGAGAGCTTCAAGGTACGAAACA 1053
 Db 505 GAAAAATGGCAAGGTTTAAAGCTGACCAACGAATTTGAGAGCTTCAAGGTGCTGATGC 564
 QY 1054 GCACGTGAGCCCTCAATTATGAGAAAGTGTGCTCCATCTGACAAAGGAAATTAACCTGTGT 1113
 Db 565 CACTGTGAGCATCATTAATGATTTCTGTGTGCTTCTGACAAAGGCACTACCTGTGAT 624
 QY 1114 AGTGAAGATGAATAACGGGTCCATCAATCAACGTACCACTGTGATGTGTGAGCCGATC 1173
 Db 625 CGTGAAGATGATGTGAGGAGCATCAACACACTACAGCTTGAAGTGTGAGAACGATC 684
 QY 1174 GCCTCAACGGCCCATCTCTCAAGCCGGAGCTGCGGCAATGCTTCAAGTGTGGAGG 1233
 Db 685 TCCGCAACGACCCATCTTCAAGGAGGCTGCTGCAACAAAGACATGAGCCCTGGGAG 744
 QY 1234 AGAGTGAAGTTTGTCTGCAAGTTTAAAGTATGATAGTCCGACCCCAATCCAGTGAATCA 1293
 Db 745 CAATGTGAAGTTCAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
 QY 1294 GCACGTGAAAAAGAACGGGAGTAAATACGGGCTCCGACGGGCTGCTTCAAGTGTCT 1353
 Db 805 GCACATTCAGAGTGAACGGGAGTAAATGATGATGATGATGATGATGATGATGATGATGAT 864
 QY 1354 CAAGCATCTGGGAGTAAATAGTTCCAAATGCAAGAA-----GTGCTGCTGTGTTAAAT 1407
 Db 865 GAAAGCTGTGAGTAAATACCAACGCAAGGAAATGAGAGTCTTCAATCAACGAAATGT 924
 QY 1408 GACCGAGCGGAGTGTGCGGGAAT 1467
 Db 925 CTCTCTTTAGAGATGCGGGGAGATATACGTGCTTGGCGGATATCTATTCGACCTCCCA 984
 QY 1468 CCAAGTCTGCTGCTCACTGCTCTGCAAAACAGCAAGCGCTGGAAGAGAAAGAGAT 1527
 Db 985 TCACCTGTGATGTTGACCGTCT-----GGAAAGCCGTGAAGAGACCAAGCTGT 1035
 QY 1528 TACAGTTTCCAGACTACTGTGAGATACCACTTATCTGCAATAGGCTTCTTAAATGCG 1587
 Db 1036 GATGACCTACCGCTCTACCTGAGATCAATTAATCTACCTACCGGAGCTTCTGATCTC 1095
 QY 1588 CTGTAATGTGTAAACAGTCACTCTGTGCGGAAATGAAGAACAGCAAGACCAAGCTT 1647
 Db 1096 CTGCAATGTGGGCTCTGTATCATCTAATGAATGAAGAGCGGACCAAGAGAGGACTT 1155
 QY 1648 CAGCAGCAGCCGGCTGTGCAAGCTGAACAAACGTATCCCTGCGGAGACAGGTATAC 1707
 Db 1156 CCATAGCCAGATGGCTGTGCAAGCTGCGCAAGAGCATCTCTGCGGAGACAGGTATAC 1215
 QY 1708 AATTTCGCTGAGTCCAGCTCTCCATGAATCTCCAAACCCCGCTGTGAGATTAACAC 1767
 Db 1216 AGTGTAGCTGACTCCAGTGCATCAATGAATCTTGGGATTTCTCTGATTCGCGCTCAG 1275
 QY 1768 ACGCTCTCTTCAACCGCAGACACCCCAATGCTGAGGAGGATCTCCGATATGAATCTTC 1827
 Db 1276 GCTC-----TCTTCAAGCGGAGCCCCATGCTGAGTGTCCGAATATAGAGTCTCC 1329
 QY 1828 AGAGACCCGAAAAATGGAAGTTTCAAGATTAAGCTGAACCTGGGAGACCCCTGGGAGA 1887
 Db 1330 TGAAGATCCCGCTGGAGCTGCAAGAGACAGACTGTCTTAAAGCAACACTTGGGCA 1389
 QY 1888 AGGTTCCTTTGGCAGTGTGATGCGGAGAGAGTGGGAATTTGAAGAGACAAAGCCAA 1947
 Db 1390 GGGCTCTCTGCGGAGAGTGTGTGCTGAGGCAATCGGCTGGATTAAGAGCAAAACCCA 1449
 QY 1948 GGAGGCGGTCAACGTGCGCTGAAGATTTGAAGATGATGCAAGAGAAAGACCTTTC 2007
 Db 1450 CCGTGTGACCAAGTGGCCCTGAAATTTGTAAGTCCGACGCAACGAGAGAGACCTGTCT 1509

QY 2008 TGATCTGTGTGAGAGATGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 2067
 Db 1510 GGAATCTATCTCGAGATGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1569
 QY 2068 TCTCTTGGAGCTGCAACAGATGAGGCTCTCTATGTCAATGATGATGATGATGATGATGATGATG 2127
 Db 1570 CTTCTTGGAGCTGCAACAGATGAGTCTCTTATGTATGATGATGATGATGATGATGATGATGATG 1629
 QY 2128 AGGCAACCTCCGAGATTAACCTCCGAGCCCGGAGCCACCCGGAGTGAAGATCTCTTATGA 2187
 Db 1630 AGGCAATCTCCGAGATTAACCTCCGAGCCCGGAGCCCTCGGAGTGAAGATCTCTTATGA 1689
 QY 2188 CATTAACCTGTGCTGAGAGAGAGATGACCTTCAAGAGCTTGTGTCAATGACCTTCA 2247
 Db 1690 CCCAGGCAACACCCCGAGAGAGAGCTGTCTTCAAGAGTGTGATTCCTGTGCTATCA 1749
 QY 2248 GCTGCGCAGAGAGATGAGTACTGTGCTTCCCAAAAATGATTTATGATGATGATGATGATGATG 2307
 Db 1750 GGTGGCTCGGGGAGATGAGTATCTTGGCTTAAGAGATGATACACCGAGACTGTGCTGC 1809
 QY 2308 CAGAAATGTTTGTGTAACAGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2367
 Db 1810 TAGGAAGCTCTGTGATGACCGAGATTAAGTATGAATGATGATGATGATGATGATGATGATG 1869
 QY 2368 AGATTAACAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2427
 Db 1870 AGCATTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1929
 QY 2428 GATGCTTCAGAGACCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2487
 Db 1930 GATGGCCCTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1989
 QY 2488 CGGGGTGTTAATGAGAGATCTTCACTTTAGGGGCTCGCCCTTACCAAGGATTTCCCT 2547
 Db 1990 TGAAGTCTCTTGTGAGAGATCTTCACTTGTGGGCTGCCCATACCCCGGTGTGCTGT 2049
 QY 2548 GGAGGAACTTTTAAAGCTGTGAG 2607
 Db 2050 GAGAGAACTTTTAAAGCTGTGAG 2109
 QY 2608 CAACGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2667
 Db 2110 CAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2169
 QY 2668 GTTCAAGAGTGTGTAAGAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2727
 Db 2170 GTTCAAGAGTGTGTAAGAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2229
 QY 2728 CTGGAACCTGAGCCAACTCTGAAACAGTATTCAGCTTATGATGATGATGATGATGATGATGATG 2786
 Db 2230 TCTGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2289
 QY 2787 --CTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2844
 Db 2290 CACCTGCTCTCAAGGAGAGAGCTGTCTTCTCATAGAGCGTTAAGCTGAGAGCCCTG 2349
 QY 2845 CTTTCTCAATGATTC 2859
 Db 2350 TCTGCTTCAACACC 2364

RESULT 8
 AKI43592 4150 bp mRNA linear HTC 21-SEP-2005
 LOCUS AKI43592
 DEFINITION Mus musculus 6 days neonate spleen cDNA, RIKEN full-length enriched library, clone: F420011n06 product: fibroblast growth factor receptor 3, full insert sequence.
 ACCESSION AKI43592.1 GI:74146955
 VERSION AKI43592.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

- Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
- 1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
- 10349636
- 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
- 11042159
- JOURNAL PUBLISHED 11042159
- REFERENCE AUTHORS
- 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishimura, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, R., Matsuda, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
- 11076861
- JOURNAL PUBLISHED 11076861
- REFERENCE AUTHORS
- 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaeerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
- 11217851
- JOURNAL PUBLISHED 11217851
- REFERENCE AUTHORS
- Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., C. Schombach, C., Gojobori, T., Schriml, L. M., Kanapir, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Bruciani, T. A., Chochia, C., Corbani, L. E., Cousins, S., Dalla, B., Driscoll, T. A., Fletcher, C. F., Forrest, A., Fraser, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, J., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lemhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagaoka, S., Numata, K., Okido, T., Pavan, W. J., Perle, G., Pesole, G., Petrovsky, N., Pillai, R., Poulos, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, P. J., Reid, J., Retou, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imokani, K., Iehi, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
PANTOM Consortium
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
- 12466851
- JOURNAL PUBLISHED 12466851
- REFERENCE AUTHORS
- 6 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aurrelija, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, P., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemmulung, P., Gingeras, T. R., Gojobori, T., Green, R. B., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Hummelbeck, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapir, A., Katoh, M., Kawasawa, Y., Keisio, J., Kitamura, H., Kitano, H., Kohlmeier, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, B. B., Mader, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Miyagawa, M., Miyake, S., Morris, K., Mortazavi, T., Muller, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. P., Ring, B. Z., Ringwald, M., Rosi, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schombach, C., Sekiguchi, K., Sempke, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Spelling, S., Stupka, E., Sugiuwa, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamashita, H., Zdobych, E., Zhu, S., Zimmer, A., Hilde, M., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, B. T., Kraus, V., Quackenbush, J., Wahlstedt, C., Mattick, J. S., Hume, D. A., Bui, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawai, J., Kawasawa, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Pleassy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
PANTOM Consortium
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
- 16141072
- JOURNAL PUBLISHED 16141072
- REFERENCE AUTHORS
- Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakamichi, M., Nakamura, M., Nishida, H., Yagi, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K. C., Hallinan, J., Mattick, J. S., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Feghhi, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.
RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
- 16141073
- JOURNAL PUBLISHED 16141073
- REFERENCE AUTHORS
- 8 (baes 1 to 4150)
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imokani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiguchi, H., Nomura, K., Ohno, M., Sakazume, N., Sato, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
- TITLE

Db 2030 GACACGGGCGATGATATCTTGGCTTTCAGAACTGATTCACAGACACTTGGCTGCACAA 2089

Qy 2312 AATGTTTGTGTAACAGAAAAACAATGATGAAATAGACAGACTTGGACTCCGACAGAT 2371

Db 2090 AAGCTCTGTGACCGAGGACATATGATGAGATTGGCGACTTGGCTGGCTGCAGAT 2149

Qy 2372 ATCAACATATATGACTTATTCACAAAAGACCAATGGCGGCTTCCACTCAATGGAG 2431

Db 2150 GTGCAACACCTGACTATCAACAGAAAGACCAAAATGGCGGCTTCTGTGAAGTGATG 2209

Qy 2432 GGTCCAGAAAGCCCTGTTTGTATGATGATATCACTCATCAGATGATGTCTGTCTCGG 2491

Db 2210 GACACGAGAGCCCTTTTGTGACGATCTACACCAAGATGATTTGGTCTTTTGGT 2269

Qy 2492 GTGTTATGTGGAGATCTTCACTTATGAGGAGGCTCGCCCTACCCAGAGATTCCTGTGAG 2551

Db 2270 GTCTCTCTCTGGAGATCTTATCGCTGGGAGGCTCAACCGTATCTGGACTCCAGTGAA 2329

Qy 2552 GAACCTTTTAAAGTCTGTAAGAGAGACACAGAAATGATTAAGCCCAATCTGCACAC 2611

Db 2330 GAGCTTTTCAAGCTGTGTAAGAGAGGACACCGCATGACAGACGACGCTGCACACAT 2389

Qy 2612 GAACGTATACATGATGATGAGAGGAGCTGTGGCATGACGCTCCAGAGACCAAGCTTC 2671

Db 2390 GACCTTACATGATGATGAGAGGAGCTGTGGCATGACGCTCCAGAGACCAAGCTTC 2449

Qy 2672 AAGCATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2731

Db 2450 AAGCATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2509

Qy 2732 GACCTTACGCAACCTCTCGAAGCATGATGATGATGATGATGATGATGATGATGATGAT 2791

Db 2510 GACCTTCTCGTGTGCTTTGAGAGCATGCTGCTGAGCATGATGATGATGATGATGATGAT 2569

Qy 2792 TCTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2842

Db 2570 TCTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2620

RESULT 9 AKI63495 3761 bp mRNA 1linear HTC 21-SBP-2005

LOCUS AKI63495 Mus musculus adult male corpora quadrigemina cDNA, RIKEN

DEFINITION full-length enriched library, clone:B230310M21 product:fibroblast

ACCESSION AKI63495 growth factor receptor 3, full insert sequence.

VERSION AKI63495.1 GI:74200956

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Bukacynska, Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 2 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

REFERENCE 3 10349636

TITLE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL PUBLISHED 11042159

REFERENCE AUTHORS

TITLE RIKEN integrated sequence analysis (RISA) system--384-format

JOURNAL PUBLISHED sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE 11076861

CONSRMT 4

TITLE Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komoto, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kaubuka, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Fleschmann, W., Gaasterland, T., Gissi, C., King, S., Kochiya, H., Knehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Bottelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seye, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weltz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontsuki, S. and Hayashizaki, Y.

CONSRMT 5

TITLE RIKEN Genome Exploration Research Group Phase II Team and the

JOURNAL PUBLISHED PANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)

REFERENCE 11217851

CONSRMT 5

TITLE Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Baralov, S., Beisel, K.W., Blake, J., Brady, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzielski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mik, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.U., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Q.D., Kamachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takekura, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kikukawa, T., Komoto, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, U., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Hayashizaki, Y.

CONSRMT 6

TITLE PANTOM Consortium Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002)

JOURNAL PUBLISHED 12468851

REFERENCE AUTHORS

Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgiil-Hemmung, P., Gigerats, T.R., Gojoodri, T., Green, R.B., Gustincich, S., Harber, M., Hayashi, Y., Hench, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jaki, M., Kamipin, A., Katoh, M., Kawasawa, Y., Keiso, Y., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.P., Lazarevic, D., Lipovich, L., Liu, J., Lium, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, P., Pang, K.C., Pavan, W.J., Pavoni, G., Peol, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Roel, B., Ruan, Y., Salzberg, S.L., Sanderlin, A., Schneider, C., Schonbach, C., Sekizuchi, K., Semple, C.A., Seno, S., Seesa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tamojia, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, B., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zaborovskiy, E., Zhu, S., Zimmer, A., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlested, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Niimura, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanuki, A., Okamura-Ono, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

FANTOM Consortium
 The transcriptional landscape of the mammalian genome
 Science 309 (5740), 1559-1563 (2005)
 16141072

7
 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishide, H., Yag, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carinici, P., Hayashizaki, Y., Wells, C., Fritsch, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engelstrom, P.G., Mizuno, Y., Feghli, M.A., Sanderlin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlested, C.

RIKEN Genome Exploration Research Group
 Antisense transcription in the mammalian transcriptome
 Science 309 (5740), 1564-1566 (2005)
 16141073

8 (bases 1 to 3761)
 Arakawa, T., Carinici, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imocani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Niimura, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanuki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
 Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://phantom.gsc.riken.jp/
 Location/Qualifiers
 1. 3761
 /organism="Mus musculus"
 /mol_type="cDNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:B230310M21"

FEATURES
 source

```

/db xref="taxon:10090"
/cdon="B230310M21"
/sex="male"
/tissue_type="corpora quadrigemina"
/tissue_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
<1..2290
/note="unnamed protein product; fibroblast growth factor
receptor 3 [MGI:95524 GB|BC053056, evidence: BLASTN,
99%, match=3761]"
putative
start codon is not identified"
/codon_start=2
/protein_id="BAE37371.1"
/db_xref="GI:74200957"
/translaction="PPEPSQOEQVAFSGSDTVELSCHPGGAATPGPTVMAWDGCTVASF
HRLIVEPQRLQVLANSHEDAGVYSCQRLTRRVLCFHSVATVDAPSDEDDDEVDVAF
DTGAPWTREPMDKLLAIPAAVTAFPCDPAAGNPPI51SWLNKGEFGEHRTIGDI
KLHNOO5LWMSVSPEDRANVTCVVENKFGSIRQYTLDLVERSPHRPILOGLPANN
OTPLISDVEFHCKVSDAOPHIOMLGHVSNVSKVDPDGPVYTVLTAGANTDLKDE
LEVLSTHNVTFEDAGEYTCIAGNSIGSHSNVSLVLPARELMETDEASVAVGVS
YGVVFFLIVAAVILCRLSPPKKKLSGSPYTHKXSRFPFLKROVSELSNMSNMTTP
LVRIARLSSEGPVLANVSEIETLPADRKWELSRITLTKPVLGSGCGVQVMAEATIGI

Query Match      29.2%; Score 905.4; DB 6; Length 3761;
Best Local Similarity 67.3%; Pred. No. 6,5e-254;
Matches 1367; Conservative 0; Mismatches 611; Indels 33; Gaps 5;

818 GAGGATGACACCGATGCTGCGGAAGATTTTGTCACTAGAGAACAGTAAACACAGAGACCA 877
260 GATCTCCATCTCTCAGGAGATGACGAGATGGGAGGACGTGCTGGAAGACACAGGGGCTT 319
878 CCATACCTGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCTGGGGCCAAAC 937
320 CCTATTGAGACTCCCGCGAGCCGATGATGAAGAACTGTGCTGTGCGCACCGCAAC 379
938 ACTGTCAAGTTTGGCTGCCCGACCGGGGGGAAACCAATGCAACCATGCGGTGCTGAAA 997
380 ACTGTCCGCTTCCGCTGCCGCTGACGCTGCGGACCACTTACCCTTCATCTCTGCTGAG 439
998 AACGGGAAGAGATTTAAGCAGAGACATTCGATTGGAAGGCTTACAAGTACGAAACCAAGAC 1057
440 AATGGCAAGAAATCCGAGGGGAGACATTCGATTGGGGGCAATCAAGCTCCGGACACAGCAG 499
1058 TGAAGCTCATTTATGGAAGATGTGTGCTCCCATCTGACCAAGGAAATTTATCCTGTGTAGT 1117
500 TGGAGCTTGGTCATGAGAAAGTGTGATCCCTCCATCGTGGCAACTAATCCTGTGTAGT 559
1118 GAGATGAATTCGGGCTTCATCATTCACACGTACCACTGATGTGTGAGACGATTCGCT 1177
560 GAGAACAAATTGGCAGCATCCGGCAGACATACATCAGATGTCTGGAACGCTCCCA 619
1178 CACCGGCCCATCTCCAGCCGAGCTGCGGCAAAATGCTTCAACAGTGTGCGAGAGAC 1231
620 CACGGGCCCATCTCGAGAGCTGTGGGCTGCGGCAACAGACGCAATCTAGGGCAGTAC 679
1238 GTAAGATTGTCTGCAAGGTTTACATGATGCCCCAGCCCACTTCACTGATCAAGAC 1297
680 GTGGAGTTCACCTGCAAGGTGTACAGCATACACAGCCACATTCAGATGCTGAAGAC 739
1298 GTGGAAGAACGCGAGTAAATACGGGGCCGACGGGCTGACCTTCAAGGTTTCTCAAG 1357
740 GTGAAGTGAACGGACGAGGTGGGGCCCTTGAACGGACGCTTACGTACTGTAAG 799
1358 CACTGCGGGATAAATAGTTCC-----AATCAGAAAGTGTGCTTGTTCATATGTAAC 1411
800 ACTGAGGCGCTAACACCAACGACGAAGAGGCTAAGAGTTCGTCTTCACAATGTCAAC 859
1412 GAGCGGATGCTGGGGAATATATATGTAAGTCTTCAATTATATGGCAGGCAACAG 1477
860 TTGAGGACGCGGGGAGTAACTGCTGCGGCGGCAATTCTATTTGGGTTTTTCCATCAG 919
1472 TCTGCTGTGCTCCTGCTCCGCAAAACAGCAAGGCGCTGGAAGGAAAAGGATTTACA 1533

```

Db	920	TCCTCGTGGCTGTGGTGTCTCCAGCTGAGGAGGAGCTGATGAAACTGATGAG-----	973
Oy	1532	GCTTCCCAAGCTACTCTGGAGATAGCCATTACTGCAATAGGGGTCTTTAATGACCTGT	1591
Db	974	GCTGGCAGCGGTGTACGACGAGCGGTCTCAAGCTACGAGGGGTGTCTTCTCTCATCTGT	1033
Oy	1592	ATGTGTAACTGATCATCTGTGCCGAATGAAGAACCAACAGACAGAACCAAGCACTTACG	1651
Db	1034	GTGTGTGACGTGTGATATCTGTGCGCTGTGCGCAGTCTCCCAAGAAAG-----GGCTTG	1087
Oy	1652	AGCCAGCGCGGTGTGACAGCTGACCAAGATATCCCTCGGGAGACAGTAACTTT	1711
Db	1088	GGCTGCGCCACGTGACAAAGGTCTC-----TGCTTCCGCTTAAACGACAGTGTG	1138
Oy	1712	TCGGCTGAGTCAAGTCTCTCATATGACTCAACACCCGCTGTGTAGGATTAACAACGC	1771
Db	1139	TCCTTGAATTTAACTCTCTCTATGAACTCCAACACCCCTTGTTCGGATTTGC-----C	1192
Oy	1772	CTCTCTTAACGGCAGACACCCCACTGTGCAAGGGGTCTCGAGTATGAACCTTCCAGAG	1831
Db	1193	CGGCTGTCTCTAGAGGAGAGTCTGTGTGCGCAATGTTTCTGAACCTTGAAGCTCTGCT	1252
Oy	1832	GACCCAAATGGGAGTTTCCAAAGATTAAGCTGACATCTGGCAGAGCCCTTGGGAAAGT	1891
Db	1253	GACCCCAAGTGGGAGCTATCCAGAGACCGGCTGACACTTGTATAGCCTCTTGGAGAAAGC	1312
Oy	1892	TGCTTTGGGCAAGTGTGATGTGGCGGAGCAGTGGGAATTTGACAAAGACCAACCGAAGAG	1951
Db	1313	TGCTTTGGACAGGTGTGTATGTGACAGAGCTATTTGGCATGACAGAGACCGTATCTGCCAG	1372
Oy	1952	GCGGTCACTGTGCGCTGTAGAGATTTTGAAGATGATGTCACAGAGAAAGACTTTCGTAT	2011
Db	1373	CTGTGACCGTGTGCGCTGTAGAGATGTCTGAAGATGATATGATGCACTGACAGAGACTGTGGAC	1432
Oy	2012	CTGTGTGTAGAGATGAGATGATGAAATGATTTGGGAAACCAAGAAATATATTAATCTT	2071
Db	1433	CTGTGATCTGAGTGTGAGATGATGAAATGATTTGGCAGACCAAGAAATATTAATCTG	1492
Oy	2072	CTTGGAGCTGTGACACAGAGATGGGCTCTCATGTCAATGTGATGATAGCTCTTAAAGGC	2131
Db	1493	CTGGGGGCTGTGACACAGAGTGGGCTCTGTATGTGTCTGTGTGAGTACGACGCAAGGGC	1552
Oy	2132	AACCTCCGAGAAATCTCCGAGCCCGAGGGCCACCCGGAGTGAAGTACTCTATGACATT	2191
Db	1553	AATCTCCGGAGTCTCTTCCGGGCGGGGGGCTCCAGGCACTGACTCTTTGATGCC	1612
Oy	2192	AACGTGTCTCTGAGGAGAGATGACTTTCAAGACTTGTGTATGCACTTACACGTG	2251
Db	1613	TGACAGGCTGACAGAGGAACAGTCACTGTCAAGGATCTAGTGTCTGTGCTTACACAGGTG	1672
Oy	2252	GCCAGAGGAGTGAAGTACTTGGGCTTCCCAAAAATGTATTCATCCAGATTTAGACGCCAGA	2311
Db	1673	GACCGGGCAATGGAATTACTTGGCTTCTGAGAGTGTATTTCAACAGAGCTTGGCTGCCAGA	1732
Oy	2312	AATGTTTGTGTAAAGAAAACATGTGTGAAAAATAGCAGACTTGTGACTGCCAGAGAT	2371
Db	1733	AAAGTCTGTGTGACCGAGAGACATGTGTATGAAGATGTGGACTTTGGCTGGCTCGAGAT	1792
Oy	2372	ATCAACAAATTAAGTATTTACAAAAGAACCAACCAATGGGCGGCTTCCAGTCAAGTGAAT	2431
Db	1793	GTGCAACAACCTGTACTTACAAAGAAAGCACAAAATGTCAAGGCTTACTGTAAAGTGAATG	1852
Oy	2432	GCTCCAGAGAGCCCTGTGTGATGATGATTAACCTATCAAGAGTGAATGTGGGCTGTGGG	2491
Db	1853	GCACCAAGAGCCCTTTTGTGACCGAGTCTTACCCACCAAGAGTGAATGTTGTCTTTTGT	1912
Oy	2492	GTGTTAATGTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCCAGGATTCCTGTGAG	2551
Db	1913	GTCTCTCTCTGTGGAGATCTTTTACGCTGGGGGGCTCAACCGTATTCGGCATCCAGTGGAA	1972
Oy	2552	GAACTTTTAACTGTCTGTAGAGAGACACAGATGATTAAGCCAGCCACTGTGACCAAC	2611

Db	1973	GAGCTTTTCAAGCTGTTGAAGAAGGGCCACCGCATGAGACAAGCAGGCAGCTGCACAT	2032
Oy	2612	GAACCTGTACATGATGATGAGAGGACTGTGGCATGTACAGTGCCCTCCAGAACACCACTTC	2671
Db	2033	GACCTGTACATGATGATGAGAGGACTGTGGCATGTACAGTGCCCTCCAGAACACCACTTC	2092
Oy	2672	AAGAGATTGGTAGAAGACTTGGATCGAAATCTCACTGTCACAACCAATGAGAAATCTTG	2731
Db	2093	AAGAGATTGGTAGAAGACTTGGATCGAAATCTCACTGTCACAACCAATGAGAAATCTTG	2152
Oy	2732	GACCTCAGCACCACTCTCGAACAGTATTAACCTTACCCTGACACAGAAAGTTCTTG	2791
Db	2153	GACCTCTCCGCGCGTTTGAAGCACTACCTCCGAGGTGGCAGAGACACGCTTAGCTCAGC	2212
Oy	2792	TCTTCAGAGATGATTTCTGTTTTTTCTTCACAGACCCCAATGCCCTTACGAACCA	2842
Db	2213	TCGTCCGAGATGACTCGGTGTTCACCCATGACCTGTACCCCCAGGTCCA	2263
RESULT 10			
BQ438964			
LOCUS			
DEFINITION	BQ438964	885 bp	mRNA linear EST 24-MAY-2002
ACCESSION	AGENCOURT 7761624 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018096		
VERSION	5', mRNA sequence.		
KEYWORDS	BQ438964 BQ438964.1 GI:21178040		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
JOURNAL	Mammalia; Homo.		
COMMENT	1 (bases 1 to 885) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@omail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LMNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LMNL at: http://image.lnl.gov Plate: LHM13218 row: h column: 01 High quality sequence stop: 770.		
FEATURES			
source	location/Qualifiers		
	1..885		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6018096"		
	/tissue_type="epitheloid carcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_id="NH_MGC_70"		
	/note="Organ: pancreas; Vector: pCMV-Sport6; Site: 1; NotI; site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."		
ORIGIN			
Query Match	25.0%; Score 777.4; DB 3; Length 885;		
Best Local Similarity	99.0%; Pred. No. 1.9e-216;		
Matches 793; Conservative 0; Mismatches 6; Indels 2; Gaps 1;			
Oy	2308	CAGAAATGTTTGGTACAGAAAACATGTGATGAAAAATAGCAGACTTGGACTCGCAG	2367
Db	1	CAGAAATGTTTGGTACAGAAAACATGTGATGAAAAATAGCAGACTTGGACTCGCAG	60
Oy	2368	AGATATCAACATATAGACTTATCAAAAGAAGACCAATGGGGGGCTTCAGTCAAGT	2427
Db	61	AGATATCAACATATAGACTTATCAAAAGAAGACCAATGGGGGGCTTCAGTCAAGT	120


```

OY 2428 GATGGCTCCAGAACCCCTGTTGATAGATATAGATCATCATGATGATGTCGTGCTT 2487
DB 121 GATGGCTCCAGAACCCCTGTTGATAGATATAGATCATCATGATGATGTCGTGCTT 180
OY 2488 CGGGGTGTTAATGTTGGAGATCTTCACTTTAGGGGGCTGCGCCCTACCCAGGGATTTCCCGT 2547
DB 181 CGGGGTGTTAATGTTGGAGATCTTCACTTTAGGGGGCTGCGCCCTACCCAGGGATTTCCCGT 240
OY 2548 GGAGAACTTTTAAAGCTGCTGAAGAGACACAGATGATAGAGCAAGCCCACTGAC 2607
DB 241 GGAGAACTTTTAAAGCTGCTGAAGAGACACAGATGATAGAGCAAGCCCACTGAC 300
OY 2608 CAAGAACTGTATCATGATGATGAGGAGCTGTGGATGCAATGCTCCCAAGACCAAC 2667
DB 301 CAAGAACTGTATCATGATGATGAGGAGCTGTGGATGCAATGCTCCCAAGACCAAC 360
OY 2668 GTTCAAGCATGTTGGTGAAGACTTGGATGCAATTTCTCTCTCAACCAATGAGAAATA 2727
DB 361 GTTCAAGCATGTTGGTGAAGACTTGGATGCAATTTCTCTCTCAACCAATGAGAAATA 420
OY 2728 CTGGACCTCAAGCCCACTCTCAAGCAGTATTCACCTGTTACCTGACACAGAAATTC 2787
DB 421 CTGGACCTCAAGCCCACTCTCAAGCAGTATTCACCTGTTACCTGACACAGAAATTC 480
OY 2788 TTGTTCTTCAGAGATGATTCGTTTTTTCTTCAGAACCCCACTGCTTACCAACATGCTT 2847
DB 481 TTGTTCTTCAGAGATGATTCGTTTTTTCTTCAGAACCCCACTGCTTACCAACATGCTT 540
OY 2848 TCTCTGATATCCACATTAACGCGAGTGTAAACATGAAATGATGTCGCTGCTGCTC 2907
DB 541 TCTCTGATATCCACATTAACGCGAGTGTAAACATGAAATGATGTCGCTGCTGCTC 600
OY 2908 CCAAAACAGAGACGAGCTGGGAACTAGCTACAGAGAGGAGACCAATGCTCCCAAG 2967
DB 601 CCAAAACAGAGACGAGCTGGGAACTAGCTACAGAGAGGAGACCAATGCTCCCAAG 660
OY 2968 CTGTTGTTCTCCACTGTATATATATGATCAGAGAGTAAATATGTAAGAAAGTATCAGC 3027
DB 661 CTGTTGTTCTCCACTGTATATATATGATCAGAGAGTAAATATGTAAGAAAGTATCAGC 720
OY 3028 ATATGTGTAAGATTTATACAGTTGAAAACTTGTATCTTCCCGAGAGG--AGAAGAG 3085
DB 721 ATATGTGTAAGATTTATACAGTTGAAAACTTGTATCTTCCCGAGAGGAGAAAGG 780
OY 3086 GTTCTGAGAGAGTGAAGCTGC 3106
DB 781 TTTCTGAGAGAGTGAAGCTGC 801

```

RESULT 11
 AUI32307 803 bp mRNA linear EST 01-AUG-2002
 LOCUS AUI32307 NT2RP3 Homo sapiens cDNA clone NT2RP3004190 5', mRNA
 DEFINITION AUI32307 NT2RP3 Homo sapiens cDNA clone NT2RP3004190 5', mRNA
 ACCESSION AUI32307
 VERSION AUI32307.1 GI:10992661
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 803)
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Makaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, K., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes

```

JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Source Location/Qualifiers
1..803
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3004190"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_id="NT2RP3"
/notes="Vector: pME18SPJ3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
ORIGIN
Query Match 24.5%; Score 759.6; DB 1; Length 803;
Best Local Similarity 98.1%; Pred. No. 3.1e-211;
Matches 788; Conservative 0; Mismatches 12; Indels 3; Gaps 2;
OY 1582 AATGCCCTGTAATGCTGTAACAGTATCTGTCGCAATGAAACAGACCAAGAGCC 1641
DB 1 AATGCCCTGTAATGCTGTAACAGTATCTGTCGCAATGAAACAGACCAAGAGCC 60
OY 1642 AGACTTGAAGCAGCCAGCCGCTGTGCAACAAGCTGACCAAGATATCTCTCGAGACA 1701
DB 61 AGACTTGAAGCAGCCAGCCGCTGTGCAACAAGCTGACCAAGATATCTCTCGAGACA 120
OY 1702 GGTAAAGTTTGGCTGATGTTCAAGTCTCTCATTAATCTCCAAACCCCGCTGGAGGAT 1761
DB 121 GGTAAAGTTTGGCTGATGTTCAAGTCTCTCATTAATCTCCAAACCCCGCTGGAGGAT 180
OY 1762 AACAAACGCTCTCTTCAACGAGACACCCCATGCTGCAAGGCTCTCCAGTATGA 1821
DB 181 AACAAACGCTCTCTTCAACGAGACACCCCATGCTGCAAGGCTCTCCAGTATGA 240
OY 1822 ACTTCCAGAGAGCCCAAAATGGAATTTCCAAAGATTAAGCTGACATGGGCAAGCCCT 1881
DB 241 ACTTCCAGAGAGCCCAAAATGGAATTTCCAAAGATTAAGCTGACATGGGCAAGCCCT 300
OY 1882 GGGAGAGGTTGCTTTGGGCAAGTGTATGCGGAGAGCATGGGAATTTGACAAAGCAA 1941
DB 301 GGGAGAGGTTGCTTTGGGCAAGTGTATGCGGAGAGCATGGGAATTTGACAAAGCAA 360
OY 1942 GCCCAAGAGGCGGTCACCGTGGCGGTGAAGATGTTGAAAGATGATGTCACAGAGAAAGA 2001
DB 361 GCCCAAGAGGCGGTCACCGTGGCGGTGAAGATGTTGAAAGATGATGTCACAGAGAAAGA 420
OY 2002 CTTTCTGATCTGTGTGTCAGAGATGAGATGATGAATGATTTGGGAAACACAGAAATAT 2061
DB 421 CTTTCTGATCTGTGTGTCAGAGATGAGATGATGAATGATTTGGGAAACACAGAAATAT 480
OY 2062 CATTAATCTTTCTGAGGCTTGACACAGATGAGGCTCTCTATGTCATAGTTGATAGC 2121
DB 481 CATTAATCTTTCTGAGGCTTGACACAGATGAGGCTCTCTATGTCATAGTTGATAGC 540
OY 2122 CTCTAAGCAACCTCGAGATATCTCCGAGCCCGAGGACACCCGGAGATGAGTACTC 2181
DB 541 CTCTAAGCAACCTCGAGATATCTCCGAGCCCGAGGACACCCGGAGATGAGTACTC 600
OY 2182 CTATGACATTAACCTGTGTTCTGAGAGCAGATGACCTTCAAGGACTTGTGTCTGAC 2241
DB 601 CTATGACATTAACCTGTGTTCTGAGAGCAGATGACCTTCAAGGACTTGTGTCTGAC 660

```


DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC c lone distribution information
 can be found through the I.M.A.G.E. Consortium/BLM at:
<http://image.llnl.gov>
 Plate: NDAM518 row: 9 column: 08
 High quality sequence stop: 676.
 Location/Qualifiers

FEATURES

SOURCE

1. 757
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30428791"
 /issue_type="Embryonic Stem cells"
 /cell_line="WA01"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1ib="NIA Human H1 Embryonic Stem Cell cDNA library (long)"

/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
 This is a long-transcript enriched cDNA library (Genome
 Res. 11: 1553-1558 (2001). [PMID: 11541991] From WA01
 cell line. Undifferentiated human ES cell line WA01/H1
 was obtained from WCell Research Institute, Inc.,
 Madison, WI, cultured according to their instructions, on
 MEF feeders. They formed round colonies with defined edges
 and were positive for alkaline phosphatase, SSEA-4, OCT3,
 OCT4, REX1, UTR, TERT, SOX2, CX43 and CX45. They are
 negative for GATA2, GATA4, PDX1, NCAM, NEST1, FLK3, SSEA-1,
 TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days
 after plating), the ES cells from 4 X 6 cm dishes were
 treated with 1 mg/ml collagenase, type IV
 (Invitrogen/GIBCO) for 5-10 min and gently scraped off
 with 5 ml pipette. RNA was purified with TRIzol Reagent
 from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558
 (2001). [PMID: 11541991] Double-stranded cDNAs were
 synthesized with an oligo (dT) primer (Invitrogen:
 5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTT-3') from
 3.4g of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lOne-linker lI-SalI, purified by phenol/chloroform
 extraction, and separated from free linkers by
 Centricon-100 column. Then, the cDNAs were amplified by
 long-range high fidelity PCR using Ex Taq polymerase
 (Takara) with a primer SalI-S for 25 cycles. The products
 were purified by phenol/chloroform extraction and
 Centricon-100 column. The cDNAs were digested with SalI
 and NotI enzymes and cloned into SalI/NotI site of
 pCMV-Sport6 plasmid vector. The average insert size is
 about 3.6kb."

ORIGIN

Query Match 23.7%; Score 735; DB 5; Length 757;
 Best Local Similarity 98.3%; Pred. No. 5.4e-204;
 Matches 741; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 1759 GATAACACAGCCCTCTCTTCAACGCGACACACCCCAAGCTGGAGGGCTTCCGAGTA 1818
 4 GGTAAATCCACCGCTCTTCAACGCGACACACCCCAAGCTGGAGGGCTTCCGAGTA 63
 1819 TGAACCTCCAGAGACCCCAAAATGGAGTTCCAGAGATAGTCACTGGCAAGCC 1878
 64 TGAACCTCCAGAGACCCCAAAATGGAGTTCCAGAGATAGTCACTGGCAAGCC 123
 1879 CCTGGAGAGAGTGTCTTGGCAAGTGTCTATGGCGAAGAGAGTGGAAATTGACAAAGA 1938
 124 CTTGGAGAGAGTGTCTTGGCAAGTGTCTATGGCGAAGAGAGTGGAAATTGACAAAGA 183
 1939 CAAGCCCAAGAGAGCGGTCAACCGTGGCGCTGAAGATGTTGAAAGATGATGCCACAGAGA 1998
 184 CAAGCCCAAGAGAGCGGTCAACCGTGGCGCTGAAGATGTTGAAAGATGATGCCACAGAGA 243
 1999 AGACCTTCTGATCTGGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2058
 244 AGACCTTCTGATCTGGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 303

QY 2059 TATCATTAATCTTTTGGAGCTTGACACAGATGGGCTCTGATGCTAATGTTAGTA 2118
 Db 304 TATCATTAATCTTTTGGAGCTTGACACAGATGGGCTCTGATGCTAATGTTAGTA 363
 QY 2119 TGCCTTAAGAGCAACCTCCGAGAAATCTCCGAGCCCGAGGCCACCGGAGATGAGTA 2178
 Db 364 TGCCTTAAGAGCAACCTCCGAGAAATCTCCGAGCCCGAGGCCACCGGAGATGAGTA 423
 QY 2179 CTCTTATGACATTAACCGTGTCTCTGAGAGACAGATACCTTCAAGACCTTGTGTATG 2238
 Db 424 CTCTTATGACATTAACCGTGTCTCTGAGAGACAGATACCTTCAAGACCTTGTGTATG 483
 QY 2239 CACTTACAGCTGGCCGAGACGAGATGAGTCTTGGCTTCCAAATATGATTTATCGAGA 2298
 Db 484 CACTTACAGCTGGCCGAGACGAGATGAGTCTTGGCTTCCAAATATGATTTATCGAGA 543
 QY 2299 TTTAGCAGCCAGAAATGTTTGTATACAGAAACATGTGATGAAATATAGCAGACTTTGG 2358
 Db 544 TTTAGCAGCCAGAAATGTTTGTATACAGAAACATGTGATGAAATATAGCAGACTTTGG 603
 QY 2359 ACTGCGCAGAGATATCAACATATATAGCTATTTACAAAAGACCAACCAATGGCGCTTCC 2418
 Db 604 ACTGCGCAGAGATATCAACATATATAGCTATTTACAAAAGACCAACCAATGGCGCTTCC 663
 QY 2419 AGTCAAGTGAATGCTCCAGAGCCCTGTTGATGAGTATGACCTCATCAGATGATGT 2478
 Db 664 AGTCAAGTGAATGCTCCAGAGCCCTGTTGATGAGTATGACCTCATCAGATGATGT 723
 QY 2479 CTGGTCTCTGGGGTGTATATGTGGAGATCTTC 2512
 Db 724 CTGGTCTCTGGGGTGTATATGTGGAGATCTTC 757

RESULT 14
 AK084850
 LOCUS
 DEFINITION
 Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: P43001102 product: fibroblast growth factor receptor 4, full insert sequence.
 AK084850
 AK084850.1 GI:26351310
 HTG: CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 REFERENCES
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL
 PUBMED
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multiplexed sequencing
 JOURNAL
 PUBMED
 11076861
 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.

TITLE Antisense transcription in the Mammalian Transcriptome

JOURNAL Science 309, 1564-1566 (2005)

REFERENCE 7

AUTHORS The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

TITLE The Transcriptional Landscape of the Mammalian Genome

JOURNAL Science 309, 1559-1563 (2005)

REFERENCE 8 (bases 1 to 3146)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hayashida, K., Hayashi, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

source

1. 3146
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM:DB:D430001L02"
/db_xref="taxon:10090"
/clone="D430001L02"
/issue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
163. 2362
/note="unnamed protein product; fibroblast growth factor receptor 4 [MGI:MGI:95525, evidence: Direct assignment] putative"
/protein_id="BAC39292.1"
/db_xref="GI:26351311"
/translation="MWLLLLLSIFQSTPLSLSEAEKEQEPCLAPILEQEQVLTVALGQPVRLCCGRTGRGHVYEGSRSLASRVGRGRLEIASFLPEDARVYLCLARGSMVYVNLTLAMDLSLTSISNDPKLSSSGHYVPOQAPYVTLPOREKTLHAPVAGNTVPRCPAANPMPTLHMLKDQAFHEHRIIGRLRHHOMSLVMSVSVSDGTVYCLVNSIGSLIRYVYLIVTLERSPHRPLQAGLPANTRAVVSADVEILCKYSDADP HIOMLKHVIVNGSSFGADGPPYQVLTITDINSSEVYLIRVVSADDEGTYCLAGN

51GLSYGAMLTLEBEDLTWTATPEARVTDIIIVYSGSLVLTLLLAGYVRQVI
RGRVROPTVLOKSLPPLARQFSLSSSSGKSLVGRVSLSSGSPPLGLVNLD
LPLDPLMFPFPRDLVLPGLDGCQGVYVRAFGMDSPRPOGTVVAVMLKDNASD
KPLADLVSEMEVWKLTIGHKIINILNLTCTQGEPLVYVECAKKNLSEFLPARRPG
PDLSPDGSRSSSEGLSPALVSCAYQVRAQVLYESRCTLHDDLARNVLTEDVMK
IADPELARGVHHIDVYKTSNGRLPVKMAAEALDRVYTHQSDVMSFGILMELFTL
GSPYFGIPEVELFSLREGRMERPPPCPSLSYLMEMECMAAASORPTFQVLEAL
DKVLVAVEBYDLRLTRGPPSPNSGASSTCSSSDSVFSDPLPERSPPFSDSOT
T"

polyA_signal
3122..3127
/note="putative"

polyA_site
3146
/note="putative"

ORIGIN

Query Match 23.4%; Score 728; DB 6; Length 3146;
Best Local Similarity 61.4%; Pred. No. 1e-201;
Matches 1270; Conservative 0; Mismatches 770; Indels 30; Gaps 5;

777 TCATGTGAATGTCACAGTGCATCTCATCCGAGATGATGAGTACACCGATGTTG 836
491 TTACGTTGCTTATGATGATGATCTCTTAACCTCATCATGATATATGAGACCCAGACAC 550
837 CCGAAGATTTGTCTAGTGAAGACATGAACAGAGACACATATCTGACCAACACAG 896
551 TCAGCAGCTCTCGAGTGTCTATGTCATCCACAGAGACACCTTACTGACACACCCC 610
897 AAAAGATGAAGAAGCGGCTCATCTGCTGCTGCGGCAACCTGTCAAGTTTCTGCTGCC 956
611 AACGATGAGAGAAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 670
957 CAGCGCGGGGGAACCAAGCCACAGCGGCTGGAAGAAACGGGAAGAGATTAAAC 1016
671 CAGCTGCAAGAAACCCAGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
1017 AGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076
731 GGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
1077 GTGTGTCTCCATCTGACAAAGGAATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
791 GTGTGTGTCTCCATCTGACAAAGGAATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 850
1137 TCAATGACAGTACCACTGTGATGTTGTGAGACGATGCGCTCAACGCGCCATCTCCAG 1196
851 TTCGTAACAGCTATCTCTGATGTCGAGACGCGCTCCGCAACGCGCCATCTCCAG 910
1197 CCGAATGCGCGCAATGCTCCCAAGTGTGCGAGAGACGTAGAGTTGTCTGCAAG 1256
911 CCGGCTCCCAAGCAACCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 970
1257 TTACAGTATGCCAGCCCAATGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATG 1316
971 TGTACAGCAGCCCAAGCCCAATGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATG 1030
1317 AATACGCGCCCAAGCGGCTGCTTCACTCAAGTTTCTCAAGCACTCGGGATTAATGTT 1376
1031 GCTTCGCGCCCAAGCGGCTTTCCTTCAAGTGTCTCAAGCACTCAAGCACTCAAGTGT 1090
1377 CCAATGAGAGTGTGCTGCTGCTTCAATGTGATGATGATGATGATGATGATGATGATGATG 1436
1091 CCGAGTGAAGTCTTGTATCTGAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
1437 GTTAGGTCTCAATTAATATGAGGCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1496
1151 GTCTGCGGCAACTCATCTGCGCTTCTCAACAGTCAACGCTGCTGCTGCTGCTGCTGCTGCTG 1210
1497 AACAGCAAGCGCTGGAAGAGAAAGATTAAGCTTCCCAAGCTACCTGGAATAG 1556
1211 A-----GGAAGACTCACTGAGCAACAGCAACCCCTGAGGCGCAAGTACACAG 1258
1557 CCAATTACTGACATAGGGGCTTCTTATGCGCTGTATGTGTGTGAACAGTATCTGTGTC 1616

Db	1259	ATATCATCTCTGATGATATCAGAGCTCAGCGTTTCGTTGTCCTCTGCTGCTGCGCGAGG	1318
Oy	1617	GAATGAGAAACAACAACCAAGAAACCAAGCTTCAGACGCAACCGGCTGTGTGACAAGCTGA	1676
Db	1319	TGTATCATCCGCAAGTCAATCCGGTGGCCACTACTCTCGCAACCTGTGCACTATACAAAGC	1378
Oy	1677	CCAAACGATCCCCCTGGCGAGACAGGTAAACAGTTTCGGCTGAGTCCAGCTCTCTCATGA	1736
Db	1379	TGTCCCGTTTCCCTTTGGCCGACAG-----TTCTCTTTGGAGTCAGAGTCTCTGTGGCA	1432
Oy	1737	ACTCCAAACACCCCGCTGTGTGAGGATTAACAACGCGCTCTTTCAAACGCAACAACCCCA	1796
Db	1433	AGTCAAGTTTGTCCCTGGTGGCG-----AGGATGTCCTCTCTCTCCACGCGCCCGCCTT	1486
Oy	1797	TGCTGGCAGGGGCTCTCCGAGTATGAACTTTCCAGAGGACCCAAAAATGGGAGTTTCCAAAG	1856
Db	1487	TGCTACAGGGCCTTGTGAATCTAGACCTGGCTCTCTGATTCGCTTTGGAAATTTCCCGGG	1546
Oy	1857	ATTAAGCTGACACTGGGCAAGCCCTTCGGAGAGAGTTGTCTTTGGCAATGTGTATGGCG	1916
Db	1547	ACAGGTTGGTGTGCGAAAGCCCTGGGAGAGGCTGCTTTGGGCAATGTGTTGTCGAG	1606
Oy	1917	AAGCAGTGGGAATTGAACAAGCAAGCCCAAGAGGCGGTACCGTGGCCGTGAAGATGT	1976
Db	1607	AGGCTTTGGTATGTGATCCCTTCGCGGCCGACCAACCAAGACCGTGGCTGTGAAGATGC	1666
Oy	1977	TGAAGATGATATCCACAGAGAAAGACTTTTCTGATCTGTGTTCAGATGAGATGATGA	2036
Db	1667	TGAAGAACAATGCTTCGACAAAGATTTTGGCAGACTGTGTCTCGAGATGAGAGTATGA	1726
Oy	2037	AGATGATTTGGGAAACAACAAGATATCATTAATCTTTTGGAGCTGTGCAACAGATGGGC	2096
Db	1727	AGCTATCGGAAAGACAACAAGACATCATCACTCTGCGGTGTGTGCACTCAGAAAGGGC	1786
Oy	2097	CTCTGTATGTCACTAGTGTGATGTGCTCTTAAAGGACACTCCGAAGATTAATCTCGAGCC	2156
Db	1787	CCCTGTACGTGATTTGTGAATGTGCGCCGCAAGGAAACCTTCGGGAATTCCTCGTGGCC	1846
Oy	2157	GGAGGCAACCCGGGATGGAATCTCTATGACATTAAACGTGTCTTGAAGACAGATGA	2216
Db	1847	GGCGCCCCCAGGCGCTGATCTCAGCCCGATGAGACTTCGAGACGCAAGACACACTCT	1906
Oy	2217	CCTTCAAGGACTTTGTGTATGCAATCACTTACAGCTGGCCGACAGAGATAGTACTTGGCT	2276
Db	1907	CTTTCCTGGCCCTTAGTCTCTGTGCTTACAGATGACCGAGAGTCAAGTATCTGAGT	1966
Oy	2277	CCCAAAATGTAATTATCGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACAATG	2336
Db	1967	CTCGAAGTGCATCCACCGGGACCTGGCTGGCCGAAATGTGCTGTGACCCAGATGATNG	2026
Oy	2337	TGATGAAATAGCAACTTTTGGACTTCGCAAGATATCAACAATATAGACTTTTCAAA	2396
Db	2027	TGATGAAGTCCCTGACTTTTGGGCTGGCACGATGTGTCCACACAAATTGACTATTAAGA	2086
Oy	2397	AGACCAACAATGGGCGGCTTCAGTCAAGTGAATGGGCTCAGAAACCCCTGTTTGAATAG	2456
Db	2087	AAACCAAGCAACGCGCGCTGCACATCAATGATGGCTCCAGAGCAATGTTTGCACCGCG	2146
Oy	2457	TATACATCATCAGATGATGTCTGGTCTTTCGGGCTGTAATGTGGAGATCTTCACTT	2516
Db	2147	TGTACACACACAGAGTGAAGTGTGATCTTTTGGGATCTCTGCTGTGGGAAATCTTCAACC	2206
Oy	2517	TAGGGGGCTCGCCCTACCCAGGGAATTCGCGTGAAGGAATCTTTTAAGCTGTGAGAGAG	2576
Db	2207	TGCGGGGCTCCCATACCTTGGATTCGAGTGAAGAGCTCTTCTCACTGCTGCGAGAGG	2266
Oy	2577	GAACAAGAAATGAATTAAGCAGCCAACTGCAACAACAATGTATGATGAGGAGCT	2636
Db	2267	GGACAAGAAATGAAGCGGCGCCCAAACTGCGCCTCAGAGCTGTATATGGGCTAATGAGGGAGT	2326
Oy	2637	GTTGGCATGATGCTGCTCCCAAGACAACGTTCAAGCAAGTTTGTATGAAGACTTGAATC	2696
Db	2327	GCTGGACCAAGCCCATCTCAAGAGGCTTATTTTAAGCAAGCTGTGTGAAGCTCTGTGA--	2386

QY	2697	GAATTCACCTCTGCACACCAATGAGGAATCTTGAGCACTGAGCAACCTCTCGAAGAGT	2756
Db	2385	-CAAGGTCCTGCTGAGCTGCTCTCTAAGATGACCTTACCTCCGCTGACCTTGGACCC	2443
QY	2757	ATTGACCTAGTATACCTCTGCACCAAGAAATTCTTCTTCAGAGATGATTCGTGTTTT	2816
Db	2444	TTTCTCCCTCCAAATGGGGGATGTCGACGACACCTGCTCTCCAG---TGACTCGGTTTTCA	2500
QY	2817	CTCCAGACCCCATGCTTACGACACCATGCC	2846
Db	2501	GCCACGACCTTGTGGCCCTCGAGCCAGGCC	2530
RESULT 15			
AK081810			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			

REFERENCE 8 (bases 1 to 2218)
 AUTHORS Akechi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
 JOURNAL Submittal (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan [E-mail:genome-res@gs.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216]

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.jp/
 URL:http://phantom.gsc.riken.jp/
 Location/Qualifiers
 1..2218
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:C130078M18"
 /db_xref="taxon:10090"
 /clone="C130078M18"
 /tissue_type="head"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="16 days embryo"
 1..2218
 /note="fibroblast growth factor receptor 2 (MGD|MG1:95523, evidence: Direct assignment)
 putative"

ORIGIN
 Query Match 23.1%; Score 719; DB 6; Length 2218;
 Best local Similarity 88.1%; Pred. No. 4,1e-199;
 Matches 817; Conservative 0; Mismatches 105; Indels 5; Gaps 3;

QY 2184 ATGACATTAAACCGTGTCTCGAGAGCAATGACCTTCAAGACTGTGTCATGCACT 2243
 DB 1 ATGACATTAAACCGTGTCTCGAGAGCAATGACCTTCAAGACTGTGTCATGCACT 60

QY 2244 ACCAGCTGGCCAGACGATGAGTACTTGGCTCCCAAAAATGATTCATCGAGATTAG 2303
 DB 61 ACCAGCTGGCCAGACGATGAGTACTTGGCTCCCAAAAATGATTCATCGAGATTAG 120

QY 2304 CAGCCAGAAATGTTTGGTAAAGAAAACAATGTAAGAAATAGCAGACTTGAAGCTG 2363
 DB 121 CTGCCAGAAACGTGTGGTAAAGAAAACAATGTAAGAAATAGCAGACTTGAAGCTG 180

QY 2364 CCAAGATATCAACAAATATGACTATTAACAAAAGACCAACCAATGAGCG-6CTTCAAGTC 2422
 DB 181 CCAAGATATCAACAAATATGACTATTAACAAAAGACCAACCAATGAGCGCTTCAAGTC 240

QY 2423 AAGTGAATGCTCCAGAACCGCTTTGATAGATATACATCATCAGAGTATGCTG 2482
 DB 241 AAGTGAATGCTCCAGAACCGCTTTGATAGATATACATCATCAGAGTATGCTG 300

QY 2483 TCCTTCGGGGTGTAAATGTGGAGATCTTCACTTTAGGGGCTCGCCTTACCCAGGGATT 2542
 DB 301 TCCTTCGGGGTGTAAATGTGGAGATCTTCACTTTAGGGGCTCGCCTTACCCAGGGATT 360

QY 2543 CCGTGGAGAACTTTTAAGCTGCTGAAGAGACACAGATGATTAAGCCAGCAAC 2602
 DB 361 CCGTGGAGAACTTTTAAGCTGCTGAAGAGACACAGATGATTAAGCCAGCAAC 420

QY 2603 TGCACCAAGAACTGTATGATGATGAGAGGACTGTGGATGACGTGCTCCAGAGA 2662
 DB 421 TGCACCAAGAACTGTATGATGATGAGAGGACTGTGGATGACGTGCTCCAGAGA 480

QY 2663 CCAAGTTCAAGCACTGGTGAAGAACTTGGATTCGAATTCCTGACCAACCAATG 2722
 DB 481 CCAAGTTCAAGCACTGGTGAAGAACTTGGATTCGAATTCCTGACCAACCAATG 540

QY 2723 GAATCTTGAGACCTGAGCAACCTCTCGAACAGTATCACTAGTTAACCTGACAGA 2782
 DB 541 GAATCTTGAGATCTGACCAAGCTCTCGAACAGTATTCCTAGTTAACCTGACAGA 600

QY 2783 AGTCTTGTCTTTCAGAGATGATTCGTTTTTCTCGAACCCCAATGCTTACAGACA 2842
 DB 601 AGTCTTGTCTTTCAGAGGAGATTCGTTTTTCTCGAACCCCAATGCTTACAGACC 660

QY 2843 TGCCTTCTCAGTATCCACATTAACGCACTGTTAAACATGATGACTGTGCTGCC 2902
 DB 661 TGCCTTCTCAGTATCCACATTAACGCACTGTTAAACATGATGATGACTGTGCTGCC 720

QY 2903 TGTCCCAAGCAGACAGACCTAGCTACCTGACAGAGGAGACCATGCTCC 2962
 DB 721 TGTCCCAAGCAGACAGACCTAGCTACCTGACAGAGGAGACCATGCTCC 780

QY 2963 CAGAGCT--TGTGTCTCACTGTATATATGATGATGACAGAGTAAATATGGAAG 3019
 DB 781 AAGAGCTGTGACAGCGCTCCACTTGTATATATGATGATGAGAGTAAATATGGAAGCA 840

QY 3020 TAATCAGCATATGTGTAAGATTATACAGTTGAAAATTGTAATCTTCCAGAGAGG 3079
 DB 841 TAATGTGTCAGTGTGTAAGATTATATACAGTTGAAAATTGTAATCTTCCAGAGAGG 899

QY 3080 AAGAGGTTTTCGAGCAGTGAAGCTGC 3106
 DB 900 AAGAGGTTTTCGATTAAGTGAAGC 926

Search completed: October 3, 2006, 01:46:41
 Job time : 14073 secs

This Page Blank (uspto)